Mathematical Analysis of SEIR Model to Prevent COVID-19 Pandemic

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Abstract

This paper is to analyze Susceptible-Exposed-Infectious-Recovered (SEIR) COVID-19 pandemic model. In this article, a modified SEIR model is constructed, and is also discussed various aspects of it with mathematical analysis to study the dynamic behavior of this model. The spread of this disease through immigration can be represented by the SEIR model. COVID-19 is a highly infectious disease that spreads through talking, sneezing, coughing, and touching. In this model, there is an incubation period during the spread of the disease. During the gestation period, a patient is attacked by SARS-CoV-2 coronavirus and shows symptoms of COVID-19, but cannot spread the disease. The horizontal transmission of COVID-19 worldwide can be represented and explained by SEIR model. Maximal control of the pandemic disease COVID-19 can be possible by the optimum vaccination policies. The study also investigates the equilibrium of the disease. In the study, a Lyapunov function is created to analyze the global stability of the disease-free equilibrium. The generation matrix method is analyzed to obtain the basic reproduction number and has discussed the global stability of COVID-19 spreading.

Keywords: SEIR epidemic model, COVID-19 pandemic, Basic reproduction number, Immunity, Vaccinated, Latent period

JEL Codes: C02, C21, C21, I15, I18

1. Introduction

No man can avoid diseases. But deadly infectious diseases can cause afraid in human lives. Millions of people in the world suffer or die every year because of infectious diseases. Comparative knowledge of the effectiveness and efficacy of different control strategies is necessary to have a desirable goal for controlling diseases [Samsuzzoha, 2012]. In the 21st century, the research on the infectious disease through mathematical modeling has increased [Ratchagar & Subramanian, 2015]. When the pandemic breakout, mathematical models play an important role in comparing, planning, implementing, evaluating, and optimizing various detection, prevention, therapeutic, and control programs and these significantly contribute for combatting the spread and control of infectious diseases [Samsuzzoha, 2012]. Compartmental transmission models have become an invaluable tool to study the dynamics of infectious diseases. Epidemiological SEIR model can predict disease control policies to reduce severe transmission [Heng & Althaus, 2020].

Mathematical epidemiology seems to have grown exponentially starting in the middle of the 20th century. Epidemic diseases cause many deaths before disappearing. SEIR model can be represented by ordinary differential equations. COVID-19 has spread worldwide through immigration and there is an incubation interval in the spread of this disease [Yang et al., 2021].

Mathematical modeling also plays an important role to measure possible disease control strategies for pandemic diseases like COVID-19. It focuses on the important aspects of the disease. It also tries to determine threshold quantities for disease survival and tries to find out the control strategies of the disease [van den Driessche, 2017]. The exposed or latent period of an infectious disease is the time interval between infection and becoming infectious. COVID-19 has an exposed or latent period, 10 to 14 days, after transmission of infection. Therefore, for a long exposure period, an exposed compartment should be included to give an SEIR model [Fine, 2003].

In the SEIR model, we consider that the total host population $N(t)$ is divided into four compartments: susceptible, $S(t)$; exposed, $E(t)$; infectious, $I(t)$; and recovered, $R(t)$. We assume

that the population has a homogeneous spatial distribution. In the model, we consider that the natural birth rate and death rate are equal, so the population is constant, i.e., $S(t)+E(t)+I(t)+R(t)=N(t)=N$, throughout the time interval $t\in[0,\infty)$ [Demirci et al., 2011].

The dynamic nature of the SEIR model can be determined by the basic reproduction number R_0. For $R_0<1$, the disease-free equilibrium is globally asymptotically stable, and the disease will not persist for a long time i.e., will disappear with time. On the other hand, if $R_0>1$, the equilibrium will be unstable and the disease will not abolish; the number of infected people may increase [Al-Sheikh, 2012].

Vaccination is a highly effective method for preventing and reducing viral infections. It is essential for the reduction of COVID-19. Therefore, mass vaccination can create herd immunity to combat the disease. In this study, we have used SEIR model equipped with the effectiveness of vaccination to reduce the COVID-19 pandemic rapidly. COVID-19 control policy with vaccination can minimize the total death due to infection and the cost related to vaccination [Biswas et al., 2014; Mohajan, 2021b].

2. Literature Review

David Greenhalgh has operated the SEIR epidemic model for an infectious disease where the death rate depends on the number of individuals in the population. He has stated three steady-state values: i) the population is extinct, ii) the population maintains itself at a constant level, but the disease is extinct, and iii) there is a unique equilibrium with the disease that remains present [Greenhalgh, 1992]. Tao Tang and his coworkers have proposed a deterministic compartmental model that includes the progression of clinical disease, individual epidemiological status, and participant behavior [Tang et al., 2020].

Puntani Pongsumpun and her coauthors solve the system of nonlinear partial differential equations in SEIR model by using the method of separation of variables. They have considered the spread of exposed and infectious populations in a contact mode of the propagation of the disease in which the populations have only local motions [Pongsumpun et al., 2013]. Andreas Hornstein has modified the basic SEIR model to integrate demand for healthcare that highlights the relative effectiveness of policy interventions, such as social distancing, quarantine, contact tracing, and random testing [Hornstein, 2020]. David Berger and his coworkers have extended the SEIR infectious disease

epidemiology model to realize the role of testing and case-dependent quarantine but they do not include contact tracing [Berger et al., 2020].

Sarah A. Al-Sheikh has investigated the existence and stability of disease-free and endemic equilibria, where the basic reproduction number plays a big role in determining their stability [Al-Sheikh, et al., 2012]. P. Widyaningsih and his coworkers have analyzed the SEIR model with immigration. In their study, they have obtained two equilibrium points that are unstable [Widyaningsih et al., 2018]. Pauline van den Driessche focuses on the basic reproduction number, R_0, for infectious diseases. First, she has developed R_0 for a threshold value to determine whether or not the disease dies out. Then, she describes the next-generation matrix method to calculate R_0 [van den Driessche, 2017]. Suwardi Annas and his coauthors have constructed the stability analysis and numerical simulation of the SEIR model on the spread of COVID-19 by considering vaccination and isolation factors as model parameters. The analysis of the model uses the generation matrix method to obtain the basic reproduction numbers and the global stability of the COVID-19 distribution model [Annas et al., 2020].

Haradhan Kumar Mohajan, in his series of papers, has tried to discuss aspects of the global pandemic COVID-19 with economic analysis for the welfare of global humanity. He stresses on social consciousness to prevent the disease. He also tries to discuss SIR model with detailed mathematical analysis [Mohajan, 2017b, 2020a, b; 2021a, b, 2022]. Md. Haider Ali Biswas and his coauthors have shown optimal control policy to test and compare different vaccination strategies of a compartmental SEIR model [Biswas et al., 2014]. Qianying Lin and her coworkers have proposed SEIR models for the COVID-19 outbreak. They have used the data from China by considering the impact of social isolation policies including governmental actions, and successfully capture the sequence of the disease [Lin et al., 2020].

Ruiwu Niu and his coworkers in the five compartmental SEIHR model have found that for COVID-19, a highly contagious disease, when the adjacent region's epidemic is not severe, a large migration rate can reduce the speed of local epidemic spreading at the price of infecting the neighboring regions. They have stressed that infected patients are isolated immediately; the transmission rate of the epidemic is more sensitive to that of the exposed persons [Niu et al., 2020].

3. Methodology of the Study

In this study, we have analyzed the epidemic SEIR model. We have formulated a mathematical SEIR model with some initial values for systems of ordinary differential equations. We have introduced some theorems with proof. We have observed that herd immunity against COVID-19 can be built through vaccination. Equilibrium analysis of COVID-19 is essential for the stability of the disease and we have tried to provide it in brief. In the analysis, we have used the generation matrix method to obtain the basic reproduction number and the global stability for COVID-19. We have taken attempts to show the immunity loss of vaccines and re-infection procedures of the vaccinated people with proper mathematical presentations due to COVID-19.

The paper is prepared to depend on the secondary data sources that are collected from previous research articles, published books, websites, etc. In the study, we have tried to maintain reliability and validity throughout the research [Chawdhury et al., 2013; Mohajan, 2013, 2014a, b, 2017a]. To make this article significant we have followed both quantitative and qualitative research methodologies [Islam et al., 2012; Mohajan, 2011, 2012, 2016, 2018a, b, 2020c].

4. Objective of the Study

The principal objective of this paper is to form an epidemic SEIR model through proper investigation to prevent the COVID-19 pandemic strongly. Some other specific objectives are;

a) to provide the background of the disease,
b) to show the mathematical calculations elaborately, and
c) to encourage people in vaccinatation for reducing the transmission of COVID-19.

5. Background of COVID-19

The SARS-CoV-2 is a large family of non-segmented, enveloped, positive-sense, single-stranded RNA viruses that typically cause mild to severe respiratory disease in humans [Centers for Disease Control and Prevention, CDC, 2020]. It is a new human coronavirus that developed at the end of December 2019 in Wuhan, Hubei Province, China [Li et al., 2020]. On 11 February 2020, the International Committee on Taxonomy of Viruses (ICTV) named the zoonotic coronavirus disease COVID-19 (“CO” stands for “corona”, “VI” for “virus” and “D” for “disease”, while “19” was for the year), and the COVID-19 virus as “Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-

CoV-2)" [ECDC, 2020]. On 11 March 2020, the WHO declared the global outbreak as a pandemic to minimize the infection and mortality rate [WHO, 2020].

Minor or major symptoms of this illness are fever (>100.4°F/38°C), dry cough, fatigue, sputum production, dyspnoea, shortness of breath, lymphopenia, anorexia, headache, hypoxemia, chills, nausea or vomiting, rhinorrhoea, muscle or joint pain, grand-glass opacities, myalgia, haemoptysis, sore throat, sneezing, nasal congestion, RNAaemia, diarrhea, etc. An infected patient faces one or more such symptoms. Some patients experienced a loss of taste, appetite, or smell. Some COVID-19-infected persons show no symptoms even after the exposure period and infected the susceptible people [Huang et al. 2020; Ren et al., 2020; Mohajan, 2021b]. Older age, diabetes, cardiovascular disease, chronic respiratory disease, asthma, hypertension, and cancer are all associated with increased risks of death worldwide from infection of COVID-19 [Yang et al., 2020]. Obesity and smoking also increase the risks of death [Wang et al., 2020].

On 30 August 2022, the disease spreads up to 228 countries and territories globally; the total confirmed deaths become 6,490,632, the total confirmed cases 606,816,698, with a total recovery of 582,652,695 and a total of 12,449,443,718 vaccine doses have been administered. On 30 December 2022, the total confirmed deaths become 6,693,938, the total confirmed cases 664,005,108, and total recovery become 636,106,351. It is uncertain when COVID-19 will abolish completely [Worldometer, 2022].

6. Elementary Discussion

Some infectious diseases incubate inside the hosts for a period of time before the hosts become infectious. Every year millions of people die worldwide due to various infectious diseases. Epidemics, such as COVID-19, spread through human interactions with the horizontal incidence. Proper management of this highly infectious disease is necessary to save the people of the world from death and infection [Ojo & Akinpelu, 2017, Mohajan, 2022].

Epidemic: An epidemic (from Greek *epi* means "upon or above" and *demos* means "people") is one "*affecting many persons at the same time, and spreading from person to person in a locality where the disease is not permanently prevalent*." Therefore, an epidemic is unusually large, and it occurred at the level of a region or community on a temporary basis. It is actively spreading; new cases of the disease substantially exceed what is expected. It is often localized to a region, but the number of those infected in that region is significantly higher than the normal. It involves not only

infectious agent, mode of transmission, latent period, infectious period, susceptibility and resistance, but also social, cultural, demographic, economic and geographic factors. For example, when COVID-19 was limited to Wuhan, China; it was an epidemic [Green et al., 2002; Intermountain Healthcare, 2021].

Endemic: An endemic (from Greek *en* means "in or within" and *demos* means "people"), on the other hand, is a constant presence in a specific location, region, or population [Phillips, 2021]. A disease is considered endemic if it is present in a population for more than 10 or 20 years. Therefore, an organism that is restricted or peculiar to a locality or region is endemic. For example, malaria is said to be endemic to tropical regions [Intermountain Healthcare, 2021].

Pandemic: A pandemic disease is an epidemic that has spread over a large area, i.e., it is "*prevalent throughout an entire country, continent, or the whole world*." A pandemic is an epidemic that travels, i.e., a pandemic has a passport [Intermountain Healthcare, 2021].

Outbreak: An outbreak is a greater than anticipated increase in the number of endemic cases. COVID-19 is both an epidemic and a pandemic; we simply call it an "outbreak". Therefore, an outbreak is a "*sudden breaking out or occurrence or eruption*." If it is not quickly controlled, an outbreak can become an epidemic and eventually a pandemic if it spreads on large scale. For example, on March 11, the WHO officially declared the COVID-19 outbreak a pandemic due to the global spread and severity of the disease [Intermountain Healthcare, 2021].

Susceptible: The susceptible (vulnerable) refers to a group of people who are not yet infected, but may be infected with the SARS-CoV-2 virus at any time [Mohajan, 2022]. The total number of susceptible people at time t is denoted by $S(t)$, where $\forall t \in [0,\infty)$. A person is placed in the $S(t)$ compartment if s/he is vulnerable to catching the disease [Biswas et al., 2014]. The susceptible population is increased by the newborn and those who have a loss of immunity due to earlier infection and vaccination. The susceptible population is reduced through vaccination, infection (moving to $E(t)$ compartment), and natural death [Samsuzzoha, 2012].

Exposed: The persons who are hosts for infectious but they initially do not show any symptoms and are not yet able to transmit the disease [Widyaningsih et al., 2018]. The total number of exposed people at time t is denoted by $E(t)$. The exposed population is increased by infected individuals that are now in the latent period. The exposed population is reduced by the recovery

(moving to class $R(t)$), natural death and the onset of infection (moving to class $I(t)$) after the end of the latent period [Samsuzzoha, 2012].

Infective: The infective refers to a group of people who have been infected and have infectivity. Infected individuals can spread the disease to susceptible individuals. After the recovery, they enter the recovered compartment [Mohajan, 2022]. The total number of infective people at time *t* is denoted by $I(t)$. The population of infective individuals is reduced by natural death, disease-related death, and recovery from the disease [Samsuzzoha, 2012].

Removals: The removed refers to a group of people who have been removed from the COVID-19 infected people, such as died, are isolated or recovered, and are immune to the SARS-CoV-2 virus [Mohajan, 2022]. Let, $R(t)$ is the number of recovered/removed individuals who are removed from the population by recovery from exposed and infective classes, immunization, hospitalization, death, or by any other means. All the individuals who recovered are considered immune. The person in the removal compartment is reduced by re-infection and natural death [Biswas et al., 2014; Samsuzzoha, 2012].

Incubation Period: The time period in which an individual with COVID-19 is infectious remains uncertain. The incubation period ranges from 1 to 14 days and the estimated median is 5 to 6 days. About 97.5% of people develop symptoms within 11.5 days of exposure [Mohajan, 2021b].

7. Analysis of SEIR Model

In many infectious diseases, there is an exposed period or a latent period after transmission of infection. The exposed persons are apparently healthy but can transmit the infection. During the exposure period, the pathogen is in the host, but in low numbers so that the host is not yet infectious [van den Driessche, 2021]. In Susceptible-Exposed-Infectious-Recovered (SEIR) model, the total population of the world at a particular time *t* is divided into four compartments: Susceptible, $S(t)$; Exposed, $E(t)$; Infectious, $I(t)$; and Recovered, $R(t)$ populations [Widyaningsih et al., 2018]. The total population size at time *t* is denoted by, $N(t)$, i.e.,

$$N(t) = S(t) + E(t) + I(t) + R(t). \quad (1)$$

At the start at $t = 0$, $N(0) = N_0 > 0$, $S(0) = S_0 > 0$, $E(0) = E_0 \geq 0$, $I(0) = I_0 > 0$, and $R(0) = R_0 \geq 0$. In this model, $E(t) + I(t)$ is the total infected population.

The SEIR model only applies to variables and parameters that are smooth, continuous functions of time. Its differential equations do not include stochastic error terms. In the basic SEIR model, the natural death rate of all individuals is equal to the birth rate, and hence, $\frac{dN(t)}{dt}=0$, then (1) indicates, $N(t)=S(t)+E(t)+I(t)+R(t)=N$, $\forall t\in[0,\infty)$. Contacted individuals are exposed by the disease, and transferred into $E(t)$ compartment; after the latent period the individuals become infectious and are caused acute morbidity, and subsequently move to $I(t)$ compartment. The major portion of the infected people in the $I(t)$ compartment recovered, and they are immune from infection for life. A small fraction of the infected people in the $I(t)$ compartment may die, thus reducing the population of the $R(t)$ compartment.

At the start, we shall establish a set of equations that do not consider births or deaths. If $b>0$ be the effective contact rate, an exposed individual able to transmit the disease with $bN(t)$ to others per unit of time and the fraction of contacts by an exposed with a susceptible is $\frac{S(t)}{N(t)}$. The number of new exposures in unit time $bN(t).\frac{S(t)}{N(t)}$ gives the rate of new exposure as $bN(t).\frac{S(t)}{N(t)}.I(t)$ $=bS(t)I(t)$. Therefore, in the $S(t)$ compartment, $bS(t)I(t)$ individuals will be decreased. Hence, the rate of change of the number of susceptible persons;

$$\frac{dS(t)}{dt}=-bS(t)I(t). \tag{2}$$

In the $E(t)$ compartment, $bS(t)I(t)$ individuals will be increased. Let, $c>0$ be the rate of exposed persons become infected. After latent period, $cE(t)$ individuals will be infected per day, where the mean exposed period is denoted by $\frac{1}{c}$. Hence, the rate of change on the number of individuals exposed can be expressed as,

$$\frac{dE(t)}{dt}=bS(t)I(t)-cE(t). \tag{3}$$

In the $I(t)$ compartment, the number of infected individuals increases, $cE(t)$ per day. Let $r>0$ be the recovered rate; the infected individuals will be recovered $rI(t)$. Hence, the rate of change of infected persons can be expressed as;

$$\frac{dI(t)}{dt}=cE(t)-rI(t). \tag{4}$$

In the $R(t)$ compartment, $rI(t)$ recovery individuals will be added. Hence, the rate of change of recovered can be expressed as;

$$\frac{dR(t)}{dt} = rI(t). \tag{5}$$

Here the parameters are all possess positive values, i.e., $a>0, b>0, c>0, \delta>0$, and $r>0$. Flowchart of populations in the SEIR model can be represented by Figure 1, where the boxes denote compartments, and arrows indicate flux between the compartments.

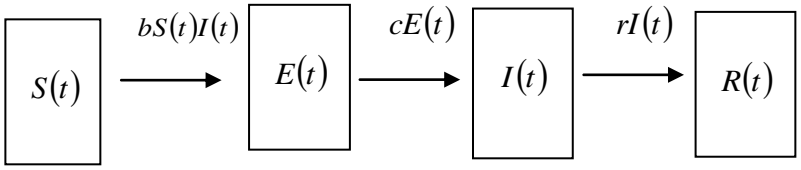

Figure 1: Flowchart of SEIR model that represents four compartments: $S(t)$, $E(t)$, $I(t)$, and $R(t)$.

Theorem 1: At $t=0$ we have $S(t)=S_0$ and $R(t)=R_0$ then,

i) $R(t)=R_0+\ln\left(\frac{S_0}{S(t)}\right)^{\frac{r}{b}}$

ii) If $R_0=0$ then, $R(t)=\ln\left(\frac{S_0}{S(t)}\right)^{\frac{r}{b}}$.

Proof: Dividing (2) by (5) we get,

$$\frac{dS(t)}{dR(t)} = \frac{-bS(t)I(t)}{rI(t)}$$

$$\frac{dS(t)}{S(t)} = \frac{-b}{r}dR(t). \tag{6}$$

Integrating (6) we get,

$$\ln S(t) = \frac{-b}{r}R(t) + C_1. \tag{7}$$

At $t=0$ we have $S(t)=S_0$ and $R(t)=R_0$, then (7) gives, $C_1 = \ln S_0 + \frac{b}{r}R_0$.

Hence, $$\ln S(t) = -\frac{b}{r}R(t) + \frac{b}{r}R_0 + \ln S_0$$

$$R(t) = R_0 + \ln\left(\frac{S_0}{S(t)}\right)^{\frac{r}{b}}. \tag{8}$$

If initially there is no removal then $R_0 = 0$; consequently,

$$R(t) = \ln\left(\frac{S_0}{S(t)}\right)^{\frac{r}{b}}. \tag{9}$$

Theorem 2: By using two parameters $S(t)$ and $R(t)$ the second-order differential equation can be formed as,

$$\ddot{R}(t) + c\dot{S}(t) + \frac{c}{b}\left(\frac{\dot{S}(t)}{S(t)}\right)^2 - \frac{c}{b}\frac{\ddot{S}(t)}{S(t)} + c\dot{R}(t) = 0.$$

Proof: Differentiating (2) with respect to *t* we get,

$$\frac{d^2S(t)}{dt^2} = -b\frac{dS(t)}{dt}I(t) - bS(t)\frac{dI(t)}{dt}$$

$$\frac{d^2S(t)}{dt^2} = \frac{1}{S(t)}\frac{dS(t)}{dt}\frac{dS(t)}{dt} - bS(t)\frac{dI(t)}{dt}, \qquad \text{by using (2), } \frac{dS(t)}{S(t)dt} = -bI(t).$$

$$\frac{d^2S(t)}{S(t)dt^2} = \frac{1}{S^2(t)}\frac{dS(t)}{dt}\frac{dS(t)}{dt} - b\frac{dI(t)}{dt}$$

$$\frac{\ddot{S}(t)}{S(t)} = \frac{\dot{S}^2(t)}{S^2(t)} - b\dot{I}(t), \qquad \text{by using } \frac{dS(t)}{dt} = \dot{S}(t) \text{ and } \frac{d^2S(t)}{dt^2} = \ddot{S}(t).$$

$$\dot{I}(t) = \frac{1}{b}\left(\frac{\dot{S}(t)}{S(t)}\right)^2 - \frac{1}{b}\frac{\ddot{S}(t)}{S(t)}. \tag{10}$$

Differentiating (10) with respect to *t* we get,

$$\frac{d^2R(t)}{dt^2} = r\frac{dI(t)}{dt}$$

$$\frac{d^2R(t)}{dt^2} = rcE(t) - r^2I(t)$$

$$\frac{d^2R(t)}{dt^2} = rcE(t) - r\frac{dR(t)}{dt}, \text{ by using (5).} \tag{11}$$

Differentiating (11) with respect to *t* we get,

$$\frac{d^3R(t)}{dt^3} = rc\frac{dE(t)}{dt} - r\frac{d^2R(t)}{dt^2}$$

$$\frac{d^3R(t)}{dt^3} = rcbS(t)I(t) - rc^2E(t) - r\frac{d^2R(t)}{dt^2}$$

$$\frac{d^3R(t)}{dt^3} = -rc\frac{dS(t)}{dt} - rc\frac{dI(t)}{dt} - r^2cI(t) - r\frac{d^2R(t)}{dt^2}, \qquad \text{by using (2) and (4).}$$

$$\dddot{R}(t) + r\ddot{R}(t) + rc\dot{S}(t) + rc\dot{I}(t) + r^2cI(t) = 0. \tag{12}$$

Equation (12) is a non-linear differential equation of three parameters; $S(t)$, $I(t)$, and $R(t)$.

Using (10) and (5) in (12) we get,

$$\dddot{R}(t)+r\ddot{R}(t)+rc\dot{S}(t)+\frac{rc}{b}\left(\frac{\dot{S}(t)}{S(t)}\right)^2-\frac{rc}{b}\frac{\ddot{S}(t)}{S(t)}+rc\dot{R}(t)=0. \tag{13}$$

If the rate of change of the acceleration of *R* is infinitesimally small then, $\dddot{R}(t)=0$, (13) becomes,

$$\ddot{R}(t)+c\dot{S}(t)+\frac{c}{b}\left(\frac{\dot{S}(t)}{S(t)}\right)^2-\frac{c}{b}\frac{\ddot{S}(t)}{S(t)}+c\dot{R}(t)=0.$$

This is a non-linear differential equation of two parameters; $S(t)$ and $R(t)$.

7.1 SEIR Model with Birth and Death

Let in a particular time *t*, during the pandemic outbreak, the population of the world is constant, so that, the birth rate is equal to the death rate. Let the birth rate be, $a>0$, and also the death rate is, $\delta>0$; consequently, $a=\delta$. Let newborn babies be susceptible, hence, the increase of susceptibility in the total population is $B(t)=aN(t)$ and $\delta S(t)$ is the natural death of susceptible persons per day, where $\delta>0$ is the natural mortality rate. Hence, the rate of change in the number of susceptible persons [Biswas et al., 2014];

$$\frac{dS(t)}{dt}=B(t)-bS(t)I(t)-\delta S(t). \tag{14}$$

From $bS(t)I(t)$ persons, $\delta E(t)$ individuals of exposed persons per day face natural death. After latent period, $cE(t)$ individuals will be infected per day. Hence, the rate of change on the number of individuals exposed can be expressed as,

$$\frac{dE(t)}{dt}=bS(t)I(t)-(c+\delta)E(t). \tag{15}$$

The infected individuals from $E(t)$ compartment will increase as, $cE(t)$ per day. Let $r>0$ be the recovered rate; the infected individuals will be recovered, $rI(t)$, and $\delta I(t)$ is natural death of infected persons per day. Hence, the rate of change of infected persons can be expressed as;

$$\frac{dI(t)}{dt}=cE(t)-(r+\delta)I(t). \tag{16}$$

From the recovered persons $rI(t)$ let, $\delta R(t)$ individuals will die naturally per day. Hence, the rate of change of recovered can be expressed as;

$$\frac{dR(t)}{dt}=rI(t)-\delta R(t). \tag{17}$$

Here the parameters are all possess positive values, i.e., $a>0, b>0, c>0, \delta>0$, and $r>0$.

Flowchart of populations in the SEIR model by considering natural birth and death can be represented as in Figure 2.

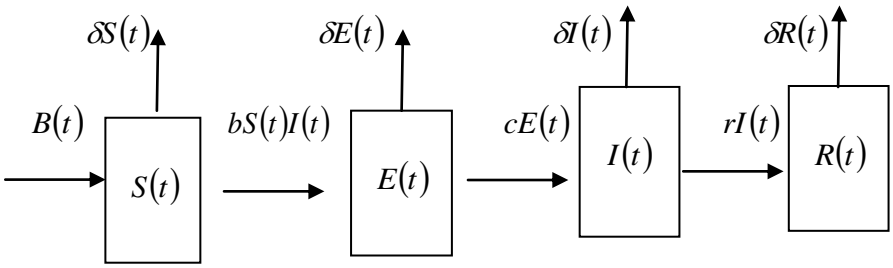

Figure 2: Flowchart of SEIR model by considering birth and natural death.

Equations (14) and (15) are highly non-linear and difficult to solve. The exact semi-analytical solution of SEIR model is impossible, but approximate solutions are possible. We assume that the number of susceptible people is double of the exposed people, i.e., $S(t)=2E(t)$; the number of exposed people is double of the infected people, i.e., $E(t)=2I(t)$, so that $S(t)=4I(t)$; and the number of infected people is four times of removed people, i.e., $I(t)=4R(t)$, so that $R(t)=\frac{1}{4}I(t)$ and $N(t)=S(t)+E(t)+I(t)+R(t) \ =4I(t)+2I(t)+I(t)+\frac{1}{4}I(t)=\frac{29}{4}I(t)$. Also, we consider the birth rate is equal to the natural death rate, i.e., $a=\delta$.

Theorem 3: We consider that $S(t)=4I(t)$, $E(t)=2I(t)$, $R(t)=\frac{1}{4}I(t)$, and $N(t)=\frac{29}{4}I(t)$, then $r=\frac{29\delta}{14}-\frac{3c}{7}$. Further, if $\delta=0.0004$ and $c=0.0005$, then $r=0.000614$.

Proof: Dividing (14) by (17) we get,

$$\frac{dS(t)}{dR(t)}=\frac{B(t)-bS(t)I(t)-\delta S(t)}{rI(t)-\delta R(t)}$$

$$\frac{4dI(t)}{\frac{1}{4}dI(t)}=\frac{\frac{29}{4}\delta I(t)-4bI(t)I(t)-4\delta I(t)}{rI(t)-\frac{1}{4}\delta I(t)}$$

$$16=\frac{\frac{29}{4}\delta-4bI(t)-4\delta}{r-\frac{1}{4}\delta}$$

$$I(t)=\frac{29\delta}{4b}-\frac{4r}{b}. \tag{18}$$

Dividing (15) by (16) we get,

$$\frac{dE(t)}{dI(t)}=\frac{bS(t)I(t)-(c+\delta)E(t)}{cE(t)-(r+\delta)I(t)}$$

$$\frac{2dI(t)}{dI(t)}=\frac{4bI(t)I(t)-2(c+\delta)I(t)}{2cI(t)-(r+\delta)I(t)}$$

$$2=\frac{4bI(t)-2(c+\delta)}{2c-(r+\delta)}$$

$$I(t)=\frac{3c}{2b}-\frac{r}{2b}. \tag{19}$$

Equalizing (18) and (19) we get,

$$\frac{7}{2}r=\frac{29\delta}{4}-\frac{3c}{2}$$

$$r=\frac{29\delta}{14}-\frac{3c}{7}. \tag{20}$$

If $\delta=0.0004$ and $c=0.0005$, then (20) gives $r=0.000614$.

Theorem 4: We consider that $S(t)=4I(t)$, $E(t)=2I(t)$, $R(t)=\frac{1}{4}I(t)$, and $N(t)=\frac{29}{4}I(t)$, then $r=-\frac{29\delta}{24}+\frac{7c}{3}$. Further, if $\delta=0.0004$ and $c=0.0005$, then $r=0.00068$.

Proof: Dividing (14) by (15) we get,

$$\frac{dS(t)}{dE(t)}=\frac{B(t)-bS(t)I(t)-\delta S(t)}{bS(t)I(t)-(c+\delta)E(t)}$$

$$\frac{4dI(t)}{2dI(t)}=\frac{\frac{29}{4}\delta I(t)-4bI(t)I(t)-4\delta I(t)}{4bI(t)I(t)-2(c+\delta)I(t)}$$

$$2=\frac{\frac{29}{4}\delta-4bI(t)-4\delta}{4bI(t)-2(c+\delta)}$$

$$I(t)=\frac{29\delta}{48b}+\frac{c}{3b}. \tag{21}$$

Dividing (14) by (16) we get,

$$\frac{dS(t)}{dI(t)} = \frac{B(t) - bS(t)I(t) - \delta S(t)}{cE(t) - (r+\delta)I(t)}$$

$$\frac{4dI(t)}{dI(t)} = \frac{\frac{29}{4}\delta I(t) - 4bI(t)I(t) - 4\delta I(t)}{2cI(t) - (r+\delta)I(t)}$$

$$4 = \frac{\frac{29}{4}\delta - 4bI(t) - 4\delta}{2c - (r+\delta)}$$

$$I(t) = \frac{29\delta}{16b} + \frac{r}{b} - \frac{2c}{b}. \tag{22}$$

Equalizing (21) and (22) we get,

$$r = -\frac{29\delta}{24} + \frac{7c}{3}. \tag{23}$$

If $\delta = 0.0004$ and $c = 0.0005$ then (23) gives, $r = 0.00068$.

7.2 Vaccination Policy

Vaccines protect us from the infection of diseases. It also keeps the community safe and stops diseases from spreading to other susceptible people. Therefore, it is equally important for personal, family, and public health. During the five decades, vaccinations have saved more than a billion lives and have prevented countless illnesses globally. COVID-19 is indeed preventable through vaccination. In a community, herd immunity is grown if the majority of people in that community are vaccinated [Nicho, 2010].

Let p is the proportion of the total population N is vaccinated and then $(1-p)$ is the proportion left unvaccinated, where $0 < p < 1$. The individuals that are vaccinated are $aN(t)p$, which are safe and will be added to the recovery compartment $R(t)$, and the unvaccinated people is $aN(t)(1-p)$, which still remain in the susceptible compartment $S(t)$. After vaccination the SEIR model can be ornamented as;

$$\frac{dS(t)}{dt} = B(t)(1-p) - bS(t)I(t) - \delta S(t) \tag{24}$$

$$\frac{dE(t)}{dt} = bS(t)I(t) - (c+\delta)E(t) \tag{25}$$

$$\frac{dI(t)}{dt} = cE(t) - (r+\delta)I(t) \tag{26}$$

$$\frac{dR(t)}{dt} = rI(t) - \delta R(t) + B(t)p. \tag{27}$$

The flowchart of SEIR model after vaccination can be given as in Figure 3.

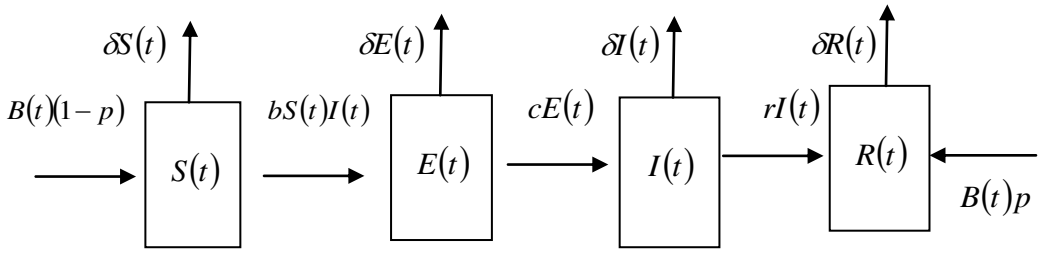

Figure 3: The flowchart of SEIR model after vaccination.

Theorem 5: We consider that $S(t) = 4I(t)$, $E(t) = 2I(t)$, $R(t) = \frac{1}{4}I(t)$, and $N(t) = \frac{29}{4}I(t)$, then $c = \frac{87\delta(2r+1)}{40c(8r+5)} + \frac{7\delta}{20c(8r+5)} + \frac{4r(2r+1)}{8r+5}$. Further, if $\delta = 0.0004$, $r = 0.00068$, and then $c = 0.00092$.

Proof: Dividing (24) by (26) we get,

$$\frac{dS(t)}{dI(t)} = \frac{B(t)(1-p) - bS(t)I(t) - \delta S(t)}{cE(t) - (r+\delta)I(t)}$$

$$\frac{4dI(t)}{dI(t)} = \frac{\frac{29}{4}\delta I(t)(1-p) - 4bI(t)I(t) - 4\delta I(t)}{2cI(t) - (r+\delta)I(t)}$$

$$4 = \frac{\frac{29}{4}\delta(1-p) - 4bI(t) - 4\delta}{2c - (r+\delta)}$$

$$I(t) = \frac{87}{160b}\delta - \frac{c}{b} + \frac{r}{b}. \tag{28}$$

Dividing (24) by (25) we get,

$$\frac{dS(t)}{dE(t)} = \frac{B(t)(1-p) - bS(t)I(t) - \delta S(t)}{bS(t)I(t) - (c+\delta)E(t)}$$

$$\frac{4dI(t)}{2dI(t)} = \frac{\frac{29}{4}\delta I(t) \times 0.3 - 4bI(t)I(t) - 4\delta I(t)}{4brI(t)I(t) - (c+\delta)I(t)}$$

$$2 = \frac{\frac{29}{4}\delta \times 0.3 - 4bI(t) - 4\delta}{4brI(t) - (c+\delta)}$$

$$I(t)=\frac{c}{2b(2r+1)}+\frac{7\delta}{80b(2r+1)}. \tag{29}$$

Equalizing (28) and (29) we get,

$$\frac{87}{160b}\delta-\frac{c}{b}+\frac{r}{b}=\frac{c}{2b(2r+1)}+\frac{7\delta}{80b(2r+1)}$$

$$c=\frac{87\delta(2r+1)}{40c(8r+5)}+\frac{7\delta}{20c(8r+5)}+\frac{4r(2r+1)}{8r+5}. \tag{30}$$

If $\delta=0.0004$, $r=0.00068$ in (30) then, $c=0.00092$.

7.3 Immunity Loss of Vaccine

Over time the immunity to vaccines decreases and after a fixed period the immunity to COVID-19 due to vaccination will be disappeared. These vaccinated but immunity-loss people will be susceptible to COVID-19. Let $e>0$ be the rate of immunity loss, then in $R(t)$ compartment, $eR(t)$ people will be reduced due to loss of immunity, and these $eR(t)$ individuals will add to $S(t)$ compartment. The system of equations in SEIR model becomes,

$$\frac{dS(t)}{dt}=B(t)(1-p)-bS(t)I(t)-\delta S(t)+eR(t) \tag{31}$$

$$\frac{dE(t)}{dt}=bS(t)I(t)-(c+\delta)E(t) \tag{32}$$

$$\frac{dI(t)}{dt}=cE(t)-(r+\delta)I(t) \tag{33}$$

$$\frac{dR(t)}{dt}=rI(t)-(\delta+e)R(t)+B(t)p\,. \tag{34}$$

The flowchart of SEIR model after immunity loss of vaccines can be given as in Figure 4.

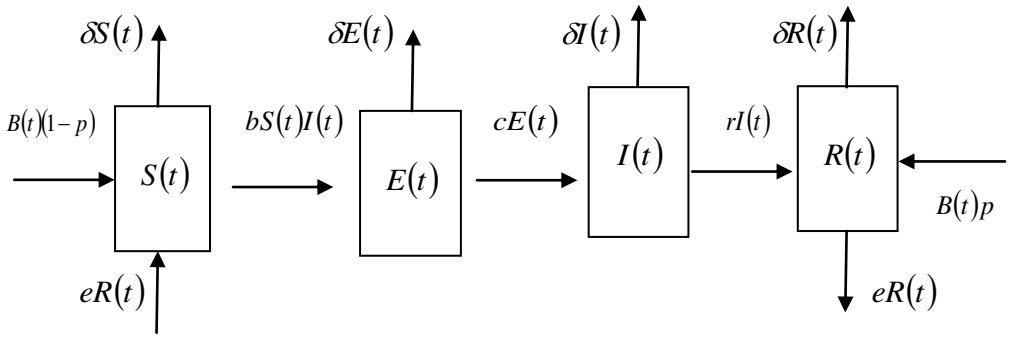

Figure 4: The flowchart of SEIR model after immunity loss of vaccine.

Theorem 6: We consider that $S(t)=4I(t)$, $E(t)=2I(t)$, $R(t)=\frac{1}{4}I(t)$, and $N(t)=\frac{29}{4}I(t)$, then $c=\frac{87\delta(2r+1)}{40c(8r+5)}+\frac{7\delta}{20c(8r+5)}+\frac{4r(2r+1)}{8r+5}$. Further, if $\delta=0.0004$, $r=0.00068$, and then $c=0.00092$.

Proof: Dividing (31) by (33) we get,

$$\frac{dS(t)}{dI(t)}=\frac{B(t)(1-p)-bS(t)I(t)-\delta S(t)+eR(t)}{cE(t)-(r+\delta)I(t)}$$

$$\frac{4dI(t)}{dI(t)}=\frac{\frac{29}{4}\delta I(t)-4bI(t)I(t)-4\delta I(t)+\frac{1}{4}eI(t)}{2cI(t)-(r+\delta)I(t)}$$

$$I(t)=\frac{29}{16b}\delta+\frac{r}{b}-\frac{2c}{b}+\frac{e}{16b}. \tag{35}$$

Dividing (31) by (34) we get,

$$\frac{dS(t)}{dR(t)}=\frac{B(t)(1-p)-bS(t)I(t)-\delta S(t)+eR(t)}{rI(t)-(\delta+e)R(t)+B(t)p}$$

$$\frac{4dI(t)}{\frac{1}{4}dI(t)}=\frac{\frac{29}{4}\delta I(t)\times 0.3-4bI(t)I(t)-4\delta I(t)+\frac{1}{4}eI(t)}{rI(t)-\frac{1}{4}(\delta+e)I(t)+\frac{1}{4}\delta I(t)\times 0.3}$$

$$16=\frac{\frac{29}{4}\delta\times 0.3-4bI(t)-4\delta+\frac{1}{4}e}{r-\frac{1}{4}(\delta+e)+\frac{1}{4}\delta\times 0.3}$$

$$I(t)=\frac{39\delta}{160b}+\frac{17e}{16b}-\frac{4r}{b}. \tag{36}$$

Equalizing (35) and (36) we get,

$$e=\frac{251\delta}{160}+5r-2c. \tag{37}$$

If $\delta=0.0004$, $r=0.00068$, $c=0.00092$ in (37) then, $e=0.0021875$.

7.4 Re-infection of the Persons

A portion of first-time infected persons that recovered may be re-infected by COVID-19 again. Let, $g>0$ be the rate of re-infected individuals; then the $gR(t)$ persons will be reduced from $R(t)$ compartment, and these $gR(t)$ people will add to the $E(t)$ compartment. After the gestation period, $gR(t)$ individuals from the $E(t)$ compartment will add to the $I(t)$ compartment. Of the newly re-

infected people, some may die. Let $h>0$, be the death rate of the re-infected individuals, where $h\neq\delta$, consequently, $hI(t)$ will be reduced in the $I(t)$ compartment, consequently, $hI(t)$ people added in $R(t)$ compartment. The system of equations in SEIR model becomes;

$$\frac{dS(t)}{dt}=B(t)(1-p)-bS(t)I(t)-\delta S(t)+eR(t) \tag{38}$$

$$\frac{dE(t)}{dt}=bS(t)I(t)-(c+\delta)E(t)+gR(t) \tag{39}$$

$$\frac{dI(t)}{dt}=(c+g)E(t)-(r+\delta+h)I(t) \tag{40}$$

$$\frac{dR(t)}{dt}=rI(t)-(\delta+e+g-h)R(t)+B(t)p\,. \tag{41}$$

In SEIR model after vaccination people re-infected by COVID-19 again can be given as in Figure 5.

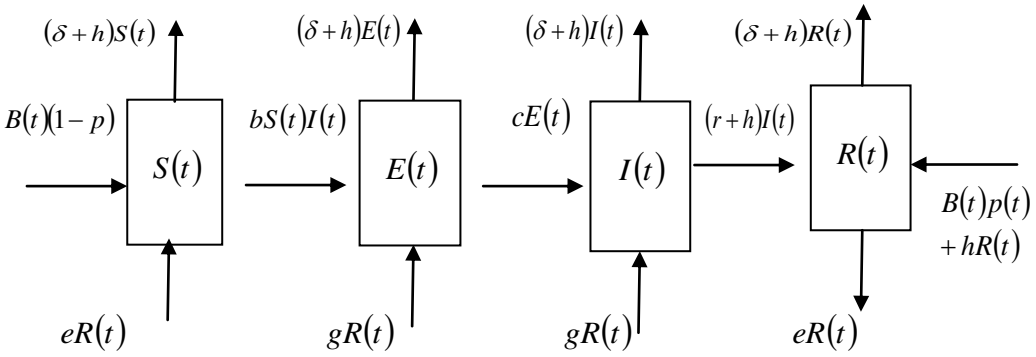

Figure 5: The flowchart of SEIR model the vaccinated people that are re-infected.

Theorem 7: We consider that $S(t)=4I(t)$, $E(t)=2I(t)$, $R(t)=\frac{1}{4}I(t)$, and $N(t)=\frac{29}{4}I(t)$, then $h=\frac{47e}{48}+\frac{25g}{24}-4r-\frac{c}{3}-\frac{957\delta}{48}$. Further, if $\delta=0.0004$, $r=0.000008$, and then $c=0.00092$, $e=0.0021875$ and $g=0.006$ in (44) then, $h=-0.006263$.

Proof: Dividing (38) by (39) we get,

$$\frac{dS(t)}{dE(t)}=\frac{B(t)(1-p)-bS(t)I(t)-\delta S(t)+eR(t)}{bS(t)I(t)-(c+\delta)E(t)+gR(t)}$$

$$\frac{4dI(t)}{2dI(t)}=\frac{\frac{29}{4}\delta I(t)\times 0.3-4bI(t)I(t)-4\delta I(t)+\frac{1}{4}eI(t)}{4bI(t)I(t)-2(c+\delta)I(t)+\frac{1}{4}gI(t)}$$

$$2=\frac{\frac{29}{4}\delta\times 0.3-4bI(t)-4\delta+\frac{1}{4}e}{4bI(t)-2(c+\delta)+\frac{1}{4}g}$$

$$I(t)=\frac{c}{3b}+\frac{87\delta}{160b}+\frac{e}{48b}-\frac{g}{24b}. \tag{42}$$

Dividing (39) by (41) we get,

$$\frac{dE(t)}{dR(t)}=\frac{bS(t)I(t)-(c+\delta)E(t)+gR(t)}{rI(t)-(\delta+e+g-h)R(t)+B(t)p}$$

$$\frac{2dI(t)}{\frac{1}{4}dI(t)}=\frac{4bI(t)I(t)-2(c+\delta)I(t)+\frac{1}{4}gI(t)}{rI(t)-\frac{1}{4}(\delta+e+g-h)I(t)+\frac{203\delta}{40}I(t)}$$

$$8=\frac{4bI(t)-2(c+\delta)+\frac{1}{4}g}{r-\frac{1}{4}(\delta+e+g-h)+\frac{203\delta}{40}}$$

$$I(t)=\frac{2r}{b}+\frac{c}{2b}-\frac{e}{2b}-\frac{9g}{16b}+\frac{h}{2b}+\frac{203\delta}{20b}. \tag{43}$$

Equalizing (42) and (43) we get,

$$\frac{2r}{b}+\frac{c}{2b}-\frac{e}{2b}-\frac{9g}{16b}+\frac{h}{2b}+\frac{203\delta}{20b}=\frac{c}{3b}+\frac{87\delta}{160b}+\frac{e}{48b}-\frac{g}{24b}$$

$$h=\frac{25e}{24}+\frac{25g}{24}-r-\frac{c}{3}-\frac{1537}{80}\delta. \tag{44}$$

If $\delta=0.0004$, $r=0.00068$, $c=0.00092$, $e=0.0021875$, and $g=0.006$ in (44) then, $h=-0.006263$. Here negative value of h indicates that re-infected people will not die, i.e., the vaccinated people has strong immunity will not die from COVID-19 infection.

7.5 Immigration Analysis

Healthy people may be infected by COVID-19 through the contact with infected individuals. We consider that all the migrated people will be infected. Let, j be the immigration rate so that $jN(t)$ newly infected people per day will increase with the previously infected individuals. We have considered that the total population in a particular time t is constant so that natural death at each compartment will change from δ to $(\delta+j)$. Hence, after immigration SEIR model can be represented as [Niu et al. 2020];

$$\frac{dS(t)}{dt} = jN(t) + B(t)(1-p) - bS(t)I(t) - (\delta + j)S(t) + eR(t) \tag{45}$$

$$\frac{dE(t)}{dt} = bS(t)I(t) - (c + \delta + g + j)E(t) + gR(t) \tag{46}$$

$$\frac{dI(t)}{dt} = (c + g)E(t) - (r + \delta + h + j)I(t) \tag{47}$$

$$\frac{dR(t)}{dt} = rI(t) - (\delta + e + g - h + j)R(t) + B(t)p\,. \tag{48}$$

Theorem 7: We consider that $S(t) = 4I(t)$, $E(t) = 2I(t)$, $R(t) = \frac{1}{4}I(t)$, and $N(t) = \frac{29}{4}I(t)$, then $h = \frac{47e}{48} + \frac{25g}{24} - 4r - \frac{c}{3} - \frac{957\delta}{48}$. Further, if $\delta = 0.0004$, $r = 0.00068$, $c = 0.00092$, $e = 0.000005$, $g = 0.000006$, and $h = 0.0000005$ then $j = 0.046$.

Proof: Dividing (45) by (47) we get,

$$\frac{dS(t)}{dI(t)} = \frac{jN(t) + B(t)(1-p) - bS(t)I(t) - (\delta + j)S(t) + eR(t)}{(c + g)E(t) - (r + \delta + h + j)I(t)}$$

$$\frac{4dI(t)}{dI(t)} = \frac{\frac{29}{4}jI(t) + \frac{29}{4}I(t)B(t) \times 0.3 - 4bI(t)I(t) - 4(\delta + j)I(t) + \frac{1}{4}eI(t)}{2(c + g)I(t) - (r + \delta + h + j)I(t)}$$

$$4 = \frac{\frac{29}{4}j + \frac{87}{40}\delta - 4bI(t) - 4(\delta + j) + \frac{1}{4}e}{2c + 2g - (r + \delta + h + j)}$$

$$I(t) = \frac{29j}{16b} + \frac{87\delta}{40b} + \frac{e}{16b} - \frac{2c}{b} - \frac{233g}{160b} + \frac{r}{b} + \frac{h}{b}\,. \tag{49}$$

Dividing (45) by (47) we get,

$$\frac{dE(t)}{dR(t)} = \frac{bS(t)I(t) - (c + \delta + g + j)E(t) + gR(t)}{rI(t) - (\delta + e + g - h + j)R(t) + B(t)p}$$

$$\frac{2dI(t)}{\frac{1}{4}dI(t)} = \frac{4bI(t)I(t) - 2(c + \delta + g + j)I(t) + \frac{1}{4}gI(t)}{rI(t) - \frac{1}{4}(\delta + e + g - h + j)I(t) + \frac{29}{4}\delta I(t) \times 0.7}$$

$$8 = \frac{4bI(t) - 2(c + \delta + g + j) + \frac{1}{4}g}{r - \frac{1}{4}(\delta + e + g - h + j) + \frac{29}{4}\delta \times 0.7}$$

$$I(t) = \frac{2r}{b} + \frac{h}{2b} + \frac{c}{2b} + \frac{203\delta}{20b} - \frac{g}{16b} - \frac{e}{2b}\,. \tag{50}$$

Equalizing (49) and (50) we get,

$$j=\frac{638\delta}{145}+\frac{40c}{29}+\frac{16r}{29}-\frac{9e}{29}+\frac{233g}{290}-\frac{8h}{29}. \tag{51}$$

If $\delta=0.0004$, $r=0.00068$, $c=0.00092$, $e=0.000005$, $g=0.000006$, and $h=0.0000005$, then $j=0.046$.

8. Equilibrium of the Model

Equilibrium points of the model can be found by setting, $\frac{dS}{dt}=\frac{dE}{dt}=\frac{dI}{dt}=\frac{dR}{dt}=0$. Hence, from (45) to (48) we get,

$$jN(t)+B(t)(1-p)-bS(t)I(t)-(\delta+j)S(t)+eR(t)=0 \tag{52}$$

$$bS(t)I(t)-(c+\delta+g+j)E(t)+gR(t)=0 \tag{53}$$

$$(c+g)E(t)-(r+\delta+h+j)I(t)=0 \tag{54}$$

$$rI(t)-(\delta+e+g-h+j)R(t)+B(t)p=0. \tag{55}$$

A disease-free equilibrium is an equilibrium when there is no spread of the disease, i.e., at an equilibrium point, $E(0)=I(0)=0$ at $t=0$ [Wintachai & Prathom, 2021]. Hence, from (55) we get,

$$(\delta+e+g-h+j)R(t)=B(t)p$$

$$(\delta+e+g-h+j)R(t)=\delta pS(t)+\delta pR(t)$$

$$(\delta-\delta p+e+g-h+j)R(t)=\delta pS(t)$$

$$\frac{R(t)}{S(t)}=\frac{\delta p}{\delta(1-p)+e+g-h+j}. \tag{56}$$

From (52) we get,

$$jN(t)+B(t)(1-p)-bS(t)I(t)-(\delta+j)S(t)+eR(t)=0$$

$$jS(t)+jR(t)+\delta S(t)(1-p)+\delta R(t)(1-p)-(\delta+j)S(t)+eR(t)=0$$

$$\{\delta(1-p)+e+j\}R(t)=\delta pS(t)$$

$$\frac{R(t)}{S(t)}=\frac{\delta p}{\delta(1-p)+e+j}. \tag{57}$$

Comparing (56) and (57) we get, $g=h=0$, i.e., there is neither re-infection nor death for re-infection in disease-free equilibrium state. For non-disease-free equilibrium; $S(t)\neq 0$, $E(t)\neq 0$, $I(t)\neq 0$, $R(t)\neq 0$. From (54) we get,

$$(c+g)E(t)-(r+\delta+h+g+j)I(t)=0$$

$$I(t)=\frac{(c+g)}{r+\delta+h+g+j}E(t). \tag{58}$$

From (53) we get,

$$I(t)=\frac{(c+\delta+g+j)E(t)-gR(t)}{bS(t)}. \tag{59}$$

Comparing (58) and (59) for $R(t)=0$ we get,

$$S(t)=\frac{(r+\delta+h+g+j)(c+\delta+g+j)}{b(c+g)}. \tag{60}$$

Equations (45) to (48) can be written as,

$$\frac{dS(t)}{dt}=-(0.7\delta+bI(t))S(t)+(j+0.3\delta)E(t)+(j+0.3\delta)I(t)+(j+0.3\delta+e)R(t) \tag{61}$$

$$\frac{dE(t)}{dt}=bS(t)I(t)-(c+\delta+g+j)E(t)+gR(t) \tag{62}$$

$$\frac{dI(t)}{dt}=(c+g)E(t)-(r+\delta+h+j)I(t) \tag{63}$$

$$\frac{dR(t)}{dt}=0.7\delta S(t)+0.7\delta E(t)+(r+0.7\delta)I(t)-(0.3\delta+e+g-h+j)R(t)+B(t)p\,. \tag{64}$$

Theorem 8: The equilibrium point of the SEIR model is locally asymptotic stable [Wintachai & Prathom, 2021].

Proof: The Jacobian method used for the SEIR model yields a biologically reasonable R_0. We consider the Jacobian matrix of the SEIR model formed by the equations (61), (62), (63), and (64) as,

$$J=\begin{bmatrix} -(0.7\delta+bI) & j+0.3\delta & j+0.3\delta & j+0.3\delta+e \\ bI & -(c+\delta+j) & 0 & g \\ 0 & c+g & -(r+\delta+h+g+j) & 0 \\ 0.7\delta & 0.7\delta & r+0.7\delta & -(0.3\delta+e+g-h+j) \end{bmatrix}.$$

Let us consider the vaccination individuals are not re-infected and there is no immigration, then $h=g=0$, $j=0$, also temporarily ignore the value of p; consequently,

$$J=\begin{bmatrix} -(\delta+bI) & \delta & \delta & \delta+e \\ bI & -(c+\delta) & 0 & 0 \\ 0 & c & -(r+\delta) & 0 \\ \delta & \delta & r+\delta & -(\delta+e) \end{bmatrix}.$$

Characteristic equation is,

$$|\lambda I-J|=0$$

$$\Rightarrow \begin{vmatrix} \lambda+\delta+bI & -\delta & -\delta & -(\delta+e) \\ -bI & \lambda+c+\delta & 0 & 0 \\ 0 & -c & \lambda+r+\delta & 0 \\ -\delta & -\delta & -(r+\delta) & \lambda+\delta+e \end{vmatrix} = 0$$

$$(\delta+e)\begin{vmatrix} -bI & \lambda+c+\delta & 0 \\ 0 & -c & \lambda+r+\delta \\ -\delta & -\delta & -(r+\delta) \end{vmatrix} + (\lambda+\delta+e)\begin{vmatrix} \lambda+\delta+bI & -\delta & -\delta \\ -bI & \lambda+c+\delta & 0 \\ 0 & -c & \lambda+r+\delta \end{vmatrix} = 0$$

$$\lambda^4 + (c+4\delta+r+bI+e)\lambda^3 + \{\delta(c+2\delta+r)+bcI+b\delta I+brI+(\delta+e)(c+3\delta+r+bI+\delta)\}\lambda^2$$
$$+ (2\delta^4+2\delta^3+2\delta^3 e+\delta^2 r+3\delta^2 e+\delta beI+\delta er+\delta e^2+breI+bceI)\lambda$$
$$+ (\delta^4+\delta^3 c+2\delta^3 e+2\delta^2 ce+\delta^2 e^2+\delta be^2+2\delta e^2+bcreI)=0$$
$$\lambda^4 + D_1\lambda^3 + D_2\lambda^2 + D_3\lambda + D_4 = 0 \qquad (65)$$

where,

$D_1 = c+4\delta+r+bI+e > 0$

$D_2 = \delta(c+2\delta+r)+bcI+b\delta I+brI+(\delta+e)(c+3\delta+r+bI+\delta) > 0$

$D_3 = 2\delta^4+2\delta^3+2\delta^3 e+\delta^2 r+3\delta^2 e+\delta beI+\delta er+\delta e^2+breI+bceI > 0$

$D_4 = \delta^4+\delta^3 c+2\delta^3 e+2\delta^2 ce+\delta^2 e^2+\delta be^2+2\delta e^2+bcreI > 0.$

Here D_1, D_2, D_3, and D_4 are positive real numbers. Therefore, all the solutions (eigenvalues) of equation (65) have negative real values, i.e., $\lambda_1, \lambda_2, \lambda_3, \lambda_4 < 0$. Therefore, the equilibrium point of the SEIR model is locally asymptotic stable.

9. Basic Reproductive Number

The basic reproduction number is denoted by, R_0, and is defined as the expected number of secondary cases produced by infection in a completely susceptible population. Actually, R_0 is not a rate and it is a dimensionless real number with units of time^{-1}. For SEIR model, R_0 is fixed over all time. R_0 is the number of secondary infections that one infected person would produce in a fully susceptible population through the entire duration of the infectious period. It provides a threshold condition for the stability of the disease-free equilibrium point. If $R_0 < 1$, the disease-free equilibrium point is locally asymptotically stable, and the disease dies will abolish. If $R_0 > 1$, the disease-free equilibrium point is unstable and the disease establishes itself in the population or an epidemic/pandemic occurs.

Now we consider that $\chi = (\chi_1, \chi_2, \chi_3, \chi_4)^T = (S(t), E(t), I(t), R(t),)^T$ be the number of people in each compartment. Consider the equation, $\frac{d\chi_i}{dt} = F_i(\chi) - V_i(\chi),\ i = 1,2,3,4$, where $F_i(\chi)$ is the rate of appearance of new infections in compartment *i*, and $V_i(\chi)$ is the rate of other transitions between compartment *i* and other infected compartments. Now, $F = \left[\frac{\partial F_i(\chi_0)}{\partial \chi_j}\right]$ and $V = \left[\frac{\partial V_i(\chi_0)}{\partial \chi_j}\right]$. Here *F* is entry wise non-negative that represents the paths to infection, and *V* is a non-singular M-matrix that represents the remaining dynamics corresponding to the compartments $E(t)$ and $I(t)$. Consequently, V^{-1} is entry wise non-negative. Let, $P(0)$ be the number of initially infected people, then $FV^{-1}P(0)$ is an entry wise non-negative vector giving the expected number of new infections. Matrix $Q = FV^{-1}$ has (i, j) entry equal to the expected number of secondary infections in compartment *i* produced by an infected individual introduced in compartment *j*. Hence, $Q = FV^{-1}$ is the next generation matrix. The dominant eigenvalues of FV^{-1} and $V^{-1}F$ are the same [van den Driessche, 2017].

To find the basic reproductive number R_0, we follow the matrices generation method by the use of seminal work of Pauline van den Driessche [van den Driessche, 2017]. Here R_0 is the dominant eigenvalue of $Q = FV^{-1}$, where

$$F = F(t) = \begin{bmatrix} 0 & bS(t) \\ c+g & 0 \end{bmatrix} \text{ and} \tag{66}$$

$$V = \begin{bmatrix} c+\delta+g+\mathrm{j} & 0 \\ 0 & r+\delta+h+j \end{bmatrix}.$$

$$V^{-1} = \frac{1}{(c+\delta+g+j)(r+\delta+h+j)} \begin{bmatrix} r+\delta+h+j & 0 \\ 0 & c+\delta+g+j \end{bmatrix}$$

$$= \begin{bmatrix} \frac{1}{c+\delta+g+j} & 0 \\ 0 & \frac{1}{r+\delta+h+j} \end{bmatrix}$$

$$Q = \begin{bmatrix} 0 & bS(t) \\ c+g & 0 \end{bmatrix} \begin{bmatrix} \frac{1}{c+\delta+g+j} & 0 \\ 0 & \frac{1}{r+\delta+h+j} \end{bmatrix}$$

$$= \begin{bmatrix} 0 & \dfrac{bS(t)}{r+\delta+h+j} \\ \dfrac{c+g}{c+\delta+g+j} & 0 \end{bmatrix}. \tag{67}$$

Using (66) and (67) we get,

$$R_0 = \frac{b(c+g)S(t)}{(c+\delta+g+j)(r+\delta+h+j)}. \tag{68}$$

Theorem 9: If $R_0 < 1$, then the disease-free equilibrium is globally asymptotic stable; on the other hand, if $R_0 > 1$, the equilibrium is unstable.

Proof: Let, $\chi(t) = \begin{bmatrix} E(t) \\ I(t) \end{bmatrix}$, where $\chi(t)$ is a zero matrix only at the disease-free equilibrium [van den Driessche, 2017; Wintachai & Prathom, 2021].

$$\frac{d\chi(t)}{dt} = \begin{bmatrix} \dfrac{dE(t)}{dt} \\ \dfrac{dI(t)}{dt} \end{bmatrix}$$

$$= \begin{bmatrix} c+\delta+g+\mathrm{j} & bS(t) \\ c+\mathrm{g} & r+\delta+h+j \end{bmatrix}$$

$$= (F(t)-V)\chi(t). \tag{69}$$

Now we define the Lyapunov function $L(t)$ as,

$$L(t) = uV^{-1}\chi(t) \tag{70}$$

where

$$u(t) = \begin{bmatrix} 1 & R_0(c+g)(r+\delta+h+j) \end{bmatrix}$$

is a 1×2 matrix. For the matrices $F(t)$ and V that are defined in (66) and (67) we can find

$$u(t)R_0 = u(t)V^{-1}F(t). \tag{71}$$

Now we see that uV^{-1} is a 1×2 matrix of positive real components and is a non-negative matrix. So that $L(t) \geq 0$, and $L(t) = 0$ is possible only if $E(t) = 0$ and $I(t) = 0$, i.e., if in the model there is no infection [Perko, 2013]. Differentiating (70) we get,

$$\frac{dL(t)}{dt} = u(t)V^{-1}\frac{d\chi(t)}{dt}$$

$$= u(t)V^{-1}(F(t)-V)\chi(t)$$

$$= \left(u(t)V^{-1}F(t) - u(t)\right)\chi(t)$$

$$= (u(t)R_0 - u(t))\chi(t), \qquad \text{by (71)}$$

$$\frac{dL(t)}{dt} = u(t)(R_0 - 1)\chi(t). \tag{72}$$

From (72) we observe that $\frac{dL(t)}{dt} < 0$ if $R_0 < 1$, i.e., the disease-free equilibrium is globally asymptotic stable. If $R_0 > 1$, then (72) implies $\frac{dL(t)}{dt} > 0$, i.e., the equilibrium is unstable.

If $R_0 < 1$ then we have, $\frac{dE(t)}{dt} + \frac{dI(t)}{dt} = 0$, then from (46) and (47) we get,

$$bS(t)I(t) - (2c + \delta + 2g + j)E(t) + gR(t) - (r + \delta + h + j)I(t) = 0. \tag{73}$$

In equation (73) we consider that $E(t) = 0$ and $R(t) = 0$, i.e., there is no people in latent period or recovery then,

$$bS(t)I(t) - (r + \delta + h + j)I(t) = 0$$

$$\frac{(c + \delta + g + j)(r + \delta + h + j)}{c + g} R_0 I(t) - (r + \delta + h + j)I(t) = 0$$

$$(r + \delta + h + j)\left\{\frac{c + \delta + g + j}{c + g} R_0 - 1\right\} = 0$$

$$(r + \delta + h + j)\left\{\frac{c + \delta + g + j}{c + g} R_0 - 1\right\} = 0. \tag{74}$$

In equation (74), $\frac{c + \delta + g + j}{c + g}$ is an improper fraction. Therefore, $R_0 < 1$ and hence from (72) we get, $\frac{dL(t)}{dt} < 0$. Consequently, the disease-free equilibrium is globally asymptotic stable. A similar reason $R_0 > 1$ implies the equilibrium is unstable.

10. Conclusions

We have observed that SEIR model is a reference model for the spread of COVID-19. In the study, we have tried to construct an SEIR model for the outbreak of COVID-19. We have investigated the impact of vaccination on the spread of COVID-19. We have perceived that vaccination is the best policy to reduce COVID-19 infection. The model supports that the vaccination rate and the efficiency of vaccines play an important role to reduce the transmission and survival of the disease. Many researchers have obtained the value of the basic reproduction number R_0 of COVID-19, and their results support that it is greater than 1. Consequently, the COVID-19 pandemic will not

terminate from the world immediately. We hope that the fatality of COVID-19 transmission will decrease gradually and eventually it will abolish from the world.

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