Mathematical Analysis of SIR Model for COVID-19 Transmission

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5 June 2022

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Abstract

Due to the recent threatening pandemic COVID-19, the research area of this disease is increasing. This paper tries to establish COVID-19 infection transmission by Susceptible-Infectious-Recovered (SIR) compartmental model for epidemic prediction and prevention. The model is built based on the secondary data of the infected persons and discharged patients. It is considered as a valuable tool in public health sector, as it can provide suggestions about the fatality of pandemic to take necessary actions for preventing the infections. COVID-19 is spreading worldwide extremely, and at present it becomes both local and global concern. This model can show the fatality of COVID-19 with time and can predict whether the disease will further spread or abolish completely. This study stresses on vaccination to reduce the infection of the disease. It can provide how many people are needed to be vaccinated to create herd immunity against COVID-19. Overtime the immunity due to vaccination may decrease and after a fixed period the immunity of COVID-19 due to vaccination may extinct completely. The article attempts to give a mathematical presentation to aware the immunity loss individuals with other susceptible. It also tries to alert the people about the re-infection of the previous COVID-19 infected persons. The aim of this study is to minimize both global economic losses and deaths due to COVID-19.

Keywords: COVID-19, SARS-CoV-2, SIR Model, Immunity, Pandemics, Vaccination, Basic Reproduction Number

1. Introduction

In the 21st century, global humanity has faced many different types of epidemics/pandemics, such as Severe Acute Respiratory Syndrome Coronavirus (SARS-CoV) (outbreaks in 2002-2003), Middle East Respiratory Syndrome Coronavirus (MERS-CoV) (outbreaks in 2012), Ebola (first outbreaks in 1976, and later in 2013), H1N1 (outbreaks in 2009), and at present SARS-CoV-2 (COVID-19) (outbreaks in December 2019). Among these outbreaks, COVID-19 is more fatal than the others. It becomes a great challenge before the global humanity to abolish the disease completely (Assiri et al., 2013; Li, 2013; Chan et al., 2020; Mohajan, 2020b). Actually the transmission nature of the COVID-19 is not fixed with change of time and real situation is more complicated than the epidemic SIR model (Zhu & Shen, 2021).

During the period of COVID-19 virus transmission, the influence of population dynamics, such as birth, death, and migration of population in this period is ignored (da Silva, 2021). Therefore, the total population N of epidemic area can be regarded as a constant over time, i.e., $N(t) = \text{constant} = N$, for all $0 \le t < \infty$. We divide the population into three homogeneous subgroups: susceptible $S(t)$, infectious $I(t)$, and recovered $R(t)$. Hence, $S(t) + I(t) + R(t) = N(t) = N$, for all $0 \le t < \infty$. The disease-free state represents, $S(t) = N$, $I(t) = 0$, and $R(t) = 0$, for all $0 \le t < \infty$ (Tang et al., 2020).

COVID-19 is a micro-parasitic disease. It spreads worldwide through human interactions. The precise nature and details of human interactions determine how epidemic grows and infection spreads. If the disease is short lived compared with the population lifetime, then demography can be ignored (Abadie et al., 2020). Epidemiological mathematical models are considered as valuable tools for investigating the spread and control of contagious disease COVID-19 (Dubey et al., 2015). After the outbreak of COVID-19, many researchers of worldwide have published articles with giving priority in epidemic mathematical models. In modern society,

epidemiological study with mathematics provides the aspects of the evolution of diseases. It captures the dynamics of acute infections that confers lifelong immunity once recovered (Rodrigues, 2016; Wacker & Schlüter, 2020).

The Susceptible-Infectious-Recovered (SIR) model of epidemics is very simple. It is one of the most popular epidemic threshold models in epidemiology that was initially proposed. It is introduced in 1927 by a Scottish biochemist, William Ogilvy Kermack (1898-1970), and a Scottish military physician and epidemiologist, Anderson Gray McKendrick (1876-1943). Later, it builds a block for the epidemic researchers and the dynamical behavior of the model is globally performed. It is based on an exponential fit for short term and long term predictions. It has only three compartments: susceptible $S(t)$, infectious $I(t)$, and recovered $R(t)$ and only two directions of changes: from susceptible to infected and from infected to recovery (Bhattacharya et al., 2015; Kermack & Mackendrick, 1927). In the SIR model, disease spread proportional to the population, the complete lack of immunity at the beginning of the epidemic, has no latency period, the short duration of the disease relative to lifespan (Zhu & Shen, 2021).

The basic reproduction number in SIR model is denoted by R_0. It 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. In this model, $R_0 = 1$ provides a threshold condition for the stability of the disease-free equilibrium point. If $R_0 < 1$, the world will be COVID-19 free in a very short time, and if $R_0 > 1$, then infected persons will transmit the diseases into susceptible people quicker than recovery rate, so the disease grow to be an epidemic (Murray, 2002; Heffernan et al., 2005).

There are numerous applications of this model, and in this study we apply it for the basic model to COVID-19 outbreak. This paper tries to establish COVID-19 infection transmission by SIR model for epidemic prediction and prevention. The model is built based on the data of the infected persons, discharged patients and discharged patients during the period of isolation and control. The mass vaccination develops herd immunization among the susceptible persons that can reduce COVID-19 transmission. It is evident that first time COVID-19 infected persons re-

infected after recovery from the disease. Also after a fixed period the vaccinated peoples loss the immunity, ultimately they become susceptible. Therefore, combined attempts including SIR model analysis are necessary to abolish this fatal disease completely from the world. The SIR model is a valuable tool in public health, as it predicts the necessities to reduce or prevent infections.

2. Literature Review

William Ogilvy Kermack and Anderson Gray McKendrick have introduced well-known SIR model for the first time in 1927. They have considered a fixed population size and have divided it into three different homogeneous groups of people: susceptible, infectious, and recovered, excluding natural births and deaths, and deaths by epidemic disease (Kermack & Mackendrick, 1927). Balram Dubey and his coauthors have investigated the global dynamics of SIR model in which the incidence rate is being considered as Beddington-DeAngelis type and the treatment rate as Holling type II. They have revealed that the disease-free equilibrium is locally asymptotically stable when reproduction number is less than one. They have also examined the existence of Hopf bifurcation by using Andronov-Hopf bifurcation theorem (Dubey et al., 2015).

Paritosh Bhattacharya and his coauthors have analyzed the compartmental SIR models for disease transmission. They have calculated the basic reproduction number and the final size of the epidemic. They have also studied the models with multiple compartments and treatment of infective (Bhattacharya et al., 2015). Rahim Uddin and Ebrahem A. Algehyne have discussed mathematical SIR model of COVID-19 in the form of differential equations and have obtained that protection, exposure, and death rates affect people with the elapse of time (Uddin & Algehyne, 2021). Wen-jing Zhu and Shou-feng Shen have constructed a reliable model based on the SIR model to analyze and assess the epidemic dynamics of COVID-19 in China. They have identified that the cure rate is 0.05 and the reproduction number is 0.4490 of COVID-19 at the end of 2020 and beginning of 2021 (Zhu & Shen, 2021). Samia Ghersheen and her coauthors have proved that for small carrying capacity K, there exists a globally stable disease-free equilibrium point. They have also established the continuity of the transition dynamics of the stable equilibrium point. They have proved that, i) for small values of K, there exists a unique

globally stable equilibrium point, and ii) the disease moves continuously as K is growing (Ghersheen et al., 2019).

Haradhan Kumar Mohajan has discussed aspects of global pandemic COVID-19 through his review papers. He has tried to create consciousness among the common people to reduce the fatality of this killer disease. He also highlights the social, economic, and health impacts in the world's poorest countries due to COVID-19 pandemic outbreak. He also emphasizes on COVID-19 vaccines to reduce both morbidity and mortality globally. He also tries to discuss SEIR model with detail mathematical analysis (Mohajan, 2020a, b, 2021a, b, c). Recently, Peter X. Song and his coworkers have proposed a modification of the SIR model to allow a state of quarantine, that is, a fraction of the susceptible population becomes quarantined and cannot be infected (Song et al., 2020). Abdon Atangana has used fractional differential equations in extended SIR and SEIR models to investigate the spread of COVID-19 in mathematical biology. They have applied novel differential and integral operators to show the effect of the lockdown (Atangana, 2020). Benjamin Wacker and Jan Schlüter have discussed both time-continuous and time-discrete SIR models. First, they introduce continuous variant with time-varying transmission and recovery rates, and then they develop different possible time-discrete SIR models (Wacker & Schlüter, 2020). Andrew G. Atkeson has introduced a simple SIR model of the progression of COVID-19 to aid understanding of how such a model might be incorporated into more standard macroeconomic models. He allows quantitative statements regarding the tradeoff between the severity and timing of suppression of the disease through social distancing and the progression of the disease in the population (Atkeson, 2020).

Curtis L. Wesley and Linda J. S. Allen have studied epidemic models with periodic demographics that include temporary immunity, isolation, and multiple strains to calculate the time-averaged basic reproduction number, which is a threshold for disease extinction (Wesley & Allen, 2009). In a compartmental model Pauline van den Driessche focuses on the basic reproduction number for infectious disease to determine whether or not the disease dies out (van den Driessche, 2017). Himel Talukder and his coauthors have estimated the basic reproduction number R_0 of the COVID-19 infection, based on the real time confirmed cases and suspected cases, in Bangladesh, to control this pandemic effectively. The value of R_0 is estimated by them

within 3.19 and 5.24, based on real time data of infected cases of COVID-19 from WHO situation report. They are confirmed that R_0 of COVID is higher than SARS and has a higher rate of transmissibility. They have stressed that for effective control of COVID, proper control measures have to be taken quickly to make the R_0 less than 1 (Talukder et al., 2020).

Joanna Nicho compares the vaccination percentage for herd immunity SIR epidemiology model against the current percentage of vaccinated individuals (Nicho, 2010). O. D. Makinde presents a SIR model with a constant vaccination technique. He shows that the vaccine has full efficacy, so that the vaccinated peoples will not be re-infected (Makinde, 2007). Later, Samuel Y. Akinyemi and his coauthors have constructed the SIR model that includes vaccination, immunity loss, and relapse (Akinyemi et al., 2016).

3. Methodology of the Study

In this paper we have formulated SIR model with some initial values for systems of ordinary differential equations, and later the model is analyzed mathematically. We have provided some theorems with proof. We have also stressed on vaccination to create herd immunity against COVID-19. Some mathematical procedures are given on the support of it if immunity of vaccines loss. We have tried to provide mathematical analysis if once infected and recovered persons are re-infected due to COVID-19. We have given a section on the basic reproduction number R_0 and stability of SIR model is given in briefly. The article is prepared depending on the secondary data sources that are collected from previous research articles, published books, websites, etc.

In the study we have tried to maintain the reliability and validity throughout the research (Mohajan, 2017). To make this article meaningful we have followed both quantitative and qualitative research methodology (Mohajan, 2018, 2020c).

4. Objective of the Study

The main objective of this article is to construct a reliable SIR model for analyzing the pandemic COVID-19 in some details. The other minor objectives of the model are as follows:

- to display the mathematical analysis more clearly,
- to analyze the theoretical explanations properly, and
- to express the usefulness of vaccine for growing herd immunity.

5. Overview of COVID-19

The SARS-CoV-2 is a new human coronavirus which developed at the end of December 2019 in Wuhan, Hubei Province, China, which affects lungs, with severe acute respiratory illness that develop a fever, dry cough, fatigue, and shortness of breath (WHO, 2020a). The most common symptoms of these disease are; fever, coughing, shortness of breath or difficulty in breathing (Lu et al., 2020). Minor to 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. A COVID-19 infected patient may experience one or more symptoms. In some cases infection happened without any symptoms. Some patients experienced loss of taste, appetite or smell (Carlos et al., 2020; Huang et al., 2020; Mohajan, 2021a, b; Ren et al., 2020; Wang et al., 2020). On 11 March 2020, the WHO declared the global outbreak as a pandemic to minimize the infection and mortality rate (WHO, 2020b). Public health responses for SARS-CoV-2 are isolation, quarantines, travel restriction, stop of workplace, closures of educational institution, and ultimately lockdown (Rothan & Byrareddy, 2020). On 12 December 2021, the disease spread up to 222 countries and territories globally; total confirmed deaths become 5,156,403, total confirmed cases 257,007,274, with total recovery 232,049,587; and also with highest deaths and infections in the USA (Worldometer, 2021).

6. Notation and Elementary Discussions

Let us consider a sufficiently large constant size of population *N*, and assume that births and natural deaths are equal. Also newborns and all people of different ages are susceptible. In this model, there are only three compartments: Susceptible $S(t)$, Infected $I(t)$, and recovered $R(t)$, for all $t \in [0,\infty)$. We assume that each individual of the total population is either susceptible, infectious or recovered from the disease with life-long immunity. The process can be represented by (Murray, 2002; Capasso, 2008),

$$S(t) \to I(t) \to R(t). \qquad (1)$$

It is a classical mathematical model of dynamic epidemical. The number of people who become infected per unit of time in epidemiology is called incidence rate. In the SIR model, incidence rate, as well as treatment rate plays an important role while analyzing the transmission of diseases. Since in SIR model an epidemic occurs relatively quickly, the model does not include births and deaths (Dubey et al., 2015). The model was built based on the data of the infected persons, discharged patients, and also discharged patients during the period of isolation and control (Harko et al., 2014). In SIR model, there is no difference between those who are recovered and those who are died; all of them are kept into compartment $R(t)$. In this model, assumes that the population is homogeneous and there is no vital dynamics, that is, the total population remains constant (da Silva, 2021). The three compartments are defined as follows (Padua & Tulang, 2010; Tang et al., 2020):

Susceptible: The susceptible refers to a group of people who are not yet infected but may be infected with the SARS-CoV-2 virus or any other virus at any time. Total number of susceptible people at time *t* is denoted by $S(t)$.

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. Total number of infective people at time *t* is denoted by $I(t)$.

Removal: The removed refers to a group of people who have been removed from the COVID-19 infected people, such as died, isolated or recovered and are immunized to the SARS-CoV-2 virus. Let $R(t)$ is the number of recovered/removed individuals who are removed from the population by recovery, immunization, hospitalization, death or by any other means. In our

model, the removed group consists of both recovered individuals, as well as the deaths caused by COVID-19.

7. Formulation of SIR Model

The SIR model is an epidemiological model that computes the theoretical number of people infected with a contagious illness within a closed population over time (Kermack & Mackendrick, 1927). In SIR model, let $b > 0$ is the contact or infection or transmission rate, and $c > 0$ is the recovery rate of the disease, and these parameters are determined depending on the fraction of the infected population, $I(t)$ changes over time (Nicho, 2010; Yang et al., 2021). Therefore, an infected individual able to transmit the disease with $bN(t)$ others in per unit time and the fraction of contacts by an infected with a susceptible is $\frac{S(t)}{N(t)}$. The number of new infection in unit time is $bN(t).\frac{S(t)}{N(t)}$ that gives the rate of new infections as $bN(t).\frac{S(t)}{N(t)}.I(t) = bS(t)I(t)$ (Bhattacharya et al., 2015). Therefore, in the $S(t)$ compartment, $bS(t)I(t)$ individuals will be decreased; whereas in the $I(t)$ compartment, $bS(t)I(t)$ individuals will be increased, and $cI(t)$ individuals will be reduced due to recovery. In the $R(t)$ compartment, $cI(t)$ recovery individuals will be added. The SIR model can be written using ordinary differential equations as (Hethcote, 1989; Murray, 2002);

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

$$\frac{dI(t)}{dt} = bS(t)I(t) - cI(t) \tag{3}$$

$$\frac{dR(t)}{dt} = cI(t) \tag{4}$$

where $r = \frac{c}{b}$ is relative removal rate. Equation (2) indicates that, $\frac{dS(t)}{dt} < 0$, i.e., in the elapse of time, the people in $S(t)$ compartment will be decreased. $I(t)$ initially increases exponentially, then moves to a plateau, and finally shrinks to zero if the disease is abolished completely after a

finite time interval (Baez-Sanchez & Bobko, 2020; Bernardi & Aminian, 2021). At $t = 0$ the initial conditions of the model are (Murray, 2002),

$$S(0) = S_0 > 0, I(0) = I_0 > 0, R(0) = 0 \text{, with } I_0 << S_0. \quad (5)$$

For disease free equilibrium, $S(t) = S_0$, $I(t) = 0$, and $R(t) = 0$. The time-dependent SIR model is much better to track the disease spread, control, and predict the future trend. Equations (2), (3), and (4) represent first-order non-linear differential equations of the SIR model (Dubey et al., 2015). Epidemic is controlled if $S_0 < r$. The flowchart of SIR model is given in Figure 1, where the boxes denote compartments, and arrows indicate flux between the compartments.

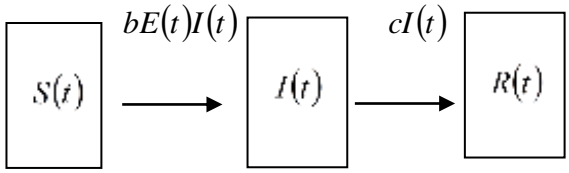

Figure 1: Flowchart of SIR model that displays the flux between the three compartments: $S(t)$, $I(t)$, and $R(t)$.

Adding (2), (3), and (4) we get (Murray, 2002),

$$\frac{dS(t)}{dt} + \frac{dI(t)}{dt} + \frac{dR(t)}{dt} = 0. \quad (6)$$

Integrating (6) we get the total population size in the SIR model as,

$$S(t) + I(t) + R(t) = N(t) = N \text{ (constant)}. \quad (7)$$

For susceptible-infectious-susceptible (SIS) case, if a susceptible becomes sick, then recovers without immunity is consider SIS, for example, the common cold, i.e., if $R(t) = 0$, i.e., if there is no recovery or no death happen due to disease we get, $S(t) + I(t) = N$, for all $t \in [0, \infty)$, and remain within the triangle (Figure 2).

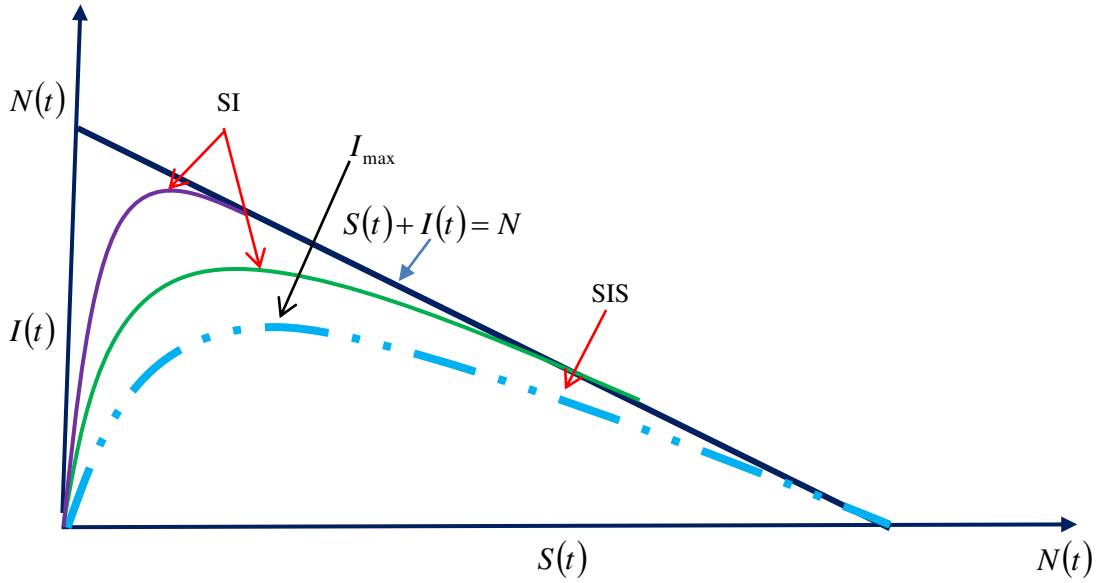

Figure 2: Solution curves for SIS.

Theorem 1: In SIR model, $S(t)$ is susceptible, and $I(t)$ is infected at an arbitrary time t. At $t=0$ the initial conditions are, $S(0)=S_0>0$, and $I(0)=I_0>0$, then,

i) $I(t)_{\max}=I_0+S_0-r+r\ln\frac{r}{S_0}$, where $r=\frac{c}{b}$ is relative removal rate and in the model r is independent of time.

ii) $S(t)=\exp\left[\ln S_0-b\left(I_0+S_0-r+r\ln\frac{r}{S_0}\right)t\right]$, for $I(t)_{\max}$, and

iii) $R(t)=c\left(I_0+S_0-r+r\ln\frac{r}{S_0}\right)t$, for $I(t)_{\max}$.

Proof: In SIR model, $S(t)$ is susceptible, and $I(t)$ infected at an arbitrary time t. At $t=0$ the initial conditions are, $S(0)=S_0>0$ and $I(0)=I_0>0$. Dividing (3) by (2) we get,

$$\frac{dI(t)}{dS(t)}=\frac{cI(t)-bS(t)I(t)}{bS(t)I(t)}=\frac{c}{bS(t)}-1=\frac{r}{S(t)}-1. \qquad (8)$$

Integrating (8) we get,

$$\int dI(t) = \int \frac{r}{S(t)} dS(t) - \int dS(t)$$

$$I(t) = r \ln S(t) - S(t) + A_1 . \quad (9)$$

Using initial conditions in (9) we get,

$$I_0 = r \ln S_0 - S_0 + A_1$$

$$A_1 = I_0 - r \ln S_0 + S_0 .$$

Hence, $$I(t) = r \ln S(t) - S(t) + I_0 - r \ln S_0 + S_0$$

$$I(t) = I_0 + S_0 - S(t) + r \ln \frac{S(t)}{S_0} .$$

$I(t)$ will be maximum if, $\frac{dI(t)}{dt} = 0$, then (3) becomes,

$$(bS(t) - c) I(t) = 0$$

$$S(t) = \frac{c}{b} = r \text{, since } I(t) \neq 0 .$$

Hence, $$I(t)_{\max} = I_0 + S_0 - r + r \ln \frac{r}{S_0} . \quad (10)$$

Using (10) in (2) we get,

$$\frac{dS(t)}{S(t)} = -b \left(I_0 + S_0 - r + r \ln \frac{r}{S_0} \right) dt .$$

Integrating we get,

$$\ln S(t) = -b \left(I_0 + S_0 - r + r \ln \frac{r}{S_0} \right) t + A_2$$

Using initial condition, $S(0) = S_0 > 0$ at $t = 0$ we get, $A_2 = \ln S_0$

Hence, $$\ln S(t) = -b \left(I_0 + S_0 - r + r \ln \frac{r}{S_0} \right) t + \ln S_0$$

$$S(t) = \exp \left[\ln S_0 - b \left(I_0 + S_0 - r + r \ln \frac{r}{S_0} \right) t \right] .$$

Using (10) in (4) we get,

$$\frac{dR(t)}{dt} = c \left(I_0 + S_0 - r + r \ln \frac{r}{S_0} \right) . \quad (11)$$

Integrating we get,

$$R(t)=c\left(I_0+S_0-r+r\ln\frac{r}{S_0}\right)t+A_3. \tag{12}$$

Using initial condition $R(0)=0$ at $t=0$ we get, $A_3=0$. Hence,

$$R(t)=c\left(I_0+S_0-r+r\ln\frac{r}{S_0}\right)t. \tag{13}$$

Theorem 2: In SIR model, $S(t)$ susceptive, and $R(t)$ is recovery/dead at an arbitrary time *t*. At $t=0$ the initial conditions are, $S(0)=S_0>0$, $R(0)=0,$ then,

i) $S(t)=e^{-\frac{1}{r}R(t)+\ln S_0}$

ii) $R(t)=r\ln\frac{S_0}{S(t)}$

iii) $t=\frac{1}{c}\int_0^R\frac{dR}{N(t)-e^{-\frac{1}{r}R(t)+\ln S_0}-R_\infty}$, where $r=\frac{c}{b}$ is relative removal rate.

Proof: Dividing (4) by (2) we get,

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

$$\Rightarrow\frac{dS(t)}{S(t)}=-\frac{b}{c}dR(t). \tag{14}$$

Integrating (14) we get,

$$\int\frac{dS(t)}{S(t)}=-\frac{b}{c}\int dR(t)$$

$$\ln S(t)=-\frac{1}{r}R(t)+A_4. \tag{15}$$

At $t=0$ the initial conditions are, $S(0)=S_0>0$ and $R(0)=0$, then (15) gives, $A_4=\ln S_0$.

Hence, $$\ln S(t)=-\frac{1}{r}R(t)+\ln S_0$$

$$S(t)=e^{-\frac{1}{r}R(t)+\ln S_0}$$

$$\frac{1}{r}R(t) = \ln S_0 - \ln S(t)$$

$$R(t) = r \ln \frac{S_0}{S(t)}.$$

Again we have,

$$S(t) + I(t) + R(t) = N(t)$$

$$\Rightarrow I(t) = N(t) - S(t) - R(t). \tag{16}$$

By using (16) in (4) we get,

$$\frac{dR(t)}{dt} = c\left[N(t) - S(t) - R(t)\right]. \tag{17}$$

Integrating (17) we get,

$$t = \frac{1}{c}\int_0^R \frac{dR(t)}{N(t) - e^{-\frac{1}{r}R(t) + \ln S_0} - R(t)}. \tag{18}$$

Equation (18) gives the time of recovery of the disease. As pandemic becomes at steady state when $t \to \infty$, hence (17) gives,

$$\frac{dR(t)}{dt} = 0. \tag{19}$$

Integrating (19) we get,

$$R(t) = \text{constant} = R_\infty, \text{ say.}$$

Then (18) becomes,

$$t = \frac{1}{c}\int_0^R \frac{dR}{N(t) - e^{-\frac{1}{r}R(t) + \ln S_0} - R_\infty}. \tag{20}$$

Theorem 3: In SIR model, $S(t)$ is susceptive, $I(t)$ infected, and $R(t)$ is recovery/dead at an arbitrary time *t*, then $\forall t \geq 0$,

i) $S_0 \leq S(t) \leq N(t)$

ii) $I_0 \leq I(t) \leq N(t)$, and

iii) $0 \leq R(t) \leq N(t)$.

Proof: i) For $t = 0$, $S(0) = S_0 > 0$ and for $0 < t < \infty$ we have,

$$S(t) = e^{-\frac{1}{r}R(t)+\ln S_0} > 0.$$

Almost all the individuals in the society are susceptible. Some of the individuals or everybody in the society has a probability of infection by COVID-19. Consequently, $S(t) \le N(t)$. For $t \to \infty$,

$$S(t) = S_\infty \le N(t).$$

Hence, $$S_0 \le S(t) \le N(t).$$

ii) For $t = 0$, $I(0) = I_0 > 0$, and for $t > 0$ we have,

$$I(t) = I_0 + S_0 - r + r \ln \frac{r}{S_0} \ge 0.$$

Almost all the individuals may be infected, i.e., some of the individuals or everybody in the society can be infected by COVID-19 or nobody can be infected. Consequently, $I(t) \le N(t)$. For $t \to \infty$,

$$I(t) = I_\infty \le N(t).$$

Hence, $$I_0 \le I(t) \le N(t).$$

iii) For $t = 0$, $R(0) = 0$, i.e., before the COVID-19 pandemic outbreak everybody in the society were COVID-19 disease free. For $0 < t < \infty$ we have,

$$R(t) = r \ln \frac{S_0}{S(t)} \ge 0.$$

Almost all the infected individuals can be recovered. Some of the infected individuals or all the members of the society can be recovered from COVID-19. On the other hand, some or all from COVID-19 infected persons may die. Both recovered and death individuals are removed from the $R(t)$ compartment. Consequently, $R(t) \le N(t)$. For $t \to \infty$ we have, $R(t) = R_\infty \le N(t)$

Hence, $$0 \le R(t) \le N(t).$$

7.1. SIR Model with Death

Let in a particular time *t*, the population of the world is constant, so that, the birth rate is equal to death rate. Let the birth rate be, $a > 0$, and also the death rate be, $\delta > 0$; consequently, $a = \delta$.

Let the new born babies are quite healthy but susceptible, i.e., $B(t)=aN(t)$ susceptible individuals will in total populations. Since b is the contact rate, in the $S(t)$ compartment, $bS(t)I(t)$ will be decreased. On the other hand, the individuals of $I(t)$ compartment, $bS(t)I(t)$ will be increased. Since c is the recovery rate of disease, in the $I(t)$ compartment, $cI(t)$ individuals will be reduced (Baez-Sanchez & Bobko, 2020; Bernardi & Aminian, 2021). In the $S(t)$, $I(t)$, and $R(t)$ compartments the amount of death are $\delta S(t)$, $\delta I(t)$, and $\delta R(t)$ respectively. Then equations of SIR model can be written as (Hethcote, 1989; Makinde, 2007);

$$\frac{dS(t)}{dt}=aN(t)-bS(t)I(t)-\delta S(t) \tag{21}$$

$$\frac{dI(t)}{dt}=bS(t)I(t)-cI(t)-\delta I(t) \tag{22}$$

$$\frac{dR(t)}{dt}=cI(t)-\delta R(t) \tag{23}$$

where $S(0)\geq 0$, $I(0)>0$, $R(0)\geq 0$. The flowchart of SIR model by considering both death and birth is given in Figure 3 (Murray, 2002).

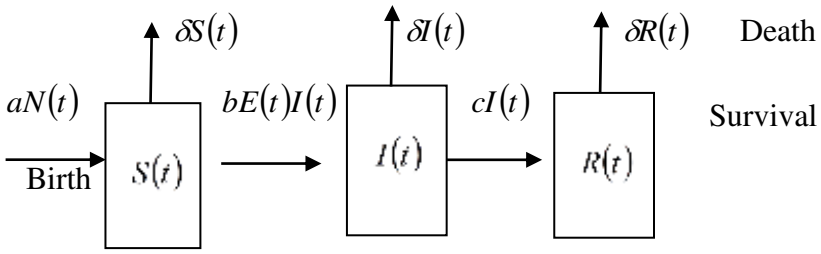

Figure 3: Flowchart of SIR model considering death and birth.

Theorem 4: In SIR model, $S(t)$ is susceptible, and $I(t)$ infected at an arbitrary time t. At $t=0$ the initial conditions are, $S(0)=S_0>0$, and $I(0)=I_0>0$. Consider birth rate equals death rate, i.e., $a=\delta$, also consider there is no removal, i.e., $R(t)=0$, then,

$$I(t)=I_0+S_0-S(t)+r\ln\frac{bS(t)-\delta}{bS_0-\delta}.$$

Proof: Dividing (22) by (21) we get,

$$\frac{dI(t)}{dS(t)}=\frac{bS(t)I(t)-cI(t)-\delta I(t)}{aN(t)-bS(t)I(t)-\delta S(t)} \tag{24}$$

If there is no removal, i.e., $R(t)=0$ we get, $N(t)=S(t)+I(t)$, also $a=\delta$, then (24) becomes,

$$\frac{dI(t)}{dS(t)}=\frac{bS(t)I(t)-cI(t)-\delta I(t)}{\delta I(t)-bS(t)I(t)}=\frac{bS(t)-c-\delta}{\delta-bS(t)}=-1+\frac{c}{bS(t)-\delta}$$

$$dI(t)=-dS(t)-\frac{cdS(t)}{\delta-bS(t)}$$

$$I(t)=-S(t)+\frac{c}{b}\ln(bS(t)-\delta)$$

$$I(t)=-S(t)+\ln(bS(t)-\delta)^{r}+A_5.$$

Using initial conditions: $S(t)=S_0$, $I(t)=I_0$ we get,

$$I_0=-S_0+\ln(bS_0-\delta)^{r}+A_5$$

$$A_5=I_0+S_0+\ln(bS_0-d)^{-r}$$

$$I(t)=I_0+S_0-S(t)+r\ln\frac{bS(t)-\delta}{bS_0-\delta}. \qquad (25)$$

Theorem 5: If all infected are removed, i.e., if all infected are recovered or some recovered and the rest (very few) are died then, $I(t)\to R(t)$, hence for $R(t)=0$ at $t=0$, then,

i) $R(t)=e^{(c-\delta)t}$,

ii) $R(t)=\frac{\delta-c}{b}\ln\{(bS(t)-\delta)(bS_0-\delta)\}$,

iii) $S(t)=\frac{\exp\left\{\frac{\delta-c}{b}e^{(c-\delta)t}\right\}}{b(bS_0-\delta)}+\frac{\delta}{b}$.

Proof: i) From (23) we get,

$$\frac{dR(t)}{R(t)}=(c-\delta)dt$$

$$\ln R(t)=(c-\delta)t+A_6.$$

Using initial condition $R(t)=0$ at $t=0$ we get, $A_6=0$.

$$\ln R(t)=(c-\delta)t$$

$$R(t)=e^{(c-\delta)t}. \qquad (26)$$

ii) Dividing (21) by (23) we get,

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

$$\frac{dS(t)}{dR(t)} = \frac{(\delta - bS(t))R(t)}{(c-\delta)R(t)}$$

$$\frac{dS(t)}{\delta - bS(t)} = \frac{1}{c-\delta} dR(t).$$

Integrating we get,

$$-\frac{\ln(\delta - bS(t))}{b} = \frac{R(t)}{c-\delta} + A_7 .$$

Using initial conditions: $S(0) = S_0$, and $R(t) = 0$ at $t = 0$ we get, $A_7 = \frac{\ln(\delta - bS_0)}{b}$.

Hence,
$$-\frac{\ln(\delta - bS(t))}{b} = \frac{R(t)}{c-\delta} + \frac{\ln(\delta - bS_0)}{b}$$

$$R(t) = \frac{\delta - c}{b} \ln\{(bS(t) - \delta)(bS_0 - \delta)\}. \quad (27)$$

iii) Equalizing (26) and (27) we get,

$$e^{(c-\delta)t} = \frac{\delta - c}{b} \ln\{(bS(t) - \delta)(bS_0 - \delta)\}$$

$$e^{(c-\delta)t} = \ln\{(bS(t) - \delta)(bS_0 - \delta)\}^{\frac{\delta - c}{b}}$$

$$\exp\{e^{(c-\delta)t}\} = \{(bS(t) - \delta)(bS_0 - \delta)\}^{\frac{\delta - c}{b}}$$

$$\exp\{e^{(c-\delta)t}\} = (bS(t) - \delta)^{\frac{\delta - c}{b}} (bS_0 - \delta)^{\frac{\delta - c}{b}}$$

$$(bS(t) - \delta) = \frac{\exp\left\{\frac{\delta - c}{b} e^{(c-\delta)t}\right\}}{(\delta b S_0 - \delta)}$$

$$S(t) = \frac{\exp\left\{\frac{\delta - c}{b} e^{(c-\delta)t}\right\}}{b(bS_0 - \delta)} + \frac{\delta}{b}. \quad (28)$$

7.2. Vaccine Efficiency of COVID-19

Individuals who have taken a full dose of vaccine and they acquire immunity to a particular infectious disease. A population is said to have herd immunity for COVID-19 if enough people are immune so that the disease would not spread. In the society, the population is homogeneously mixing and the immune people are distributed uniformly in the population. Herd immunity is obtained by the vaccination to a higher percentage people. After growing immunization, the individuals move from the $S(t)$ compartment to the $R(t)$ compartment, where death will not be happened in these immunized people (Nicho, 2010).

It is now proved that COVID-19 is preventable through vaccination. If enough people are immune, COVID-19 will not spread. As COVID-19 is highly contagious, to grow herd immunity, mass people need to be vaccinated that will prevent the initial spread of the disease. The model predicts how many people should be vaccinated so that the entire community will be in herd immunity. In our model, we consider that our vaccine is 100% efficacy. As a result, our vaccine gives permanent immunity to the vaccinated people. 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 vaccinated will avoid the susceptible class and move directly to the recovered class. On the other hand, the unvaccinated individuals will go into the susceptible class. Therefore, the total populations that are vaccinated is $aN(t)p$, which will be added in the recovery compartment $R(t)$. On the other hand, the unvaccinated populations is $aN(t)(1-p)$, which still remain in the susceptible compartment $S(t)$ (Porwal et al., 2015). After vaccination the equations of SIR model can be written as;

$$\frac{dS(t)}{dt} = aN(t)(1-p) - bS(t)I(t) - \delta S(t) \tag{29}$$

$$\frac{dI(t)}{dt} = bS(t)I(t) - cI(t) - \delta I(t) \tag{30}$$

$$\frac{dR(t)}{dt} = cI(t) - \delta R(t) + aN(t)p\,. \tag{31}$$

The flowchart of herd immunity formed by vaccinated people is given in Figure 4.

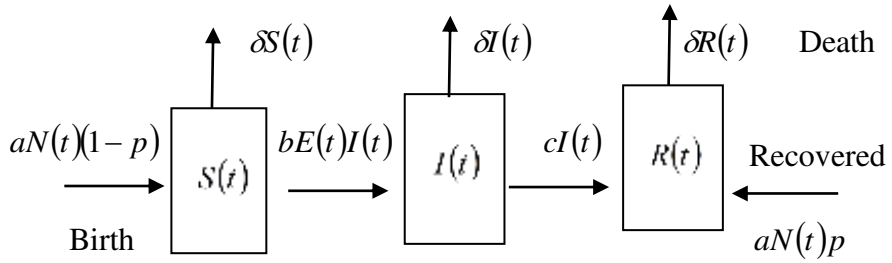

Figure 4: Flowchart of SIR model after vaccination considering death and birth.

Theorem 6: In SIR model, assume, $p = 0.5$, $S(t) = 4I(t)$, and $R(t) = 0$, i.e., $N(t) = S(t) + I(t) = 5I(t)$, then, $\delta = \frac{17}{47}c$.

Proof: Dividing (28) by (29) we get,

$$\frac{dS(t)}{dI(t)} = \frac{\delta N(t)(1-p) - bS(t)I(t) - \delta S(t)}{bS(t)I(t) - cI(t) - \delta I(t)}. \tag{32}$$

Let us consider that there is no more death happen except natural death, i.e., $R(t) = 0$, and $N(t) = S(t) + I(t)$, then (32) becomes,

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

$$\frac{dS(t)}{dI(t)} = \frac{-\delta pS(t) + \delta(1-p)I(t) - bS(t)I(t)}{bS(t)I(t) - cI(t) - \delta I(t)}. \tag{33}$$

Equation (33) is highly non-linear, and we impose a condition to obtain an approximate solution, such that, $S(t) = 4I(t)$, i.e., susceptible individuals are four times of infected individuals then,

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

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

$$16bI(t) - 4c - 4\delta = -4\delta p + \delta(1-p) - 4bI(t)$$

$$20bI(t) = 4c + 5\delta - 5\delta p$$

$$I(t) = \frac{4c + 5\delta - 5\delta p}{20b}. \tag{34}$$

Dividing (29) by (31) for $N(t)=S(t)+I(t)=5I(t)$, we get,

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

$$\frac{dS(t)}{dR(t)}=\frac{-\delta pS(t)+\delta(1-p)I(t)-bS(t)I(t)}{cI(t)-\delta R(t)+\delta S(t)p+\delta I(t)p}. \tag{35}$$

Equation (35) is highly non-linear and we impose two conditions, such that, $S(t)=4I(t)$, and $I(t)=4R(t)$ then,

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

$$16=\frac{-4\delta p+\delta(1-p)-4bI(t)}{c-\frac{\delta}{4}+4\delta p+\delta p}$$

$$-4bI(t)=16c-5\delta+85\delta p$$

$$I(t)=\frac{5\delta-16c+85\delta p}{4b}. \tag{36}$$

Equalize (34) and (36) we get,

$$\frac{4c+5\delta-5\delta p}{5}=5\delta-16c+85\delta p$$

$$4\delta-17c+86\delta p=0.$$

Let $p=0.5$, then

$$4\delta-17c+43\delta=0$$

$$\Rightarrow\delta=\frac{17}{47}c. \tag{37}$$

In this situation the death rate is $\frac{17}{47}$ times the infection rate, i.e., if $c=47$, then $\delta=17$.

7.3. Immunity Loss of Vaccine

In section 7.2 we have assumed that vaccine is 100% efficacy. In real field, no vaccine gives full protection to COVID-19 or other epidemic disease. Therefore, vaccinated individuals are not fully immunized. Overtime the immunity due to vaccination will decrease and after a fixed

period the immunity of COVID-19 due to vaccination will be disappeared. At that situation, the vaccinated people will be susceptible to COVID-19 (Fine et al., 2011; Akinyemi et al., 2016). Let $e > 0$ be the rate of immunity loss, then in $R(t)$ compartment, $eR(t)$ people will reduced due to loss of immunity, and these $eR(t)$ individuals will add in $S(t)$ compartment (Milligan & Barrett, 2015). The system of equations in SIR model becomes,

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

$$\frac{dI(t)}{dt} = bS(t)I(t) - cI(t) - \delta I(t) \tag{39}$$

$$\frac{dR(t)}{dt} = cI(t) - \delta R(t) + aN(t)p - eR(t). \tag{40}$$

The flowchart after immunity loss of vaccine can be shown as in Figure 5;

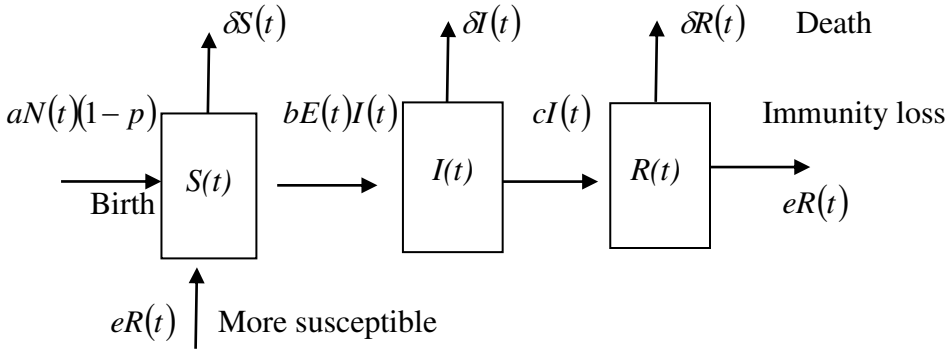

Figure 5: Flowchart of SIR model after immunity loss of vaccine considering death and birth.

Theorem 7: In SIR model, if $p = 0.5$, and $R(t) = 0$, i.e., $N(t) = S(t) + I(t) = 5I(t)$, and $S(t) = 4I(t)$, then, $e = \frac{152}{43}c + \frac{370}{43}\delta$,. Further, if $c = 0.035$, $\delta = 0.007$, then, $e = 0.18395$.

Proof: Dividing (43) by (44) we get,

$$\frac{dS(t)}{dI(t)} = \frac{aN(t)(1-p) - bS(t)I(t) - \delta S(t) + eR(t)}{bS(t)I(t) - cI(t) - \delta I(t)}. \tag{41}$$

Equation (41) is highly non-linear and we impose some conditions to find an approximate solution, such that, $N(t) = S(t) + I(t) = 5I(t)$, and $p = 0.5$, $a = \delta$, then (41) gives,

$$\frac{4dI(t)}{dI(t)} = \frac{-\frac{3}{2}\delta I(t) - 4bI(t)I(t) + \frac{1}{4}eI(t)}{4bI(t)I(t) - cI(t) - \delta I(t)}$$

$$4 = \frac{-\frac{3}{2}\delta - 4bI(t) + \frac{1}{4}e}{4bI(t) - c - \delta}$$

$$20bI(t) = 4c + \frac{5}{2}\delta + \frac{1}{4}e$$

$$I(t) = \frac{4c + \frac{5}{2}\delta + \frac{1}{4}e}{20b}.$$

$$I(t) = \frac{c}{5b} + \frac{\delta}{8b} + \frac{e}{80b}. \tag{42}$$

Dividing (38) by (42) we get,

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

$$\frac{4dI(t)}{\frac{1}{4}dI(t)} = \frac{\frac{5}{2}\delta I(t) - 4bI(t)I(t) - 4\delta I(t) + \frac{1}{4}eI(t)}{cI(t) - \frac{1}{4}\delta I(t) + 5aI(t)p - \frac{1}{4}eI(t)}$$

$$16 = \frac{\frac{5}{2}\delta - 4bI(t) - 4\delta + \frac{1}{4}e}{c - \frac{1}{4}\delta + \frac{5}{2}a - \frac{1}{4}e}$$

$$I(t) = \frac{4c}{b} + \frac{75}{8b}\delta - \frac{17}{16b}e. \tag{43}$$

Equalizing (41) and (43) we get,

$$\frac{43e}{40} = \frac{19c}{5} + \frac{37}{4}\delta$$

$$e = \frac{152}{43}c + \frac{370}{43}\delta. \tag{44}$$

For $c = 0.035$, $\delta = 0.007$, from (44) we have, $e = 0.18395$.

7.4. Re-infected of COVID-19

A portion of first time infected persons that are recovered may be re-infected again. Some people of the world are re-infected again by COVID-19 (Akinyemi et al., 2016). 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 in the $I(t)$ compartment. Of the new 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 (Widyaningsih et al., 2018). The system of equations in SIR model becomes;

$$\frac{dS(t)}{dt} = aN(t)(1-p) - bS(t)I(t) - \delta S(t) + eR(t) \tag{44}$$

$$\frac{dI(t)}{dt} = bS(t)I(t) - cI(t) + gR(t) - (\delta + h)I(t) \tag{45}$$

$$\frac{dR(t)}{dt} = (c+h)cI(t) + aN(t)p - (\delta + e + g)R(t). \tag{46}$$

The flowchart after re-infected by epidemic disease or pandemic becomes as in Figure 6;

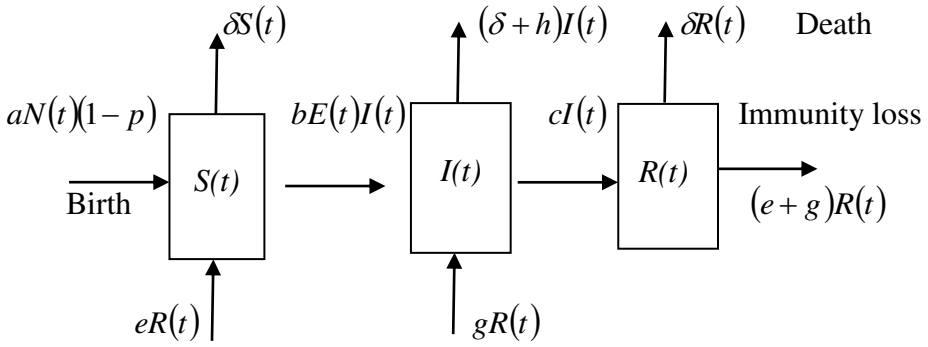

Figure 6: Flowchart of SIR model after re-infected considering death and birth.

Theorem 8: In SIR model, if $p = 0.5$, and $I(t) = 4R(t)$, and $S(t) = 4I(t)$, $g > 0$ be the rate of re-infected, and $h > 0$, be the death rate of the re-infected, $h = -c + \frac{g}{4} + \frac{9\delta}{4} + \frac{e}{4}$. Also if $c = 0.035$, $\delta = 0.0070$, $e = 0.18395$, let $g = 0.00001$, then, $h = 0.02676$.

Proof: Dividing (39) by (40) we get,

$$\frac{dS(t)}{dI(t)}=\frac{aN(t)(1-p)-bS(t)I(t)-\delta S(t)+eR(t)}{bS(t)I(t)-cI(t)+gR(t)-(\delta+h)I(t)} \tag{47}$$

Equation (40) is highly non-linear and we impose some conditions to find an approximate solution, such that, $N(t)=S(t)+I(t)+R(t)=4I(t)+I(t)+\frac{1}{4}I(t)=\frac{21}{4}I(t)$, $I(t)=4R(t)$, and $S(t)=4I(t)$, and $p=0.5$, $a=\delta$, then (47) gives,

$$\frac{4dI(t)}{dI(t)}=\frac{\frac{21}{8}\delta I(t)-4bI(t)I(t)-4\delta I(t)+\frac{1}{4}eI(t)}{4bI(t)I(t)-cI(t)+\frac{1}{4}gI(t)-(\delta+h)I(t)}$$

$$4=\frac{\frac{21}{8}\delta-4bI(t)-4\delta+\frac{1}{4}e}{4bI(t)-c+\frac{1}{4}g-(\delta+h)}$$

$$I(t)=\frac{c}{5b}-\frac{g}{20b}+\frac{53\delta}{80b}+\frac{h}{5b}+\frac{e}{80b}. \tag{48}$$

Dividing (39) by (41) we get,

$$\frac{dS(t)}{dR(t)}=\frac{aN(t)(1-p)-bS(t)I(t)-\delta S(t)+eR(t)}{(c+h)cI(t)+aN(t)p-(\delta+e+g)R(t)}$$

$$\frac{4I(t)}{\frac{1}{4}I(t)}=\frac{\frac{21}{8}\delta I(t)-4bI(t)I(t)-4\delta I(t)+\frac{1}{4}eI(t)}{(c+h)I(t)+\frac{21}{8}\delta I(t)-\frac{1}{4}(\delta+e+g)I(t)}$$

$$16=\frac{\frac{21}{8}\delta-4bI(t)-4\delta+\frac{1}{4}e}{c+h+\frac{21}{8}\delta-\frac{1}{4}(\delta+e+g)}$$

$$16c+16h+42\delta-4e-4g=\frac{21}{8}\delta-4bI(t)+\frac{1}{4}e$$

$$I(t)=-\frac{315\delta}{32b}+\frac{17e}{16b}+\frac{g}{b}-\frac{4c}{b}-\frac{4h}{b}. \tag{49}$$

Equalize (48) and (49) we get,

$$\frac{c}{5b}-\frac{g}{20b}+\frac{53\delta}{80b}+\frac{h}{5b}+\frac{e}{80b}=-\frac{4c}{b}+\frac{g}{b}-\frac{315\delta}{32b}+\frac{17e}{16b}-\frac{4h}{b}$$

$$h = -c + \frac{g}{4} - \frac{1681\delta}{160} + \frac{e}{4}. \tag{50}$$

We choose, $c = 0.035$, $\delta = 0.0007$, $e = 0.18395$, let $g = 0.00001$, then from (48) we get, $h = 0.003636$.

8. Stability of SIR Model

For the equilibrium points the equations (20), (21), and (22) should be equated to zero, i.e.,

$$\frac{dS(t)}{dt} = \frac{dS(t)}{dt} = \frac{dS(t)}{dt} = 0. \tag{51}$$

From (21) we get,

$$(bS(t) - c - \delta)I(t) = 0$$

$$S(t) = \frac{c+\delta}{b}. \tag{52}$$

From (22) we get,

$$cI(t) - \delta R(t) = 0$$

$$R(t) = \frac{c}{\delta} I(t). \tag{53}$$

From (20) we get,

$$N(t) - bS(t)I(t) - \delta S(t) = 0$$

$$N(t) = (bI(t) + \delta)S(t) = (bI(t) + \delta)\left(\frac{c+\delta}{b}\right) = N$$

$$I(t) = \left(\frac{N}{c+\delta}\right) - \frac{\delta}{b} \tag{54}$$

$$R(t) = \frac{c}{\delta}\left\{\left(\frac{N}{c+\delta}\right) - \frac{\delta}{b}\right\}. \tag{55}$$

9. Basic Reproductive Rate in SIR Model

In epidemiology, the basic reproduction number is the expected number of cases directly generated by one case in a population where all the individuals are susceptible to infection

(Fraser et al., 2009). In epidemiology, it is considered as one of the most important quantities and the number of invectives of it is produced by a primary infective in a fully susceptible virgin population (Ebraheem et al., 2021). It is not a biological constant for a pathogen, because it is affected by other factors, such as environmental conditions and the behavior of the infected population. It does not by itself give an estimate of how fast an infection spreads in the population (Delamater et al., 2019). There is no general method to calculate the basic reproduction number. It is widely varies depending on country, culture, calculation, stage of the outbreak. Different authors take different methods to determine R_0 for controlling the disease (Linka et al., 2020). If $R_0 < 1$, the infection is faded out in a population. If the infected individuals present in the population, there will be an epidemic if and only if $\frac{dI}{dt} > 0$ (Cao & Zhou, 2013). From (31) we get,

$$\Rightarrow bS(t)I(t) > (c+\delta)I(t)$$
$$\Rightarrow bS(t) > (c+\delta). \quad (56)$$

Let us consider initially at $t = 0$, death rate, $\delta = 0$, then from (56) we get (Bhattacharya et al., 2015),

$$bS_0 > c, \text{ i.e., } bS_0 - c > 0. \quad (57)$$

The initial behavior of COVID-19 is governed by the nature of $(bS_0 - c)$, i.e., of $\left(b\frac{S_0}{c} - 1\right)$. In SIR model, the term $b\frac{S_0}{c}$ is called basic reproductive rate at $t = 0$ and is denoted by (van den Driessche, 2017),

$$R_0 = b\frac{S_0}{c} = \frac{S_0}{r} = \frac{S_0}{S(t)}. \quad (58)$$

A key parameter in epidemiology is R_0 that represents the initial rate of spread of the disease. It is a threshold parameter for the SIR model (Khan et al., 2014). If $R_0 < 1$, disease free equilibrium of COVID-19 will be locally asymptotically stable. Then the number of infectious individuals decreases monotonically to zero and the disease will not spread. In this case, the introduced infected will recover or die without being able to replace themselves by new infections. If $R_0 > 1$, the COVID-19 will be unstable and number of infected persons will increase and the disease

will spread. For $R_0 = 1$, there will be a sharp threshold between the disease dying out or causing an epidemic (Heffernan et al., 2005; Linka et al., 2020).

10. Conclusions and Recommendation

In this study we have tried to discuss aspects of SIR model for the pandemic outbreak of COVID-19. It is considered as a powerful and flexible tool to understand the spread of disease and performing public health interventions. We observe that the SIR model provides a basic framework for the investigation of the pandemic COVID-19. Proper guidance and advices can help individuals to prevent and control of global pandemic in timely. In the model, the growth of infections and the duration of the pandemic COVID-19 are analyzed with detail mathematical calculations. We have seen that a susceptible individual becomes infectious after the buildup exposure is formed larger than its resistance level. In this paper, the vaccination, herd immunity grows and loss, re-infection, and abolish policy COVID-19 are discussed in some details. In this study we have tried to analyze the growth of infections, transmission, fatality, and the duration of the COVID-19 outbreak with the help of mathematical and theoretical analysis. We have also observed that if more people are vaccinated, more herd immunity will grow against highly contagious disease COVID-19. Vaccination program will be success only if a large portion of the population receives the vaccines. So that, to make the world COVID-19 free, a large portion of the global population irrespective of nation, religion, region, poor, and rich, must bring under vaccination. The public health officials, social workers, governments and common people must encourage actively others for vaccinating all the people.

References

Abadie, A., Bertolotti, P., Deaner, B., Sarker, P., & Shah, D. (2020). *Epidemic Modeling and Estimation*. Institute for Data, Systems, and Society, MIT.

Akinyemi, S. Y., Ibrahim, M. O., Usman, I. G., & Odetunde, O. (2016). Global Stability Analysis of SIR Epidemic Model with Relapse and Immunity Loss. *Applied Science Mathematical Theory*, 2(1), 1-12.

Assiri, A., Al-Tawfiq, J. A., Al-Rabeeah, A. A., & Al-Hajjar, A. et al. (2013). Epidemiological, Demographic, and Clinical Characteristics of 47 Cases of Middle East Respiratory Syndrome Coronavirus Disease from Saudi Arabia: A Descriptive Study. *The Lancet Infectious Diseases*, 13, 752-761.

Atangana, A. (2020). Modelling the Spread of COVID-19 with New Fractional-Fractal Operators: Can the Lockdown Save Mankind before Vaccination? *Chaos Solitons Fractals*, 136, 109860.

Atkeson, A. G. (2020). On Using SIR Models to Model Disease Scenarios for COVID-19. Federal Reserve Bank of Minneapolis, *Quarterly Review*, 41(1), 1-35.

Baez-Sanchez, A. D., & Bobko, N. (2020). On Equilibria Stability in an Epidemiological SIR Model with Recovery-dependent Infection Rate. *Tend˙encias em Matem´ atica Aplicada e Computacional*, 21(3), 409-424.

Bernardi, F., & Aminian, M. (2021). Epidemiology and the SIR Model: Historical Context to Modern Applications. *CODEE Journal*, 14(1), Article 4.

Bhattacharya, P., Paul, S., & Biswas, P. (2015). Mathematical Modeling of Treatment SIR Model with Respect to Variable Contact Rate. *International Proceedings of Economics Development and Research*, 83, 34-41.

Cao, H., & Zhou, H. (2013). The Basic Reproduction Number of Discrete SIR and SEIS Models with Periodic Parameters. *Discrete and Continuous Dynamical Systems Series B*, 18(1), 37-56.

Capasso, V. (2008). *Mathematical Structures of Epidemic Systems (2^{nd} Ed.)*. Heidelberg: Springer.

Carlos, W. G., Cruz, C. S., Cao, B., Pasnick, S., & Jamil, S. (2020). Novel Wuhan (2019-nCoV) Coronavirus. *American Journal of Respiratory and Critical Care Medicine*, 201(4), 7-8. https://doi.org/10.1164/rccm.2014P7

Chan, J. F.-W., Yuan, S., Kok, K.-H., To, K. K.-W., Chu, H., & Yang, J. et al. (2020). A Familial Cluster of Pneumonia Associated with the 2019 Novel Coronavirus Indicating Person-to-Person Transmission: A Study of a Family Cluster. *Lancet*, 395, 514–523. https://doi.org/10.1016/S0140-6736(20)30154-9

da Silva, A., (2021). Modeling COVID-19 in Cape Verde Islands: An Application of SIR Model. *Computational and Mathematical Biophysics*, 9, 1-13.

Delamater, P. L., Street, E. J., Leslie, T. F., Yang, Y. T., & Jacobsen, K. H. (2019). Complexity of the Basic Reproduction Number (R_0). *Emerging Infectious Diseases*, 25(1), 1-4.

Dubey, B., Dubey, P., & Dubey, U. S. (2015). Dynamics of an SIR Model with Nonlinear Incidence and Treatment Rate. *Applications and Applied Mathematics: An International Journal*, 10(2), 718-737.

Ebraheem, H. K., Alkhateeb, N., Badran, H., & Sultan, E. (2021). Delayed Dynamics of SIR Model for COVID-19. *Open Journal of Modelling and Simulation*, 9, 146-158.

Fine, P., Eames, K., & Heymann, D. L. (2011). Herd Immunity: A Rough Guide. *Clinical Infectious Diseases*, 52(7), 911-916.

Fraser, C., Donnelly, C. A., Cauchemez, S., Hanage, W. P., van Kerkhove, M. D., & Hollingsworth, T. D., et al. (2009). Pandemic Potential of a Strain of Influenza A (H1N1): Early Findings. *Science*, 324(5934), 1557-1561.

Ghersheen, S., Kozlov, V., Tkachev, V., & Wennergren, U. (2019). Mathematical Analysis of Complex SIR Model with Coinfection and Density Dependence. *Computational and Mathematical Methods*, 1, e1042.

Harko, T., Lobo, F. S. N., & Mak, M. K. (2014). Exact Analytical Solutions of the Susceptible-Infected-Recovered (SIR) Epidemic Model and of the SIR Model with Equal Death and Birth Rates. Applied Mathematics and Computation. 236, 184-194.

Heffernan, J. M., Smith, R. J., & Wahl, L. M. (2005). Perspectives on the Basic Reproductive Ratio. *Journal of the Royal Society Interface*, 2(4), 281-293.

Hethcote, H. W. (1989). Three Basic Epidemiological Models. In Levin S. A., Hallam T. G., & Gross L. J. (Eds.), Applied Mathematical Ecology. *Biomathematics*, vol. 18, pp. 119-144. Springer, Berlin, Heidelberg. https://doi.org/10.1007/978-3-642-61317-3_5

Huang, C., Wang, Y., Li, X., Ren, L., Zhao, J., & Hu, Y. et al. (2020). Clinical Features of Patients Infected with 2019 Novel Coronavirus in Wuhan, China. *Lancet*, 395(10223), 497–506. https://doi.org/10.1016/S0140-6736(20)30183-5

Kermack, N. O., & Mackendrick, A. G. (1927). Contribution to Mathematical Theory of Epidemics. *Proceedings of the Royal Society of London*, 115(772), 700-721.

Khan, A., Hassan, M., & Imran, M. (2014). Estimating the Basic Reproduction Number for Single-Strain Dengue Fever Epidemics, 3, 12.

Li, F. (2013). Receptor Recognition and Cross-Species Infections of SARS Coronavirus. *Antiviral Research*, 100(1), 246-254.

Linka, K., Peirlinck, M. & Kuhl, E. (2020). The Reproduction Number of COVID-19 and Its Correlation with Public Health Interventions. *Computational Mechanics*, 66, 1035-1050. https://doi.org/10.1007/s00466-020-01880-8

Lu, H., Stratton, C. W., & Tang, Y. W. (2020). Outbreak of Pneumonia of Unknown Etiology in Wuhan China: The Mystery and the Miracle. *Journal of Medical Virology*, 92(4), 401-402. https://doi.org/10.1002/jmv.25678

Makinde, O. D. (2007). Adomian Decomposition Approach to a SIR Epidemic Model with Constant Vaccination Strategy. *Applied Mathematics and Computation*, 184(2), 842-848.

Milligan, G., N., & Barrett, A. D. (2015). *Vaccinology: An Essential Guide*. Chichester, West Sussex: Wiley Blackwell.

Mohajan, H. K. (2017). Two Criteria for Good Measurements in Research: Validity and Reliability. *Annals of Spiru Haret University Economic Series*, 17(3), 58-82.

Mohajan, H. K. (2018). Qualitative Research Methodology in Social Sciences and Related Subjects. *Journal of Economic Development, Environment and People*, 2(1), 19-46.

Mohajan, H. K. (2020a). The COVID-19 in Italy: Remedies to Reduce the Infections and Deaths. *Malaysian Journal of Medical and Biological Research*, 7(2), 59-66.

Mohajan, H. K. (2020b). Most Fatal Pandemic COVID-19 Outbreak: An Analysis of Economic Consequences. *Annals of Spiru Haret University Economic Series*, 20(2), 127-146.

Mohajan, H. K. (2020c). Quantitative Research: A Successful Investigation in Natural and Social Sciences. *Journal of Economic Development, Environment and People*, 9(4), 52-79.

Mohajan, H. K. (2021a). *Aspects of Global COVID-19 Pandemic*. Lambert Academic Publishing, Germany.

Mohajan, H. K. (2021b). Global COVID-19 Pandemic: Prevention and Protection Techniques. *Journal of Economic Development, Environment and People*, 10(1), 51-72.

Mohajan, H. K. (2021c). Mathematical Analysis of SEIR Model to Prevent COVID-19 Pandemic (Unpublished Manuscript).

Murray, J. D. (2002). *Mathematical Biology I: An Introduction*. Springer-Verlag, New York, Inc.

Nicho, J. (2010). The SIR Epidemiology Model in Predicting Herd Immunity. *Undergraduate Journal of Mathematical Modeling*, 2(2), 8.

Padua, R. N., & Tulang, A. B. (2010). A Density–Dependent Epidemiological Model for the Spread of Infectious Diseases. *Liceo Journal of Higher Education Research*, 6(2), 1-30.

Porwal, P., Shrivastava, P., & Tiwari, S. K. (2015). Study of Simple SIR Epidemic Model. *Advances in Applied Science Research*, 6(4), 1-4.

Ren, L. L., Wang, Y. M., Wu, Z. Q., Xiang, Z. C., Guo, L., & Xu, T. et al. (2020). Identification of a Novel Coronavirus Causing Severe Pneumonia in Human: A Descriptive Study. *Chinese Medical Journal*, 1-10. https://doi.org/10.1097/CM9.0000000000000722

Rodrigues, H. S. (2016). Application of SIR Epidemiological Model: New Trends. *International Journal of Applied Mathematics and Informatics*, 10, 92-97.

Rothan, H. A., & Byrareddy, S. N. (2020). The Epidemiology and Pathogenesis of Coronavirus Dieses (COVID-19) Outbreak. *Journal of Autoimmunity*, 109, 102433. https://doi.org/10.1016/j.jaut.2020.102433

Song, P. X., Wang, L., Zhou, Y., He, J., Zhu, B., Wang, F., Tang, L. & Eisenberg, M. (2020). An Epidemiological Forecast Model and Software Assessing Interventions on COVID-19 Epidemic in China. MedRxiv preprint.

Talukder, H., Debnath, K., Raquib, A., Uddin, M. M., & Hussain, S. (2020). Estimation of Basic Reproduction Number (R_o) of Novel Coronavirus (COVID-19) from SEIR Model in Perspective of Bangladesh. *Journal of Infectious Diseases and Epidemiology*, 6, 144.

Tang, T., Cao, L., Lan, C.-Y., & Cao, L. (2020). SIR Model for Novel Coronavirus-Infected Transmission Process and Its Application. https://doi.org/10.21203/rs.3.rs-16297/v1

Uddin, R., & Algehyne, E. A. (2021). Mathematical Analysis of COVID-19 by Using SIR Model with Convex Incidence Rate. *Results in Physics*, 23, 103970.

van den Driessche, P. (2017). Reproduction Numbers of Infectious Disease Models. *Infectious Disease Modelling*, 2, 288-303.

Wacker, B., & Schlüter, J. (2020). Time-Continuous and Time-Discrete SIR Models Revisited: Theory and Applications. *Advances in Difference Equations*, 2020, 556.

Wang, C., Hornby, P. W., Hayden, F. G., & Gao, G. F. (2020). A Novel Coronavirus Outbreak of Global Health Concern. *Lancet*, 395(10223), 470-473. http://dx.doi.org/10.1016/S0140-6736(20)30185-9

Wesley, C. L., & Allen, L. J. S. (2009). The Basic Reproduction Number in Epidemic Models with Periodic Demographics. *Journal of Biological Dynamics*, 3(2-3), 116-129.

WHO (2020a). *Novel Coronavirus–China*. Geneva, Switzerland: World Health Organization.

WHO (2020b). *WHO Characterizes COVID-19 as a Pandemic*. World Health Organization (WHO).

Widyaningsih, P., Saputro, D. R. S., & Nugroho, A. W. (2018). Susceptible Exposed Infected Recovery (SEIR) Model with Immigration: Equilibria Points and Its Application. AIP Conference Proceedings 2014, 020165 (2018), AIP Publishing.

Worldometer (2021). COVID-19 Coronavirus Pandemic. American Library Association (ALA).

Yang, W., Zhang, D., Peng, L., Zhuge, C., & Hong, L. (2021). Rational Evaluation of Various Epidemic Models Based on the COVID-19 Data of China. *Epidemics*, 37, 100501. https://doi.org/10.1016/j.epidem.2021.100501

Zhu, W., & Shen, S. (2021). An Improved SIR Model Describing the Epidemic Dynamics of the COVID-19 in China. *Results in Physics*, 25, 104289.