CHANGING PERCEPTION THROUGH THE ART OF MATHEMATICAL MODELING

Sayooj Aby Jose[1*] and Raja R.[2,3]

[1]*Department of Mathematics, Alagappa University, Karaikudi-630 004, India*

[2]*Ramanujan Centre for Higher Mathematics, Alagappa University, Karaikudi-630 004, India*

[3]*Lebanese American University, Beirut, Lebanon*

[*]*Corresponding author: Sayooj Aby Jose, Email; sayoojaby999@gmail.com*

Abstract

Nowadays, infectious diseases are disorders caused by organisms - such as bacteria, viruses, fungi or parasites. Many organisms live in and on our bodies. They're normally harmless or even helpful. But certain microbes have the potential to cause disease in specific situations. It is possible for some infectious diseases to spread from person to person. Others are spread by animals or insects. In this study, we build certain fundamental models, such as SI, SIR, SIRS, and SEIR, and in numerical simulations, we take into account random parameters to determine the dynamics of the model's behavior. Finally, we present several studies in mathematical modeling of real situation relevant to epidemiology and population dynamic systems.

Keywords: *Art of mathemtical modeling, changing perception, infectious diseases.*

THAY ĐỔI NHẬN THỨC
THÔNG QUA NGHỆ THUẬT MÔ HÌNH TOÁN HỌC

Sayooj Aby Jose[1*] và Raja R.[2,3]

[1]Khoa Toán, Trường Đại học Alagappa, Ấn Độ

[2]Trung tâm Toán cao cấp Ramanujan, Trường Đại học Alagappa, Ấn Độ

[3]Trường Đại học Lebanese American, Lebanon

[*]Tác giả liên hệ: Sayooj Aby Jose, Email: sayoojaby999@gmail.com

Tóm tắt

Ngày nay, các bệnh truyền nhiễm là những rối loạn do sinh vật gây ra - chẳng hạn như vi khuẩn, vi rút, nấm hoặc ký sinh trùng. Nhiều sinh vật sống trong và trên cơ thể người. Những sinh vật này thường vô hại hoặc thậm chí hữu ích. Nhưng một số vi khuẩn có khả năng gây bệnh trong những tình huống cụ thể. Một số bệnh truyền nhiễm có thể lây lan từ người này sang người khác. Một số khác lây lan bởi động vật hoặc côn trùng. Trong nghiên cứu này, chúng tôi xây dựng một số mô hình cơ bản bao gồm SI, SIR, SIRS và SEIR, và trong các mô phỏng số, chúng tôi tính đến các tham số ngẫu nhiên để xác định động lực học của hành vi của mô hình. Cuối cùng, chúng tôi trình bày một số nghiên cứu về mô hình toán học của tình huống thực tế liên quan đến dịch tễ học và các hệ thống động dân số.

Từ khóa: Các bệnh truyền nhiễm, nghệ thuật mô hình toán học, thay đổi nhận thức.

1. Introduction

A model is a deliberate rendering of reality. Modeling entails researching processes and physical items, then employing replicas of those objects in other physical environments to simulate the behavior of the systems being researched. Even if a real-world issue can be generalized, it is rarely converted into a mathematical one. The ensuing mathematical issue might not be solvable. Therefore, it is important to idealize, simplify, or approximate the problem by another problem that is somewhat similar to the original problem and can be translated into and solved mathematically (Brauer & Castillo-Chavez, 2012). Since it existed through the use of mathematical models, physicists, mathematicians, engineers, astronomers, statisticians, and biologist are researching a wide range of problems well (Braun, 1993).

The word *epidemiology* is derived from the Greek words *epi* (upon), *demos* (the people), and *logos* (study, science), and means literally "the study of what is upon the people." More specifically, it is a branch of science within medicine that focuses on understanding the dynamics of a disease within a population, trying to predict the course of the disease, and ultimately coming up with ways to control it. Although it is applicable to any disease, such as cancer, metabolic syndrome, and swine influenza, we are specifically interested in human contagious diseases. Based on a few presumptions, the dynamics of the diseases are simulated and put into systems of nonlinear differential equations. The model's various parameters describe the rate of disease transmission, disease survival, disease recovery, population life expectancy, rate of immune system deterioration over time, and other aspects that are unique to a given disease.

2. Basic terminology

The models come in a variety of sorts based on the number of compartments. We must first comprehend several fundamental terms:

- Susceptible: An individual who is not infected but is at risk of getting sick.

- Exposed: A person who has the infection but does not show any outward symptoms.

- Infectious: An individual who is exhibiting symptoms of the illness and is contagious.

- Recovered/Removed: After receiving therapy, etc., the symptoms vanish, and the patient is no longer contagious.

- Incubation Period: It is the amount of time between being exposed to the infection and experiencing the first noticeable symptoms of the disease.

- Endemic: A disease is said to be endemic if it frequently affects a population or a specific region.

- Epidemic: If there are noticeably more cases of a disease within a short period of time in a particular community, it is considered to be in epidemic stage.

- Pandemic: A disease is said to be pandemic if it is prevalent in the entire country or the world.

Each of these classes has a different number of members, hence S(t), I(t), and R(t) are functions of time *t*. The sizes of these three classes add up to the overall population size *N*: N = S(t) +I(t) +R(t).

Next, we make assumptions in order to simplify reality in order to create a model. The Kermack-McKendrick model's first presumption is that diseased people are likewise contagious. The model's second presumption is that the size of the entire population doesn't change. Systems of ODEs that describe the dynamics in each class make up epidemiological models. The dynamics of susceptible, infectious, and recovered individuals are part of one of the most basic models. Kermack and McKendrick first proposed the approach in 1927 (Kermack & McKendrick, 1927). The system of nonlinear equations in epidemiology produces two equilibrium points: the disease-free equilibrium point and the endemic equilibrium point. By equating the system of equations to zero and finding the values of the relevant variables, these equilibrium points can be found. Only taking into account nonnegative solutions to the nonlinear system of differential equations is always useful from a biological perspective.

In epidemiology, the reproduction number gives the number of secondary cases one infectious individual will produce in a population consisting only of susceptible individuals. Mathematically, the reproduction number plays the role of a threshold value for the dynamics of the system and the disease. The basic reproduction number R_0 is equal to the spectral ratio of the matrix $J_f.J_v^{-1}$, where $F(z)$ is the rate of appearance of new

infections, $V(z)$ is the rate of transfer of individuals in and out of the infected compartment, and z describes the linearization of the reduced system around the disease free equilibrium, according to research by Diekmann and Heesterbeek and Van den Driessche and Watmough. Consider that any matrix's spectral ratio corresponds to its biggest eigenvalue. The fundamental reproduction number, R_0, as stated by Driessche et al. (Driessche & Watmough, 2002), may therefore be calculated as $R_0 = \rho(J_f.J_v^{-1})$, where J_f and J_v are the Jacobian matrices associated with $F(z)$ and $V(z)$ while ρ denotes the spectral radius of the matrix $J_f.J_v^{-1}$.

3. Some basic models and its dynamics

In this section we deal with SI, SIR, SIRS and SEIR models.

SI (Susceptible-Infected) Model: A fundamental epidemiological model for describing the spread of infectious diseases is the SI model. It goes without saying that there are only two possible states for people: susceptible or infected. Susceptible people are those who have not yet caught the disease, whereas infected persons are those who have. The SI model is employed to forecast both the number of people who will eventually become infected and its rate at which the disease will spread. The system in (1) is represented by the schematic diagram in Figure 1.
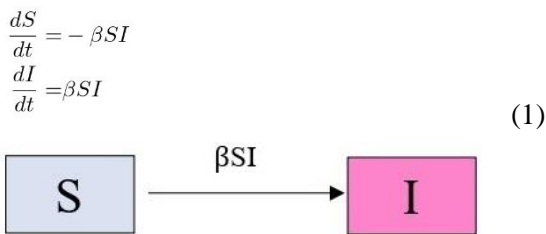
$$\frac{dS}{dt} = -\beta SI$$
$$\frac{dI}{dt} = \beta SI$$

$$(1)$$

Figure 1. Schematic Diagram of SI Model

SIR (Susceptible-Infected-Recovered) Model: The SIR model, an extension of the SI model, is used to explain how infectious diseases spread among people who may alternate between the three stages of susceptible, infected, and recovery. According to this paradigm, a person may go from being vulnerable to becoming sick, then from becoming infected to recovering. This model is used to forecast the number of individuals who will be infected over time, as well as the rate at which the disease will spread and the rate at which individuals will recover from the disease. The

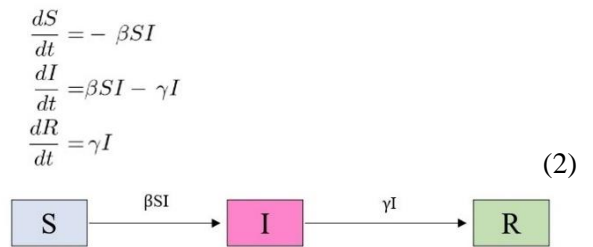schematic diagram in Figure 2 illustrates the system in (2):

$$\frac{dS}{dt} = -\beta SI$$
$$\frac{dI}{dt} = \beta SI - \gamma I$$
$$\frac{dR}{dt} = \gamma I$$

$$(2)$$

Figure 2. Schematic Diagram of SIR Model

SIRS (Susceptible-Infected-Recovered-Susceptible) Model: The SIRS model, an extension of the SIR model, is used to explain how infectious diseases spread among people who can alternate between four states: susceptible, infected, recovered, and susceptible once more. According to this paradigm, people can go from being susceptible to becoming sick, from becoming infected to recovering, and then from recovering to becoming susceptible once again. This model is used to forecast the amount of people who will contract the disease over time, as well as the rate at which the disease will spread and the rate at which individuals will recover from and become re-infected with the disease. The system (3) is depicted by the schematic diagram in Figure 3.
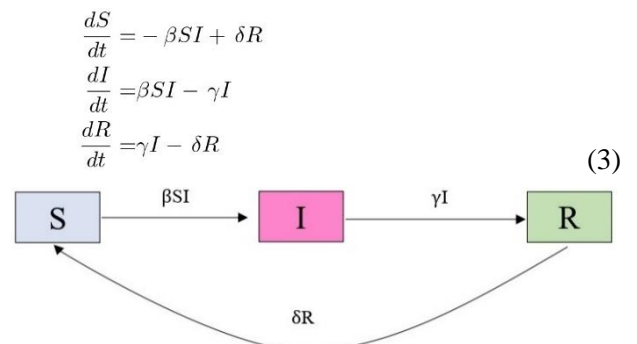
$$\frac{dS}{dt} = -\beta SI + \delta R$$
$$\frac{dI}{dt} = \beta SI - \gamma I$$
$$\frac{dR}{dt} = \gamma I - \delta R$$

$$(3)$$

Figure 3. Schematic Diagram of SIRS Model

Susceptibility-Exposed-Infection-Recovery (SEIR) Mode: As an extension of the SIRS model, the SEIR model is used to explain how infectious diseases spread among people who can alternate between four states: susceptible, exposed, infected, and recovered. According to this concept, people can go from being susceptible to being exposed, from being exposed to infected, and finally from infected to recovered. The number of people who will eventually interact with the disease, the rate at which it will spread, and the rate at which people

will be exposed to, develop it and recover from it are all predicted using this model. The schematic diagram of the system in (4) is shown in Figure 4.

$$\frac{dS}{dt} = -\beta SI + \delta R$$
$$\frac{dE}{dt} = \beta SI - \eta E$$
$$\frac{dI}{dt} = \eta E - \gamma I$$
$$\frac{dR}{dt} = \gamma I - \delta R$$

(4)
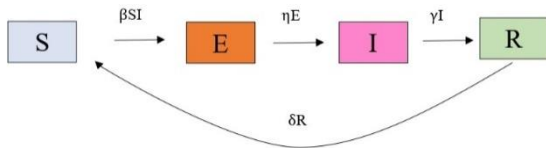
Figure 4. Schematic Diagram of SEIRS Model

Table 1. Description of Parameters of the models

Parameters	Description
β	Disease transmission rate
η	Progression rate to symptom development
γ	Recovery rate
δ	Rate of leaving the recovered class

4. Numerical Simulations

We conducted research using the four sets of random parameters listed in Table 2, Table 3, and Table 4. It displays various cases.

Table 2. Case I

Parameters	β	η	γ	δ
Value(day^{-1})	0.00213	0.03134	0.08	0.214

Table 3. Case II

Parameters	β	η	γ	δ
Value(day^{-1})	0.000513	0.0134	0.08	0.00414

Table 4. Case III

Parameters	β	η	γ	δ
Value(day^{-1})	0.0000613	0.134	0.08	0.0414

Figures 5 to 8 are displayed in Case I, Figure 9 to Figure 12 in Case II, and Figures 13 Figure 16 in Case III. Discuss each of the three scenarios in detail. The rate of change in susceptible individuals can be seen in Figure 5. We can deduce from Figure 5 that it initially reached its peak value, then decreased, and after 15 days, it has reached a steady state. The stimulation of those who were exposed is seen in Figure 6. Individuals that are exposed are 60 on the first day, and as time goes on, that number rises to 160 by day 15. We can

observe that it does not change beyond day 15. It appears to be at a steady value. In Figure 7, an illustration of infected people is displayed. Figure 7 shows that the number of infected people is 40 on the initial day, followed by an abrupt decrease. After day 10, the rate of declining behavior slowed, and after day 15, it started to become steady. The rate of change for recovered individuals is seen in Figure 8. The recovery rate significantly increases from the first day to day five. Then, on day 5, it reaches its highest point. It reached a steady state once the growth slowed.
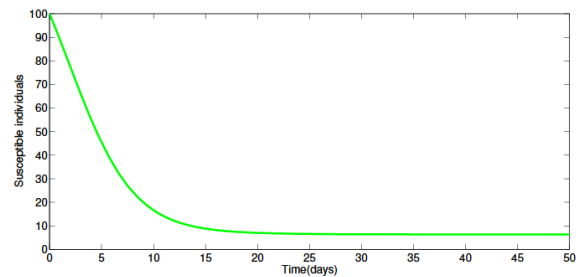

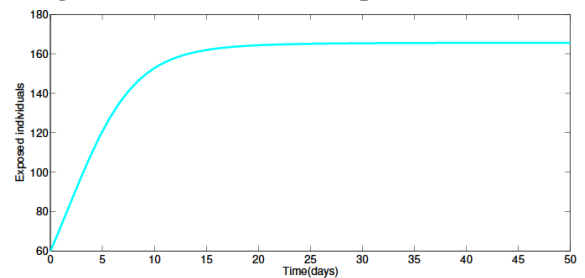**Figure 5. Simulation of susceptible individuals**

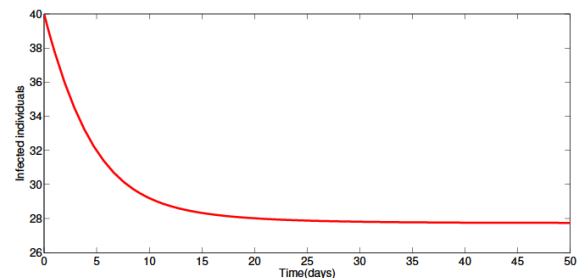**Figure 6. Simulation of exposed individuals**

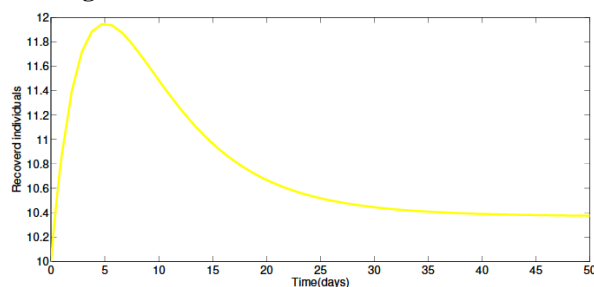**Figure 7. Simulation of infected individuals**

Figure 8. Simulation of recovered individuals

Figure 9 depicts the change rate in those who are susceptible. It reaches a maximum value of 100 on the initial day. then daily reduces progressively. The simulations of exposed people are shown in Figure 10. We may infer from the graph that the rate of exposed people is 60 on the initial day, then it rises and reaches its peak again on the day following 30. Around that, it progressively gets smaller after day 35. Figure 11 describes the rate of change in infected people with 40 initially infected. After that, it becomes smaller every day. The simulation of recovered persons is shown in Figure 12. From this figure, we can conclude that 10 people recovered on the first day, and then number increases daily.
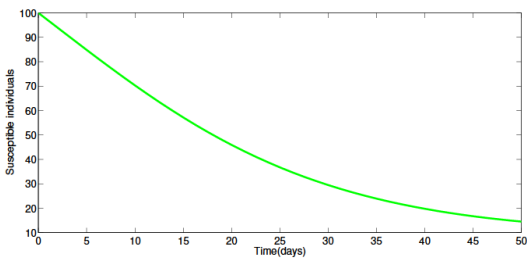
We can understand susceptible persons from Figure 13. There is a slight growth at the start of day 5. Then, from day 5, it increases quickly. Figure 14 depicts the simulation of exposed individuals. On the initial day, it is 60. After the 35th day, it decreases exponentially and turns to zero. Figure 15 shows the rate of change of infected individuals at the starting day is 40 then increases at the day 5 it attains maximum value 50. Then it decreases gradually. From Figure 16, we can understand at initially 10. Then it increases gradually, and it attains its maximum after day 20 is 50. Then it decreases gradually.

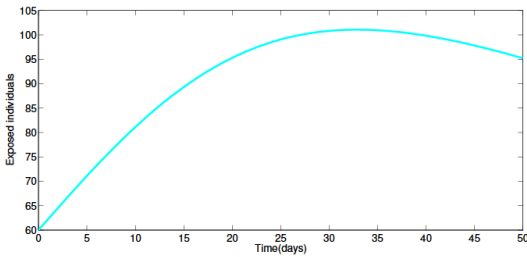
Figure 9. Simulation of susceptible individuals

Figure 10. Simulation of exposed individuals
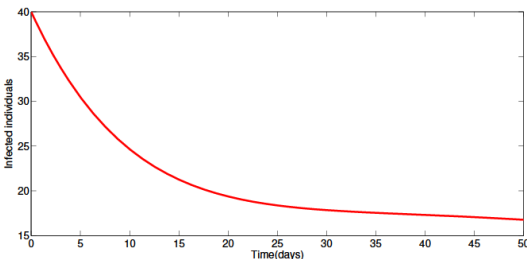
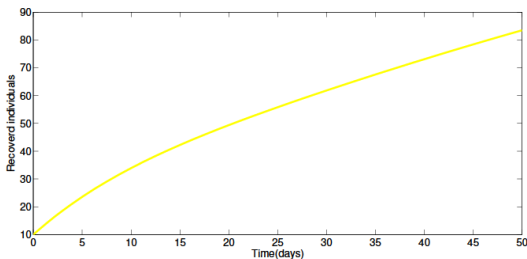**Figure 11. Simulation of infected individuals**

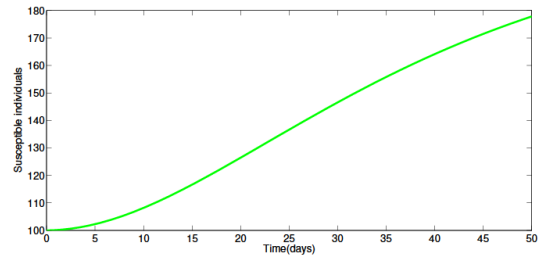**Figure 12. Simulation of recovered individuals**

Figure 13. Simulation of susceptible individuals

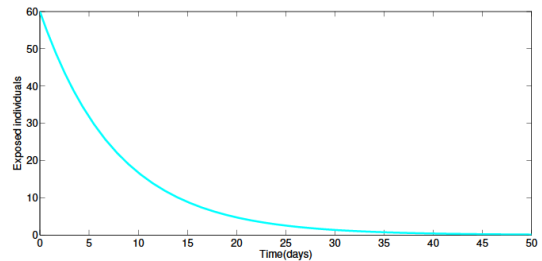**Figure 14. Simulation of exposed individuals**
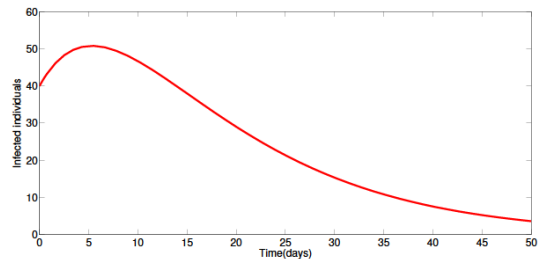

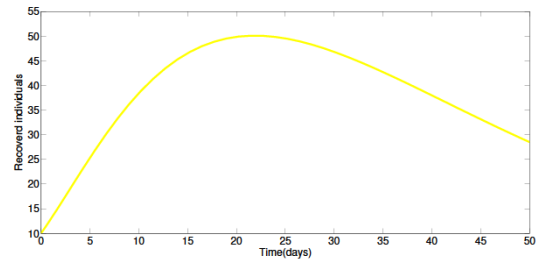**Figure 15. Simulation of infected individuals**

Figure 16. Simulation of recovered individuals

5. Mathematical modeling on real life scenario

As a result of the 2019-nCoV pandemic, the globe is nearly at a stop. More than 6.58 million lives were already lost. In addition to COVID-19, millions of people are dying from infectious diseases such as the swine flu, Ebola, Zika, plague, tuberculosis, and others (Jose et al., 2023; Ojo et al., 2021; Zafar, Ali, et al., 2021; Zafar, Tunç, et al., 2021). Controlling these infectious diseases was difficult due to the propensity of the bacteria, viruses, and parasites that cause them to change over time. Currently, COVID-19 is the most recent epidemic disease wreaking havoc on the entire planet. After evolving in China in late December of the year 2019 and rapidly spreading to other regions of the world, COVID-19 is a respiratory disease (Aba Oud et al., 2021; Mahmoudi et al., 2021). It is the newest kind of virus caused by SARS COV-2 (Ivorra et al., 2020). Some of the early pandemic models, particularly those used to examine the first wave of cases (Giordano et al., 2020; Ivorra et al., 2020; Kucharski et al., 2020; Li et al., 2020), did not take into account all of the unique aspects of the COVID-19 pandemic (undetected deaths, unreported cases, social distancing, quarantine, etc.). Gonzalez-Parra et al., 2021 (Gonzalez-Parra et al., 2021) investigated two distinct COVID-19 virus variants and provided a mathematical model for any more novel variants. In order to reflect the disease's transmission dynamics in more detail, a small number of researchers (Gonzalez-Parra et al., 2021; Tilahun et al., 2020; Tong et al., 2021) have included the influence of vaccines in their suggested models. Sah et al., 2021, (Sah et al., 2021) discovered the effects of precipitated vaccination distribution, which can lessen the burden caused by the various coronavirus strains. A Susceptible-Latent-Mild-Critical-Removed (SLMCR) compartmental model of the transmission of COVID-19 disease was demonstrated by Rahman and Kuddus in 2021 (Rahman & Kuddus, 2021). A model of several vaccination techniques was supplemented by Aguilar-Canto et al. in 2022 (Aguilar-Canto et al., 2022). Reetha et al. (Thomas et al., 2022) construct a mathematical modeling on Covid -19 in India, they are formulate four different SEIRS models and find the solution of the Models using Homotopy Perturbation Method. And also find that the last model by considering the effect of asymptomatic

patients and improve immunity by our food habits and taking some exercise like yoga, precaution by continuous awareness given by health officials. The model details are in below:

Many nations sealed their borders and instituted a state of lockdown to impede internal travel as a precaution to slow the rate of infection or contain the spread of the virus. However, some nations, like India, where there are more migrant workers than other nations, are seeing a rise in the number of migrant workers returning home. Additionally, migratory workers are returning home inside the nation, from one state to another. Therefore, the impact of the immigration inflow on the population is not insignificant. The previous model can be altered in this situation as indicated below.

$$\frac{dS}{dt} = A - \pi SI + \omega R - \mu S$$
$$\frac{dE}{dt} = \pi SI - (\mu + \varepsilon)E$$
$$\frac{dI}{dt} = \varepsilon E - (\mu + \gamma + d)I$$
$$\frac{dR}{dt} = \gamma I - (\omega + \mu)R \qquad (5)$$

People are taking precautions as a result of ongoing education provided by health experts and governments through media, including social media, avoiding unnecessary outings, routinely washing their hands, wearing a mask outside, etc. Additionally, people are able to exercise caution by reading the published route maps of infected patients. Additionally, by changing our eating habits and engaging in activities like yoga, we can boost our immunity. We alter the model (5) together with innate immunity and precaution to create the SEIRS model. Then the following form's model:

$$\frac{dS}{dt} = A - \pi SI + (1 - \nu)\sigma E + \omega R - \mu S$$
$$\frac{dE}{dt} = \pi SI - (\mu + \varepsilon)E$$
$$\frac{dI}{dt} = (\sigma \nu + \varepsilon)E - (\mu + \gamma + d)I$$
$$\frac{dR}{dt} = \gamma I - (\omega + \mu)R \qquad (6)$$

The transmission method of 2019-nCoV is often clear from symptomatic individuals. That could happen as a result of droplets that come out when you cough, sneeze, etc. Yet, even singing, exhaling loudly at a gym, or yelling for someone to hear you in a nightclub might result in 2019-nCoV

symptoms. Fundamentally, when you express air under pressure, it may happen in any circumstances through droplet transmission. Also, based on the data at hand, identified asymptomatic 2019-nCoV individuals cannot be avoided. We alter the model (6) together with asymptomatic infected class. then the following form's model:

$$\frac{dS}{dt} = A - \pi S(I + P) + (1 - \nu)\sigma E + \omega R - \mu S$$
$$\frac{dE}{dt} = \pi S(I + P) - (\sigma + \tau + \mu + \varepsilon)E$$
$$\frac{dI}{dt} = (\sigma\nu + \tau\kappa + \varepsilon)E + \delta P - (\mu + \gamma + d)I$$
$$\frac{dP}{dt} = (1 - \kappa)\tau E - (\delta + \lambda + \mu)P$$
$$\frac{dR}{dt} = \gamma I + \lambda P - (\omega + \mu)R$$
$$(7)$$

Mosquito borne diseases are the most dangerous diseases caused by mosquitoes such as Aedes aegypti, Aedes albopictus, Anopheles etc. Because, throughout the world 7, 20, 000 deaths are caused by mosquitoes. This fact makes the mosquito the world's deadliest animal. The optimal way to control mosquito borne diseases is by controlling the mosquito population. Wolbachia is an endo symbiotic bacterium found by Wolbach in 1924. This bacterium works as a population suppression factor and virus blocking agent in mosquitoes. In (Joseph Dianavinnarasi et al., 2020), the authors studied the interaction dynamics between Wolbachia and non-Wolbachia mosquitoes in the presence of delay and uncertainty in the control input. The interval of stable region is found, and the stability of the proposed results is analyzed via spectral theory. Moreover, in (Dianavinnarasi et al., 2022; Joseph Dianavinnarasi et al., 2021), the linear matrix inequality theory is initially introduced into the newly proposed derivative called Caputo-Fabrizio derivative. And analyzed the usefulness of using this derivative over life cycle model of both Wolbachia and non-Wolbachia mosquitoes. The author proved that using CF derivative one can analyze up to Exponential stability results not up to Mittag Leffler stable. In (Dianavinnarasi et al., 2021), the transmission dynamics of Wolbachia among both population in fractional and integer order models. An impulsive control strategy is implemented when there is an invasion in Wolbachia. In (Joseph et al., 2022), the authors discussed the non-fragile control synthesis to control sugarcane borer using its own egg parasitoid as a control, system dynamics is

analyzed using linear matrix inequality theory and Lyapunov theory. The authors proved that the proposed model is globally exponentially stable.

The eco-epidemic model essentially depicts a predator-prey relationship in which populations of either predators or preys are affected by infectious diseases. Not only is the relationship between a predator and prey threatened, but so is the rise in death rates brought on by the presence of infectious diseases. Even though the disease may affect both prey and predator, some researchers concentrate on the eco-epidemic model, in which the diseased population serves as the prey (Alzahrani et al., 2018; Dutta et al., 2022; Jana et al., 2022; Jose, Raja, Zhu, et al., 2022b; Jose, Ramachandran, et al., 2022; Pal et al., 2022; Rezapour et al., 2022; Saifuddin et al., 2016). This circumstance is supported by the eco-epidemic model for pest management on fields and plantations (Costa & dos Anjos, 2015; Liu et al., 2014; Yu et al., 2019). In addition to the epidemic aspect, they also involve some ecological components such as the Allee effect (Costa & dos Anjos, 2015; Saifuddin et al., 2016; Yu et al., 2019), predator switching (Pal et al., 2022), prey refuge (Pal et al., 2022), harvesting (Pal et al., 2022), and competition (Saifuddin et al., 2016). To obtain more advanced novelty, they also integrate some mathematical ways such as using fractional-order differential equation (Nugraheni et al., 2017; Rezapour et al., 2022; Zafar, Tunç, et al., 2021) and delay differential equation (Dutta et al., 2022; Jana et al., 2022) which considered more suitable for specific cases. One simple eco-epidemic model is given by Panigoro et al (Panigoro et al., 2021). They propose a simpler mode compared to the above models. This model is almost similar to the eco-epidemic model given by Nugraheni et al. (Nugraheni et al., 2017) and Saifuddin et al. (Saifuddin et al., 2016). They strengthen the novelty of their research results in the different presentations. Two fractional operators are used simultaneously namely Caputo and Atangana-Baleanu-Caputo derivative. In preliminaries, they show that both operators have a unique solution when the initial values are non-negative. The local and global stability of equilibrium points as well as the existence of Hopf bifurcation are investigated only for the Caputo operator due to the limitation of the theoretical support of the Atangana-Baleanu-Caputo operator. The interesting results are shown by the numerical

simulations. By applying a similar numerical scheme using Adam-Bashforth-Moulton for fractional derivative, all dynamics are qualitatively the same for the equilibrium points which have real eigenvalues. The difference between those operators occurs in the interior point when the eigenvalues are a pair of complex conjugate numbers with positive real parts. Hopf bifurcation occurs on both operators, but they have different bifurcation points with respect to the order of the derivative as the bifurcation parameter. The model with the Caputo operator experienced the Hopf bifurcation compared to the model with the Atangana-Baleanu-Caputo operator. This means there exist some values on the order of the derivate where those operators give different stability conditions.

In order to comprehend the dynamics of corruption transmission and to decide on intervention techniques to root out corruption, mathematical models with optimal control analyses are helpful. Numerous authors have discussed the epidemiological corruption modelling technique, including (Abdulrahman, 2014; Brianzoni et al., 2011; Khan, 2000). A mathematical model for dynamic corruption was created and examined by the authors of (Cuervo-Cazurra, 2016). The basic reproduction number, as well as the corruption-free and endemic equilibrium points, were identified. For the dynamics of corruption in (Athithan et al., 2018) the authors used a SIR model. They further developed the model by adding optimum control using a single optimal control strategy. A corruption prevention model created by Khan et al. (Khan, 2000) showed that perfect corruption prevention is feasible if the ratio between the rate of dismissals and the rate of corruption is equal to one. With reference to our current situation, Sayooj et al. (Jose, Raja, Alzabut, et al., 2022) developed a mathematical model for correction that established stability corresponding to the corruption free equilibrium point (CFEP) and corruption persistence equilibrium point (CPEP). Through figures, they show the effectiveness of the results of the numerical simulation. The importance of education, political awareness, punishment, and transparency of political acts is also demonstrated using an optimum control model. The model is follows:

$$\frac{dI_S(t)}{dt} = \nu\Psi - \lambda_{I_S} I_S(t) I_C(t) + \theta\psi_{I_T} I_T(t) - \gamma I_S(t)$$

$$\frac{dI_R(t)}{dt} = \lambda_{I_S} I_S(t) I_C(t) + \lambda_{I_R} I_R(t) I_C(t) - (\psi_{I_R} + \gamma) I_R(t)$$

$$\frac{dI_C(t)}{dt} = \beta\psi_{I_R} I_R(t) - \lambda_{I_R} I_R(t) I_C(t) - (\psi_{I_C} + \gamma) I_C(t)$$

$$\frac{dI_P(t)}{dt} = \psi_{I_C} I_C(t) - (\psi_{I_P} + \gamma) I_P(t)$$

$$\frac{dI_T(t)}{dt} = \psi_{I_P} I_P(t) + (1 - \beta)\psi_{I_R} I_R(t) - (\gamma + \psi_{I_T}) I_T(t)$$

$$\frac{dI_I(t)}{dt} = (1 - \nu)\Psi + (1 - \theta)\psi_{I_T} I_T(t) - \gamma I_I(t) \tag{8}$$

Mathematical models are important in comprehending and studying various facets of human life (Ginoux et al., 2019; Helbing et al., 2015; Rajasekar et al., 2021). Mathematical models (Balatif et al., 2018; Huo, Chen, et al., 2017; Huo, Huang, et al., 2017) can be used to study social behavior's or the spread of infectious disease. Numerous statistical models have been created and investigated in the area of alcohol in an effort to further minimize the number of drinkers (Adu et al., 2017; Agrawal et al., 2018). To the best of our knowledge, only a few scholarly articles have been written on substance addiction. Sayooj et al. (Jose, Raja, Zhu, et al., 2022a) developed a model for substance addictions and shown the significance of awareness and Strong determination. The stability and bifurcation have also been examined, along with the number of addiction generation cases. Here is the model:

$$\frac{dS(t)}{dt} = \Pi + \zeta\delta R(t) - \theta_1 S(t) A_3(t) - \omega S(t)$$

$$\frac{dA_1(t)}{dt} = \theta_1 S(t) A_3(t) - (\theta_2 + \psi_2 + \vartheta_3 + \omega) A_1(t)$$

$$\frac{dA_2(t)}{dt} = (1 - \vartheta_2)\psi_2 A_1(t) - (\theta_3 + \psi_1 + \omega + \omega_2) A_2(t)$$

$$\frac{dA_3(t)}{dt} = ((1 - \vartheta_1)\psi_1 + \theta_3) A_2(t) + (\vartheta_3 + \theta_2) A_1(t) - (\nu + \omega + \omega_3) A_3(t)$$

$$\frac{dR(t)}{dt} = \vartheta_1\psi_1 A_2(t) + \nu A_3(t) - (\omega + \delta) R(t)$$

$$\frac{dQ(t)}{dt} = (1 - \zeta)\delta R(t) + \vartheta_2\psi_2 A_1(t) - \omega Q(t) \tag{9}$$

6. Conclusions

These studies indicate that the practice of mathematical modeling has the ability to alter how we view the world. We can better grasp the complexity of our environment and how it impacts us by using mathematical models to examine data and make predictions. We may also find patterns and trends in data using mathematical modeling, which can then be utilized to make judgments and come up with solutions. Ultimately, mathematical modeling can help us to better understand our world and make more informed decisions.

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