Mathematical Modeling of Reservoir-Mediator-Human Dynamical Transmission of COVID-19 Outbreak

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Abstract

Coronaviruses are highly transmissible and are pathogenic viruses of the 21st century worldwide. The outbreak of Coronavirus disease 2019 (COVID-19), caused by severe acute respiratory syndrome (SARS) coronavirus 2 (SARS-CoV-2). In general, SARS-CoV-2 viruses are originated in bats or other wild animals and outbreak was originated from the Wuhan city of China at the end of December 2019. At the same time, the transmission of the infection to the human is caused by domestic animals that represent in the habitat the mediator. We especially emphasized the interaction of reservoir, mediator, and human the spread of coronavirus through our proposed model. In this paper, we reviewed currently information and established a model of differential equations, which has twelve ODEs with effective parameters to discuss the spread of the infection from the natural reservoir to the mediator, and from them to the human. We show analytical results as boundedness, non-negativity of solution, disease-free equilibrium point, endemic equilibrium point, basic reproduction number, steady state and numerical simulation. We aimed to estimate the numerical result of our model showed that the new incidence of symptomatic and asymptomatic infections, deaths, and isolations under quarantine scenarios. COVID-19 transmission rate among natural reservoir-mediator-human is the main theme of this study.

Keywords

COVID-19, SARS CoV-2, Reservoir-mediator-human Transmission, Mathematical model and ODE45.

1. Introduction

Mathematical modeling is an important tool to analyze several complex phenomena surrounding us. When a real system change concerning time, then it is referred to as a dynamical system. A dynamical system can be described by using a system of ordinary differential equations (ODEs) or a system of partial differential equations (PDEs) depending on the real (physical or chemical or biological or social) problems. These are sometimes called the ODE or PDE models respectively. In this paper, we propose a new deterministic ODE model, which has twelve ODEs, for the study of transmission of infectious disease of COVID-19. COVID-19 is an active research topic not only in the community of mathematical epidemiology group **(**Badr et al. 2020**)** but also the problem is of interests in various scientific communities including the group of modeling biological systems , biomedical engineering and signal processing, etc. To prepare a new mathematical model for a specific disease, some population-specific assumptions are important to make the model simple. However, the principal of model parsimony is also important, which is simply states as "a mathematical model should be as simple as possible and as complex as necessary". It also includes the parameter estimation from the source of real outbreaks information. A new mathematical model grants us to know the asymptotic prediction of infectious outbreaks shortly of a particular area of a country or of a country (Suwardi et al. 2020) by using the present data of outbreaks and also allow us to understand the basic epidemiological processes **(**Jose et al. 2020**)**. Thehe first, simplest and most basic proposed ODE model in the study of epidemiology is the three compartmental SIR (susceptible, infected, and recovered) model proposed by Kermack and McKendrick in 1927. Several modifications of the SIR model was published to understand the infectious outbreaks in humans and other animals. Modeling approach was also used to predict and understand several infectious diseases such as HIV-infection, influenza pandemic, H1F1 epidemic, pseudo-periodic 1918 pandemic influenza (known as Spanish flu) **(**Roy and

Robert 1979**)**, 2002/2003 SARS epidemic in Asia, etc. The agents of infectious diseases are mainly viruses, bacteria, and protozoa. The fundamental characteristics or biological dynamics of different infectious diseases are different. A basic model needs to modify based on a particular disease so that the model behavior and results adapt to the field data. Therefore, in this study, we propose a new model to understand the dynamics of an ongoing pandemic coronavirus disease 2019 (COVID19), caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), emerging in December 2019 in Wuhan city of China. There are already proposed mathematical models for COVID-19 to understand the current global outbreaks.COVID-19 outbreaks transmitted rapidly throughout the world and causing subversive health problems. The non-pharmaceuticals interventions, such as social-distancing (three or six feet), isolation or hospitalization for confirmed cases, home quarantine for susceptible cases, contact-tracing, washing hands for 20 s, use of face-masks in public places and some cases at home, etc. are the only way to suppress the pandemic burden as no vaccine or antiviral medicines are not yet invented by the researchers or healthcare management. As of 16 October 2020, 39 million cases have been reported across 189 countries and territories, but the WHO estimates that around 800 million people in total may have been infected. The disease has killed 1.09 million people; more than 26.9 million have recovered. The United States is now the epicenter of the current pandemic of the coronavirus. The record shows that 8,352,652 is of confirmed total cases and 224,393 deaths in US. In Bangladesh COVID-19 causes 388,569 infectious, 5,660 deaths and 303,972 recovered cases. The first three cases (two men and one woman) of COVID-19 in Bangladesh was confirmed on March 8, 2020. Two men were Italy returnees and the woman was a family member of one of them. It is clear from the data of the developed countries that people of 65 years older and above are at high risk of deaths, however, in the case of Bangladesh it is 40 years and above. An estimated 60% of known infectious diseases and 75% of all new, emerging, or re-emerging diseases in humans have animal origins. SARS-CoV-2 is the newest of seven coronaviruses found in humans, all of which came from bats. Bats were also the source of the viruses causing Ebola, rabies, Nipah and Hendra virus infections, Marburg virus disease, and strains of Influenza A virus. Until earlier this year, most people had never heard of the term “wild animal market or wet market,” but the coronavirus pandemic has thrust it into the limelight. A wet market in Wuhan, China, called the Huanan Seafood Wholesale Market, is believed to be the source of COVID-19.Somewhat akin to farmer’s markets and found around

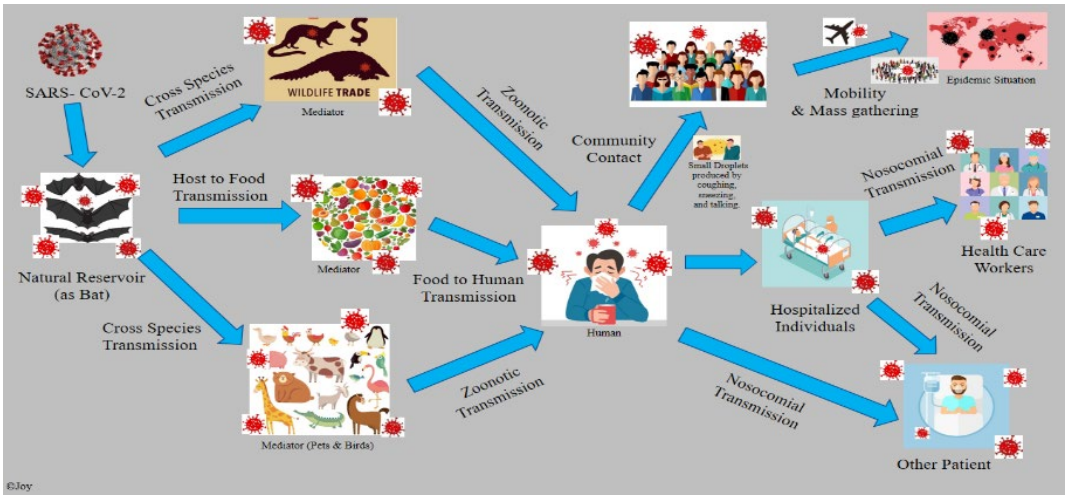

Figure 1.2. A biological diagram reservoir-mediator-human transmission of Covid-19

2. Mathematical Model Formulation of COVID-19

To understand the transmission of COVID-19 as well as its outbreak, we propose a mathematical model that can predict the dynamics of transmission in three sectors. They are natural reservoir (Bat), mediator and human. For the formulation of the model, we impose the following assumptions or facts:The reservoir (Bat) sector were divided into four compartments: We assume S_b represents susceptible individuals, E_b represents exposed individuals, I_b represents infected individuals and R_b represents removed individuals. N_b refer to the total number of reservoir as bat population. The mediator sector has a single compartment: The Covid-19 in mediator (the seafood, wild animal market, fruits) was denoted as M . We assumed that the consume/purchase rate of the mediator was λ . Therefore, the rate of the Covid-19 in M imported form the reservoir was λI_b . So that the virus in M will apart from this

compartment as the rate is εM .The human sector were divided into seven compartments: We assume S_p represents susceptible individuals, E_p represents exposed people, Q_p represents quarantine individuals, I_p represents symptomatic infected individuals, I_{sp} represents isolated individuals, A_p represents asymptomatic infected individuals and R_p represents recovered individuals. N_p refers to the total number of human population.`

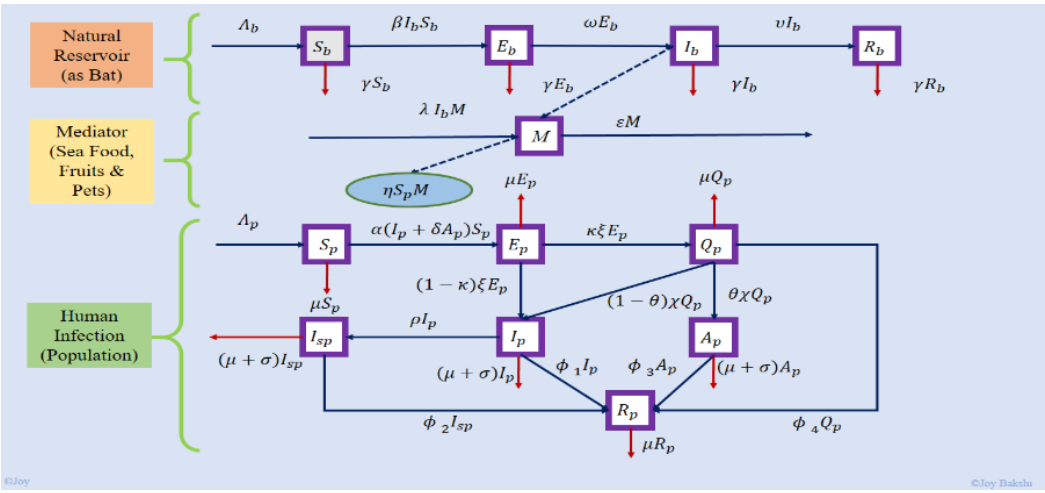

Figure 2.1. A schematic diagram of reservoir-mediator-human transmission of COVID-19 model.

The schematic representation of our assumptions underlying the model is depicted in Figure. 2.1.
Under the above-mentioned assumptions, the model leads to the following system of nonlinear ordinary differential equations;

$$\frac{dS_b(t)}{dt} = \Lambda_b - \beta I_b S_b - \gamma S_b$$
$$\frac{dE_b(t)}{dt} = \beta I_b S_b - \omega E_b - \gamma E_b$$
$$\frac{dI_b(t)}{dt} = \omega E_b - \upsilon I_b - \gamma I_b$$
$$\frac{dR_b(t)}{dt} = \upsilon I_b - \gamma R_b$$
$$\frac{dM(t)}{dt} = \lambda M I_b - \varepsilon M$$
$$\frac{dS_p(t)}{dt} = \Lambda_p - \alpha(A_p + \delta I_p)S_p - \eta S_p M - \mu S_p \quad (2.1)$$
$$\frac{dE_p(t)}{dt} = \alpha(A_p + \delta I_p)S_p + \eta S_p M - \kappa\xi E_p - (1-\kappa)\xi E_p - \mu E_p$$
$$\frac{dQ_p(t)}{dt} = \kappa\xi E_p - \theta\chi Q_p - (1-\theta)\chi Q_p - \phi_4 Q_p - \mu Q_p$$
$$\frac{dI_p(t)}{dt} = (1-\kappa)\xi E_p + (1-\theta)\chi Q_p - \rho I_p - \phi_1 I_p - (\mu+\sigma)I_p$$
$$\frac{dI_{sp}(t)}{dt} = \rho I_p - \phi_2 I_{sp} - (\mu+\sigma)I_{sp}$$
$$\frac{dA_p(t)}{dt} = \theta\chi Q_p - \phi_3 A_p - (\mu+\sigma)A_p$$

$$\frac{dR_p(t)}{dt} = \phi_1 I_p + \phi_2 I_{sp} + \phi_3 A_p + \phi_4 Q_p - \mu R_p$$

With the initial conditions; $S_b(0) = S_{b0} \geq 0, E_b(0) = E_{b0} \geq 0, I_b(0) = I_{b0} \geq 0, R_b(0) = R_{b0} \geq 0, M(0) = M_0 \geq 0,$ $S_p(0) = S_{p0} \geq 0, E_p(0) = E_{p0} \geq 0, .Q_p(0) = Q_{p0} \geq 0, I_p(0) = I_{p0} \geq 0, I_{sp}(0) = I_{sp0} \geq 0, A_p(0) = A_{p0} \geq 0$ and $R_p(0) = R_{p0} \geq 0$ .The description of parameters are presented in the following tables Table 2.1.

Table 2.1 Description of Parameters and Numerical Values

Parameter	Description	Values
Λ_b	Recruitment rate of bat	-
γ	The death rate of bat	-
β	The transmission rate S_b to E_b	-
ω	The transmission rate E_b to I_b	-
υ	The recovery rate of bat	-
λ	The purchase/consume rate of reservoir	1.5-3
ε	Life time of virus rate	0.1
η	The transmission rate W to S_p	1.5
Λ_p	Recruitment rate of bat	67446.82054
μ	The death rate of human	0.0000391
σ	The death rate due to CoVid-19	0.06891
α	The transmission rate S_p to E_p	1.5-3
κ	Rate of infection type-I	0.26556
χ	Rate of infection type-II	0.19230
ξ	The proportion of quarantine rate of human	0.24754
θ	The proportion of asymptomatic infection rate of human	0.5
ρ	Isolation rate	0.26190
δ	Multiple of the transmissibility of A_p to that of I_p	1
ϕ_1	The recovery rate of symptomatic infectious individuals	0.05090
ϕ_2	The recovery rate of isolation individuals	0.07048
ϕ_3	The recovery rate of asymptomatic infectious individuals	0.05311
ϕ_4	The recovery rate of quarantine individuals	0.05071

3. Mathematical Analysis of the Model

3.1 Positivity of the Solution

Here, we check the positivity of each compartment. We must have the positive values of these biological compartments. To test the positivity of the following compartments, we need to see the required lemma-1.

Lemma-3.1: If $S_b(0) > 0, E_b(0) \geq 0, I_b(0) \geq 0, R_b(0) \geq 0, M(0) \geq 0, S_p(0) \geq 0, E_p(0) \geq 0, .Q_p(0) \geq 0$ $I_p(0) \geq 0, I_{sp}(0) \geq 0, A_p(0) \geq 0$ and $R_p(0) \geq 0$ then the existing solution of our model system of nonlinear equations are all positive.

$$\frac{dS_b(t)}{dt} = \Lambda_b - \beta I_b S_b - \gamma S_b \qquad (3.1)$$

In order to find the possibility, From (3.1) we have;

$$\frac{dS_b(t)}{dt} \geq \Lambda_b - \gamma S_b \text{ or, } \frac{dS_b(t)}{dt} + \gamma S_b \geq \Lambda_b \qquad (3.2)$$

Hence the integrating factor of the equation is $I.F = e^{\int \gamma dt} = e^{\gamma t}$

Multiplying both side of (3.2) equation by $e^{\gamma t}$ we get,

$e^{\gamma t}.\frac{dS_b(t)}{dt}+e^{\gamma t}.\gamma S_b \geq e^{\gamma t}.\Lambda_b$ or, $\frac{d}{dt}(S_b e^{\gamma t}) \geq e^{\gamma t}.\Lambda_b$

$d(S_b e^{\gamma t}) \geq e^{\gamma t}.\Lambda_b dt$ (3.3)

Integrating both side (3.3)we get, $S_b e^{\gamma t} \geq \frac{e^{\gamma t}.\Lambda_b}{\gamma}+c_1$ (3.4)

where c_1 *i*s a constant. Applying the initial condition at $t=0, S_b(t) \geq S_b(0)$

$$S_b(0) \geq \frac{e^{\gamma t}.\Lambda_b}{\gamma}+c_1 \Rightarrow S_b(0)-\frac{\Lambda_b}{\gamma} \geq c_1 \quad (3.5)$$

Putting the value of c_1 into (3.5) equation, we get

$S_b e^{\gamma t} \geq \frac{e^{\gamma t}.\Lambda_b}{\gamma}+S_b(0)-\frac{\Lambda_b}{\gamma} \Rightarrow S_b(t) \geq \frac{\Lambda_b}{\gamma}+(S_b(0)-\frac{\Lambda_b}{\gamma})e^{-\gamma t}$

Hence, $S_b(0)>0$ at $t=0$ and $t \to \infty$. Similarly, we can find the possibility of $E_b, I_b, R_b, M, S_p, E_p, Q_p, I_p, I_{sp}, A_p$ and R_p.

Therefore, it is proved that $S_b(0)>0, E_b(0) \geq 0, I_b(0) \geq 0, R_b(0) \geq 0, M(0) \geq 0, S_p(0) \geq 0, E_p(0) \geq 0,$ $Q_p(0) \geq 0, I_p(0) \geq 0, I_{sp}(0) \geq 0, A_p(0) \geq 0$ and $R_p(0) \geq 0$

3.2 Boundedness

Here, we check the bounded-ness of human compartments. To test the bounded-ness of the following compartments, we need to see the required lemma-2.

Lemma 3.2: The closed region Ω is a positively invariant set for the COVID-19 model for human population with non-negative initial conditions in $\Re_+^8$.

Proof: Adding all the eight component equations of the model (2.1) for human population and using the relation $N_p = S_p + E_p + Q_p + I_p + I_{sp} + A_p + R_p + M$

We have, $\frac{dN_p}{dt} = \Lambda - \sigma(I_p + I_{sp} + R_p) - N_p$

Using standard comparison theorem,

$\frac{dN_p}{dt} \leq \Lambda - \mu N_p$ or, $\frac{dN_p}{dt} + \mu N_p \leq \Lambda$ or, $N_p(t) \leq N(0)e^{-\mu t} + \frac{\Lambda}{\mu}(1-e^{-\mu t})$. It is clear from that $N_p(t) \leq \frac{\Lambda}{\mu}$ if $N(0) \leq \frac{\Lambda}{\mu}$.

That is Ω is a positively invariant set under the flow presented in the COVID-19 model .Further, if, then $N_p(t)$ again approaches to $\frac{\Lambda}{\mu}$ and the number of infected population $E_p, Q_p, I_p, I_{sp}, A_p$ and M approach to zero for larger *t*. So all solutions in $\Re_+^8$ of the model eventually enters in Ω that is it is an attracting set.

3.3 Disease-free equilibrium Point (DFE)

The DFE of the Covid-19 transmission model (2.1) can be obtained by setting

$\frac{dS_b(t)}{dt} = \frac{dE_b(t)}{dt} = \frac{dI_b(t)}{dt} = \frac{dR_b(t)}{dt} = \frac{dM(t)}{dt} = \frac{dS_p(t)}{dt} = \frac{dE_p(t)}{dt} = \frac{dQ_p(t)}{dt} = \frac{dI_p(t)}{dt} = \frac{dI_{sp}(t)}{dt} = \frac{dA_p(t)}{dt} = \frac{dR_p(t)}{dt} = 0$

Since we have considered the DFE, $E_b(t) = I_b(t) = R_b(t) = M(t) = S_p(t) = E_p(t) = Q_p(t) = I_p(t) = I_{sp}(t) = A_p(t) = R_p(t) = 0$

Thus the aforementioned system reduces to

$\Lambda_b - \beta I_b S_b - \gamma S_b = 0 \qquad \therefore S_b = \frac{\Lambda_b}{\gamma}$

and $\Lambda_p - \alpha(A_p + \delta I_p)S_p - \lambda S_p M - \mu S_p = 0 \qquad \therefore S_p = \frac{\Lambda_p}{\mu}$,

Therefore, the DFE point is $E_{dfe} = \left(\frac{\Lambda_b}{\gamma}, 0, 0, 0, 0, \frac{\Lambda_p}{\mu}, 0, 0, 0, 0, 0, 0\right)$.

3.4 Endemic Equilibrium Point (EE)

The EE of the Covid-19 transmission model (2.1) can be obtained by setting

$$\frac{dS_b(t)}{dt} = \frac{dE_b(t)}{dt} = \frac{dI_b(t)}{dt} = \frac{dR_b(t)}{dt} = \frac{dM(t)}{dt} = \frac{dS_p(t)}{dt} = \frac{dE_p(t)}{dt} = \frac{dQ_p(t)}{dt} = \frac{dI_p(t)}{dt} = \frac{dI_{sp}(t)}{dt} = \frac{dA_p(t)}{dt} = \frac{dR_p(t)}{dt} = 0$$

Therefore, the EE point is

$$S_p^* = \frac{(\nu+\gamma)(\gamma+\omega)}{\beta\omega}\ ; E_p^* = \frac{\Lambda_b}{\gamma+\omega} - \frac{\gamma^2}{\beta\omega} - \frac{\nu\gamma}{\beta\omega}\ ; I_p^* = \frac{\Lambda_b\omega}{(\nu+\gamma)(\gamma+\omega)} - \frac{\gamma}{\beta}$$

$$R_b^* = \frac{\nu\left(\beta\Lambda_b\omega - \nu\gamma^2 + \omega\gamma^2 + \gamma^3 + \nu\gamma\omega\right)}{\beta\gamma(\nu+\gamma)(\gamma+\omega)}\ ; M^* = 0$$

$$S_p^* = \frac{x_3x_5x_7\ (\mathrm{x}_4 + \theta\xi)}{\alpha\chi(\theta\mathrm{x}_4\mathrm{x}_7 - \theta\kappa\mathrm{x}_4\mathrm{x}_7 + \delta\kappa\mathrm{x}_7\xi + \delta\theta\mathrm{x}_7\xi + \kappa\theta\mathrm{x}_5\xi - 2\delta\kappa\theta\mathrm{x}_7\xi)}$$

$$E_p^* = \frac{-\left(\mu\mathrm{x}_3\mathrm{x}_4\mathrm{x}_5\mathrm{x}_7 + \mu\theta\mathrm{x}_3\mathrm{x}_5\mathrm{x}_7\xi - \alpha\Lambda_p\chi\delta\mathrm{x}_4\mathrm{x}_7 + \alpha\Lambda_p\chi\delta\kappa\mathrm{x}_4\mathrm{x}_7 - \alpha\Lambda_p\chi\delta\kappa\mathrm{x}_7\xi - \alpha\Lambda_p\chi\delta\theta\mathrm{x}_7\xi - \alpha\Lambda_p\chi\kappa\theta\mathrm{x}_5\xi + 2\alpha\Lambda_p\chi\delta\kappa\theta\mathrm{x}_7\xi\right)}{\alpha\chi\mathrm{x}_3(\delta\mathrm{x}_4\mathrm{x}_7 - \delta\kappa\mathrm{x}_4\mathrm{x}_7 + \delta\kappa\mathrm{x}_7\xi + \delta\theta\mathrm{x}_7\xi + \kappa\theta\mathrm{x}_5\xi - 2\delta\kappa\theta\mathrm{x}_7\xi)}$$

$$Q_p^* = \frac{-\left(\kappa\mu x_3x_4x_5x_7 - \alpha\Lambda_p\chi\delta\kappa x_4x_7 + \kappa\mu\theta x_3x_5x_7\xi + \alpha\Lambda_p\chi\delta\kappa^2\ x_4\ x_7 - \alpha\Lambda_p\chi\delta\kappa^2 x_7\xi - \alpha\Lambda_p\chi\kappa^2\ \theta x_5\xi + 2\alpha\Lambda_p\chi\delta\kappa^2\ \theta x_7\xi\ - \alpha\Lambda_p\chi\delta\kappa\theta x_7\xi\right)}{\alpha x_3\left(x_4 + \theta\xi\right)(\delta x_4x_7 - \delta\kappa x_4x_7 + \delta\kappa x_7\xi + \delta\theta x_7\xi + \kappa\theta x_5\xi - 2\delta\kappa\theta x_7\xi)}$$

$$I_p^* = \frac{-\left(\left(x_4 - \kappa x_4 + \kappa\xi + \theta\xi - 2\kappa\theta\xi\right)\ \left(\begin{array}{l}\mu x_3x_4x_5x_7 + \mu\theta x_3x_5x_7\xi - \alpha\Lambda_p\chi\delta x_4x_7 + \alpha\Lambda_p\chi\delta\kappa x_4x_7 - \alpha\Lambda_p\chi\delta\kappa x_7\xi - \\ \alpha\Lambda_p\chi\delta\theta x_7\xi - \alpha\Lambda_p\chi\kappa\theta x_5\xi + \ 2\alpha\Lambda_p\chi\delta\,\kappa\theta\ x_7\xi\end{array}\right)\right)}{\left(\alpha x_3x_5\left(x_4 + \theta\xi\right)\ (\delta x_4x_7 - \delta\kappa x_4x_7 + \delta\kappa x_7\xi + \delta\theta x_7\xi + \kappa\theta x_5\xi - 2\delta\kappa\theta x_7\xi)\right)}$$

$$I_{sp}^* = \frac{-\left(\rho\left(x_4 - \kappa x_4 + \kappa\xi + \theta\xi - 2\kappa\theta\ \xi\right)\ \left(\begin{array}{l}\mu x_3x_4x_5x_7 + \mu\theta x_3x_5x_7\xi - \alpha\Lambda_p\chi\delta x_4x_7 + \alpha\Lambda_p\chi\delta\kappa x_4x_7 - \\ \alpha\Lambda_p\chi\delta\kappa x_7\xi - \alpha\Lambda_p\chi\delta\theta x_7\xi - \alpha\Lambda_p\chi\kappa\theta\ x_5\xi + 2\alpha\Lambda_p\chi\delta\kappa\theta x_7\xi\end{array}\right)\right)}{\left(\alpha x_3x_5x_6\left(x_4 + \theta\xi\right)\left(\delta x_4x_7 - \delta\kappa x_4x_7 + \delta\kappa x_7\xi + \delta\theta x_7\xi + \kappa\theta\ x_5\xi - 2\kappa\theta x_7\xi\right)\right)}$$

$$A_p^* = \frac{-\left(\begin{array}{l}\kappa\mu\theta^2x_3\ x_5\ x_7\xi^2 - \alpha\Lambda_p\chi\ \kappa^2\theta^2\ x_5\xi^2\ + \ \kappa\mu\theta x_3x_4x_5x_7\xi\ - \ \alpha\Lambda_p\chi\delta\kappa\theta^2x_7\xi^2 - \\ \alpha\Lambda_p\chi\delta\kappa^2\ \theta x_7\xi^2\ + 2\alpha\Lambda_p\chi\delta\kappa^2\ \theta^2\ x_7\xi^2 - \alpha\Lambda_p\chi\delta\kappa\theta x_4x_7\xi + \alpha\Lambda_p\chi\delta\kappa^2\ \theta x_4x_7\xi\end{array}\right)}{\alpha x_3\ x_7\ \left(x_4 + \theta\xi\right)\ \left(\delta x_4x_7 - \delta\kappa x_4x_7 + \ \delta\kappa x_7\xi + \kappa\theta\ x_7\xi + \kappa\theta x_5\xi - 2\delta\kappa\theta x_7\xi\right)}$$

$$R_p^* = -\frac{\left(\begin{array}{l}\left(\mu x_3x_4x_5x_7 + \mu\theta x_3x_5x_7\xi - \alpha\Lambda_p\chi\delta x_4x_7\ + 2\alpha\Lambda_p\chi\delta\kappa x_4x_7 - \alpha\Lambda_p\chi\delta\kappa\ x_7\xi - \alpha\Lambda_p\chi\delta\theta x_7\xi - \alpha\Lambda_p\chi\kappa\theta x_5\xi + 2\alpha\Lambda_p\chi\delta\kappa\theta x_7\xi\right) \\ \left(\phi_2\rho x_4x_7 + \phi_1x_4x_6x_7 - \kappa\phi_2\rho x_4x_7 + \kappa\phi_2\rho x_7\xi - \kappa\phi_1x_4x_6x_7 + \kappa\phi_4x_5x_6x_7 + \kappa\phi_1x_6x_7\xi + \phi_2\rho\theta\ x_7\xi + \phi_1\theta x_6x_7\xi - 2\kappa\phi_2\rho\theta x_7\xi - 2\kappa\phi_1\theta x_6x_7\xi + \kappa\phi_3\theta x_5x_6\xi\right)\end{array}\right)}{\alpha\mu x_3x_5x_6x_7\left(x_4 + \theta\xi\right)\ \left(\delta x_4x_7 - \delta\kappa x_4x_7 + \delta\kappa x_7\xi + \delta\theta x_7\xi\ + \kappa\theta x_5\xi - 2\delta\kappa\theta x_7\xi\right)}$$

where,

$x_1 = \gamma + \omega, x_2 = \nu + \gamma, x_3 = \kappa\chi + \mu - (\kappa - 1)\chi, x_4 = \theta\xi + \phi_4 + \mu - (\theta - 1)\xi, x_5 = \phi_1 + \mu + \sigma, x_6 = \phi_2 + \mu + \sigma, x_7 = \phi_3 + \mu + \sigma.$

3.5 Basic Reproduction Number

The basic reproduction number is defined as the expected number of secondary infections produced by single typical infected individuals in a completely susceptible population. It is a key epidemiological quantity, because it determines the size and duration of epidemics. The basic reproduction number is shown that when $R_0 < 1$, then throughout the infectious period, each infective will produce less than one new infective on the average. This implies that the disease will die out. So we can write if $R_0 < 1$ then the disease dies out or extinct. When $R_0 > 1$, then throughout the infectious period, each infective will produce less than one new infective on the average. This implies that the disease will persist. So we can write if $R_0 > 1$ then the epidemic disease exists. This means that there will be an outbreak.

It is obtained by taking the dominant eigenvalue of $G = \left[\frac{\partial F_i}{\partial y_j}\left(E_{dfe}\right)\right]\left[\left[\frac{\partial V_i}{\partial y_j}\left(E_{dfe}\right)\right]\right]^{-1}$

where, F_i is the gains to infectious compartments, V_i is the losses from infectious compartments and E_{dfe} is the diseases free equilibrium (DFE).The DFE point is $E_{dfe} = \left(\frac{\Lambda_b}{\gamma}, 0, 0, 0, 0, \frac{\Lambda_p}{\mu}, 0, 0, 0, 0, 0, 0\right)$ Now we get from the model of the system of equations (2.1)

$$F_i = \begin{pmatrix} 0 \\ \alpha(A_p + \delta I_p)S_p + \lambda S_p M) \\ 0 \\ 0 \\ 0 \\ 0 \end{pmatrix} \qquad G_i = \begin{pmatrix} -a.M.I_b + \varepsilon M \\ -\alpha(A_p + \delta I_p)S_p - \lambda S_p M + \kappa\xi E_p + (1-\kappa)\xi E_p + \mu E_p \\ -\kappa\xi E_p + \theta\chi Q_p + (1-\theta)\chi Q_p + \phi_4 Q_p + \mu Q_p \\ -(1-\kappa)\xi E_p - (1-\theta)\chi Q_p + \rho I_p + \phi_1 I_p + (\mu+\sigma)I_p \\ -\rho I_p + \phi_2 I_{sp} + (\mu+\sigma)I_{sp} \\ -\theta\chi Q_p + \phi_3 A_p + (\mu+\sigma)A_p \end{pmatrix}$$

Hence, we have the basic reproduction number for the considered model is

$$R_0 = \frac{\alpha\xi(\delta k_2 k_5 - \delta k_2 k_5 \kappa + \chi k_3 \kappa\theta + \chi\delta k_5 \kappa - \chi\delta k_5 \kappa\theta)}{k_1 k_2 k_3 k_5}$$

where, $k_1 = \kappa\xi + (1-\kappa) + \mu; k_2 = \theta\chi + (1-\theta)\chi + \phi_4 + \mu; k_3 = \rho + \phi_1 + \mu + \sigma; k_3 = \phi_2 + \mu + \sigma; k_5 = \phi_3 + \mu + \sigma$

3.6 Steady State

In this section, we shall study the stability analysis of the disease-free equilibrium point $E_{dfe} = (\frac{\Lambda_b}{\gamma}, 0, 0, 0, 0, \frac{\Lambda_p}{\mu}, 0, 0, 0, 0, 0, 0)$ whose stability has been investigated in the next theorem.

Theorem 1 If $R_0 > 1$, then the E_{dfe} is unstable and it is stable if $R_0 < 1$.

Proof: The Jacobian matrix corresponding to the system (2.1) at DFE $E_{dfe} = (\frac{\Lambda_b}{\gamma}, 0, 0, 0, 0, \frac{\Lambda_p}{\mu}, 0, 0, 0, 0, 0, 0)$ is

$$J_{dfe} = \begin{bmatrix} -\gamma & 0 & -\beta\frac{\Lambda}{\gamma} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & -x_1 & \beta\frac{\Lambda}{\gamma} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \omega & -x_2 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \nu & -\gamma & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & -\varepsilon & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & -\eta\frac{\Lambda}{\mu} & -\mu & 0 & 0 & -\alpha\delta\frac{\Lambda}{\mu} & 0 & -\alpha\frac{\Lambda}{\mu} & 0 \\ 0 & 0 & 0 & 0 & \eta\frac{\Lambda}{\mu} & 0 & -x_3 & 0 & \alpha\delta\frac{\Lambda}{\mu} & 0 & \alpha\frac{\Lambda}{\mu} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \kappa\chi & -x_4 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & -(\kappa-1)\chi & -(\theta-1)\xi & -x_5 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \rho & -x_6 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & \theta\xi & 0 & 0 & -x_7 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & \phi_4 & \phi_1 & \phi_2 & \phi_3 & -\mu \end{bmatrix}$$

The characteristic equation is $|J - kI| = 0$

where, $x_1 = \gamma + \omega; x_2 = V + \gamma; x_3 = \mu + \chi\kappa - \chi(\kappa - 1); x_4 = \mu + \phi_4 + \xi\theta - \xi(\theta - 1); x_5 = \mu + \phi_1 + \rho + \sigma;$

$x_6 = \mu + \phi_2 + \sigma; x_7 = \mu + \phi_3 + \sigma;$

$$a_1 = \eta\Lambda_p / \mu; a_2 = (\alpha\Lambda_p)/\mu; a_3 = (\beta\Lambda_b)/\gamma; a_4 = \theta\xi; a_5 = \chi\kappa;$$

$$\therefore \left[(\varepsilon + k)(\gamma + k)^2(k + \mu)^2(k + x_6)\{p_0k^6 + p_1k^5 + p_2k^4 + p_3k^3 + p_4k^2 + p_5k - p\}\right] = 0$$

Where, $p = (a_3\omega - x_1x_2)(x_3x_4x_5x_7 - a_2a_4a_5x_5 + a_2a_4a_5\delta x_7 + a_2a_5\delta x_4x_7 - a_2a_5\delta x_7\xi - a_2\chi\delta x_4x_7)$

The six eigenvalues are $(k_1, k_2, k_3, k_4, k_5, k_6) = (-\varepsilon, -\gamma, -\gamma, -\mu, -\mu, -x_6)$

Since, $-\varepsilon, -\gamma, -\gamma, -\mu, -\mu, -x_6$ are negative roots of characteristic polynomial. We use Rouwth-Herwitz criterion to show that the reaming polynomial, $p_0k^6 + p_1k^5 + p_2k^4 + p_3k^3 + p_4k^2 + p_5k - p_6 = 0$ has negative real roots. The first condition for the criteria p_1 must be positive and clearly when $R_0 < 1$, then p_2, p_3, p_4, p_5 and p_6 are all positive. Now if $R_0 < 1$ then it is clear that p_2, p_3, p_4, p_5 and $p_6 > 0$ .Since p_1, p_2, p_3, p_4, p_5 and p_6 are same sign so according to Rouwth-Herwitz criteria the other eigenvalues have negative real part. Now if $R_0 > 1$ then at least one eigenvalue have positive real part. Therefore, the dieaseas free equilibrium E_{dfe} is locally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$.

4. Numerical Analysis

We perform numerical simulations of our model proposed in (2.1) by the ODE45-solver using MATLAB programming. For demonstrating the analytical results, we have taken some hypothetical data. The parameters of the dynamical model are based on real-world observation. Our main goal is to illustrate the result by numerical simulations considered from a qualitative, rather than a quantitative point of view. Along with the verification of our analytical observations, these numerical results are very much important from the practical point of view. The numerical result shows different behavior of our dynamical model. We have used a set of suitable parameter values in table 2.1.

In Figures 4.1 we see the variation of quarantined population and symptomatic infectious population with time 10 months for the different quarantine rate. From Figures 4.1, we observe that quarantined population and symptomatic infectious population increases as the quarantine rate of human increases in the world. Due to the decrease in the quarantine rate of human in the world, quarantined population and symptomatic infectious population also decreases.

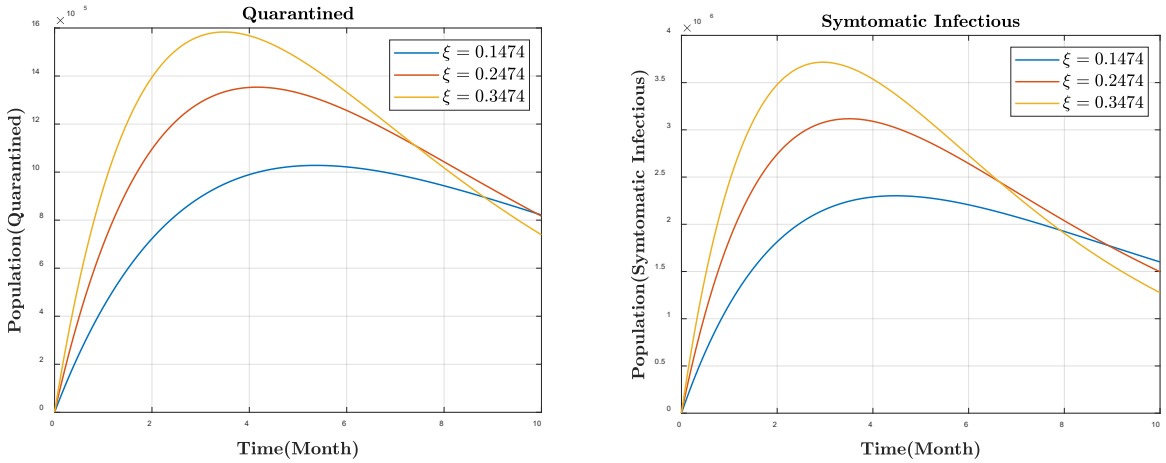

Figure 4.1. Graph of symptomatic infected human of covid-19 transmission for our model (2.1) where time span 0 to 10 months and $\xi_1 = 0.14754; \xi_2 = 0.24754; \xi_3 = 0.34754$.

In Figures 4.2 we see the variation of symptomatic infectious population and asymptomatic infectious population with time 10 months for the different infection rate. From Figures 4.2, we observe that quarantined population and symptomatic infectious population increases as the infection rate of human increases in the world. Due to the decrease in the infection rate of human in the world, symptomatic infectious population and asymptomatic infectious population also decreases.

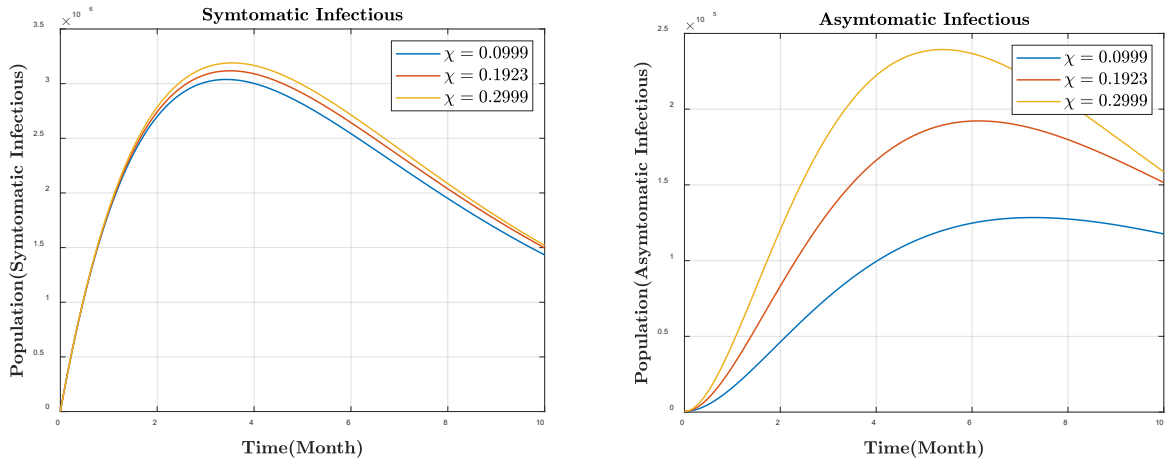

Figure 4.2. Graph of symptomatic infected and asymptomatic infected human of covid-19 transmission for our model (2.1) where time span 0 to 10 days and $\chi_1 = 0.0999; \chi_2 = 0.1923; \chi_3 = 0.2999$.

In Figures 4.3 we see the variation of isolated population with time 10 months for the different isolation rate. From Figures 4.3, we observe that isolated population increases as the isolation rate of human increases in the world. Due to the decrease in the isolation rate of human in the world, isolated population also decreases.

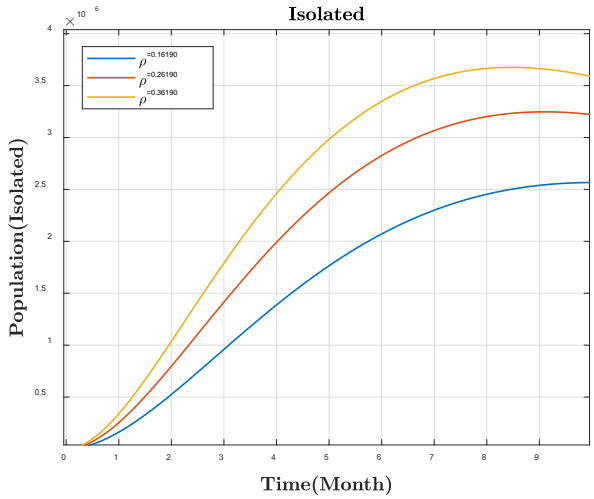

Figure 4.3. Graph of isolated human of covid-19 transmission for our model (2.1) where time span 0 to 10 months and $\rho_1 = 0.16190; \rho_2 = 0.26190; \rho_3 = 0.36190$.

In Figures 4.4 we see the variation of isolated population and recovered population with time 10 months for the different recovery rate of isolation. From Figures 4.4, we observe that isolated population increases as the recovery rate of isolation of human decreases and recovered population increases as the recovery rate of isolation of human increases in the world. Due to the decrease in the recovery rate of isolation of human in the world, isolated population and recovered population also decreases and due to the decrease in the recovery rate of isolation of human in the world, isolated also increases.

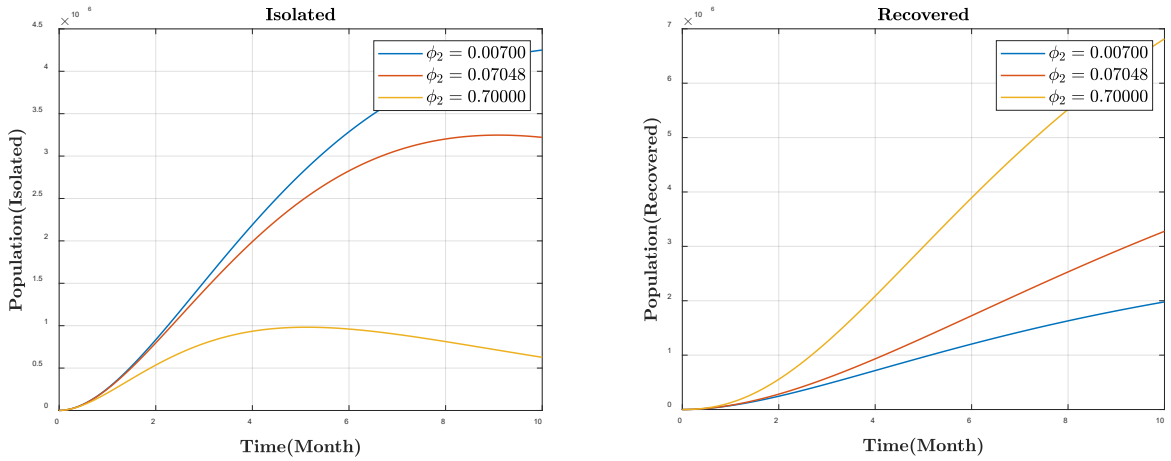

Figure 4.4. Graph of isolated and recovered human of covid-19 transmission for our model (2.1) where time span 0 to 10 months and $\phi_2 = 0.00700; \phi_2 = 0.07048; \phi_2 = 0.70000$.

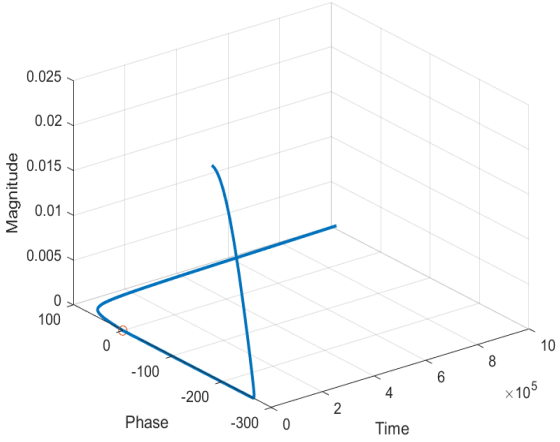

Figure 4.5. Phase Portrait Graph of mediator and human compartments of covid-19 transmission for our model (2.1) where time span 0 to 10 months.

5. Conclusion

COVID-19 pandemic is the second world disaster after the World War II, government of all countries has taken some policies to control the catastrophic nature of the deadly disease in their own capacity. In this paper, we have analyzed the behavior of outbreak from reservoir, mediator and human transmission. The mathematical model used in this paper is a system of nonlinear differential equations which includes the parameter named transmission of Covid-19 of reservoir, mediator and human. A dynamical model of reservoir, mediator and human, has been introduced at first. Then the equilibrium points of the model have been determined. The stability analysis at the interior points has been tested which ensures the validity of the model. The analytical analysis is included with positivity test, equilibrium point, stability at steady state point and stability at disease free equilibrium point. In the schematic diagram, we used twelve compartments. Those compartments are called variables. Here we directly discuss about variables are symptomatic infectious individuals, isolation individuals, asymptomatic infectious individuals and quarantine individuals of Covid-19 outbreak. These three variables are interconnected. We have presented the numerical results with its discussions which show that if transmission of virus increases, Covid-19 diseases will be increased.

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