



MATHEMATICAL AND COMPUTATIONAL INVESTIGATION OF THREE STRAIN DYNAMIC TRANSMISSION NETWORK MODEL OF THE ZONOTIC COVID-19 EPIDEMIC

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Abstract

The COVID-19 epidemic, commonly known as the coronavirus flu epidemic, is a worldwide COVID-19 epidemic caused by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). The new virus was discovered in December 2019 during an epidemic in Wuhan, China. In our suggested model, we have focused on the relationship between the reservoir, the mediator, and the individual during the transmission of the coronavirus. To better understand, how an infection spreads from a natural reservoir to a mediator and finally to a person, we have built a model that includes twelve ordinary differential equations with effective parameters. In this study, we have provided boundedness, non-negative solution, disease-free and endemic equilibrium point, stability analysis for the equilibrium points, sensitivity analysis, basic reproduction number, and numerical simulation. The epidemic indicator fundamental reproduction number is derived from the largest eigenvalue of the next-generation matrix. To establish the numerical output of the model, it was assessed if the new incidence of symptomatic and asymptomatic infections, deaths, and isolations under quarantined situations was larger than the existing incidence. A major goal of this study is to curtail COVID-19 from spreading through natural reservoirs to human via intermediate hosts.

Keywords: COVID-19, Reservoirs, Basic Reproduction Number, Transmission Network, Numerical Simulation

Introduction

In the study of infectious diseases, mathematics has a long history. Each year, infectious diseases take millions of lives and sicken billions. With advancements in sanitation, antibiotics, vaccinations, medical knowledge, and medical treatment, infectious diseases may be eliminated from the human population. They remain the leading cause of death in developing nations. The findings indicate the development of novel infectious diseases as well as the reemergence of previously existing diseases. When an infectious agent is transferred from an infected person to a susceptible one, an infectious illness ensues (the host). Numerous individuals have utilized

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mathematical models to forecast the spread of disease. There have been several mathematical models constructed to examine the transmission of diseases, viruses, and parasites (Dym, 2004). Kermack and McKendrick established the SIR (susceptible, infected, and recovered) paradigm in 1927. The SIR model has been modified to allow for the investigation of human and non-human animal illnesses (Kermack & McKendrick, 1933). We forecasted and analyzed the 2002–2003 SARS epidemic in Asia using modeling. Viruses, bacteria, and protozoa are all examples of infectious disease agents. Infectious diseases have unique underlying characteristics or biological dynamics. A core model must be updated to fit the field data for each sickness (Last, 1988). Thus, we have presented a fresh viewpoint in this study on the dynamics of an epidemic of coronavirus infection (COVID-19) generated by the SARS-CoV-2 (WHO, 2020). Already, mathematical models based on COVID-19 have been constructed to explain contemporary global epidemics. COVID-19 outbreaks are quickly spreading around the world, causing health issues. Researchers and the healthcare administration have not created any epidemic vaccinations or antiviral drugs. The main non-pharmaceutical methods of curing sick people are: three or six feet of social distance; isolation and hospitalization for confirmed infections; home quarantine for vulnerable patients; contact tracing; and wearing face masks in public and sometimes at home (Rothan, 2020). As of May 19, 2022, the WHO estimates that over 525,289,105 people may have been infected. Over 494,990,323 individuals have recovered and 6,294,930 individuals' deaths have been attributed (Worldometer, 2022). The current coronavirus outbreak has reached the United States. There were 84,692,706 confirmed cases and 1,028,014 deaths in the United States (Worldometer, 2022). In Bangladesh, COVID-19 infected 1,953,103 people, killed 29,127 and recovered 1,900,138 (Worldometer, 2022). Bangladesh reported three COVID-19 issues on March 8, 2020 (two males and one female). The woman was linked to one of the returnees from Italy (IEDCR, 2020). The evidence from developed countries demonstrates unequivocally that people over the age of 65 have an increased risk of death. It is 40 years and above in Bangladesh. Many think that 60–70% of existing infections and 75% of new, emerging, or re-emerging diseases are caused by animals. SARS-CoV-2 is the most recently discovered coronavirus in humans. In addition, bats carry Ebola, rabies, Nipah, and Hendra virus strains (Last, 1988). This coronavirus outbreak has revived the "wild animal market" and the "wet market". COVID-19 might have originated at Wuhan's Huanan Seafood Wholesale Market. individuals (Rothan, 2020). Wet markets offer fresh fish, meat, veggies, and herbs. Some wet markets sell live chickens, fish, and shellfish. They are often eaten in China. Wild meat is occasionally sold at damp markets. Exotics offered in the Huanan market included bats, snakes, beavers, porcupines, and crocodiles. Local markets in India, Latin America, and Africa sell wild animal flesh (bushmeat). Close animal interaction has been linked to Ebola and HIV. SARS and the pathogen causing the Wuhan epidemic are both coronaviruses. Coronaviruses are a broad group of viruses that may infect people, camels, cats, and bats. Fruit consumption may be contaminated by bats. The fruit may be a viral entrance route for farmed animals like civets. The COVID-19 virus has been found in cats and dogs, the CDC reports (Maron, 2021). This occurred after close interaction with COVID-19-infected people. The incubation time for COVID-19 is 2–14 days (Biswas et al., 2020). COVID-19 symptoms include fever, chills, exhaustion, pains, headaches, sore throat, congestion, nasal congestion, nausea, vomiting, diarrhea, and loss of smell (Biswas et al., 2021). Most serious cases (80%) have no previous symptoms and are corona positive. (WHO, 2020). It's tough to maintain a six-foot social barrier in Bangladesh (e.g., raw vegetable markets, shopping malls, festivals, and so on). So the situation in Bangladesh worsens.

Materials and Methods

Biological model formulation

The 'SARS-CoV-2 viruses' are the main causes of COVID-19 diseases. Many researchers think that SARS-CoV-2 comes from a natural reservoir (Maron, 2021). They predicted that it was a bat. We mentioned it as a natural reservoir of viruses. The virus spreads from bats to other species. It is called "cross-species transmission". We mentioned that it is a natural reservoir of viruses. The virus is transmitted into the human population via a mediator, which is known as zoonotic transmission. After that, the virus was transmitted from

human to human, causing a serious outbreak. In Figure 1, a biological model of the reservoir-mediator-human network of COVID-19 transmission is displayed.

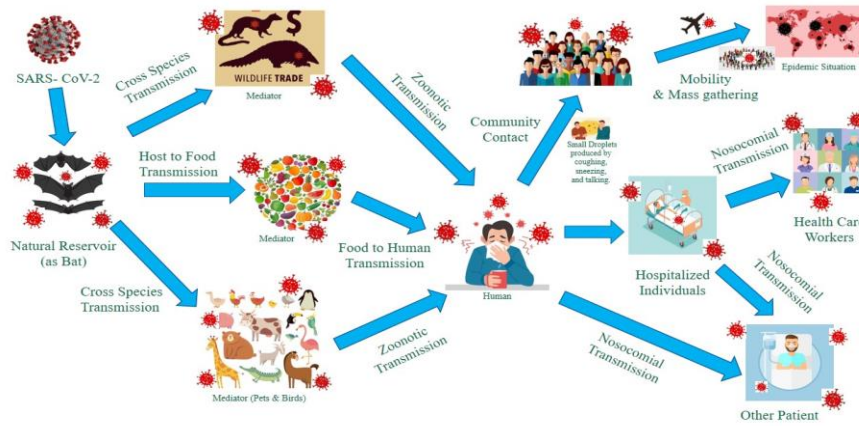


Figure 1. A biological diagram of the reservoir-mediator-human network transmission of COVID-19 model.

Mathematical model formulation

For this purpose, we have assumed that the SARS CoV-2 was transmitted among the reservoir individuals as a bat, and then the host interacted with the seafood market, fruits, vegetables, and domestic animals which were defined as mediator. People revealed to the mediator and got the presumption of the infectious disease. To understand the transmission of COVID-19 and its epidemic, we have built a mathematical model capable of simulating the transmission characteristics in three major sections. They are bats, mediators, and humans. The following assumptions or facts were required for the formulation of the model:

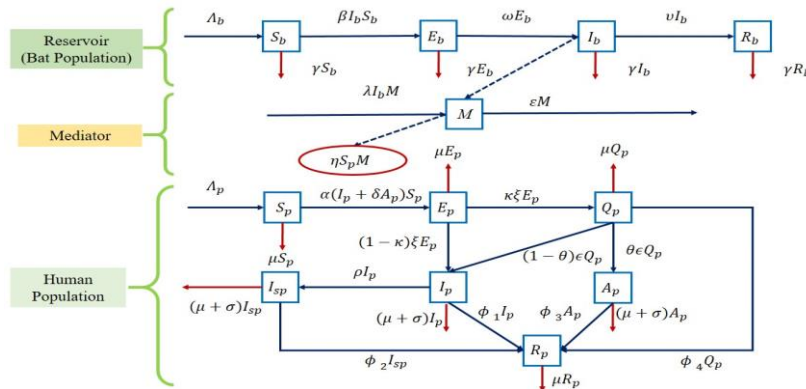


Figure 2. A diagrammatic representation of the COVID-19 reservoir-mediator-human transmission network (A1) The reservoir network (Bat) was separated into four compartments: We have assumed that S_b represents susceptible bats, E_b represents exposed bats, I_b represents infected bats and R_b represents removed bats. N_b denotes the total number of bat population as reservoir. The recruitment rate of the reservoir individuals is Λ_b and the natural death rate of reservoir is γ . The S_b will be infected through appropriate

contact with I_b and the rate of transmission from susceptible bats to exposed bats was denoted as β . The transmission rate from exposed bats to infected bats was defined as ω . The recovery rate of bats was defined as ν .

(A2) The mediator network consists of only one compartment: The mediator of Covid-19 infections (the market for fish, wild animals, and fruits) was denoted as M . We predicted the rate of consumption or purchasing of the mediator to be λ , and that the prevalence of Covid-19 in the acquired was $\frac{I_b}{N_b}$, therefore, the rate of virus transmission of the Covid-19 in M shipped from the reservoir was λI_b where, N_b was the total number of the reservoir. Rate of viral longevity is ε . Therefore, the virus of M will be omit from this section as the transmission rate is εM .

(A3) Seven compartments of the human network were generated: We have assumed $S_p, E_p, Q_p, I_p, I_{sp}, A_p$ and R_p symbolizes as susceptible human, exposed human, quarantine human, symptomatic infected human, isolated human, asymptomatic infected human, and recovered human respectively. The total number of the human population is N_p . The recruitment rate of human is Λ_p and the natural death rate is μ . The S_p will be infected through appropriate contact with M, I_p and A_p . The transmission rate from susceptible to exposed human was defined as α . κ and χ represent the rate of type-1 and type-2 human infection respectively. ξ is the proportion of the quarantine infection rate of human. θ is the proportion of asymptomatic infection rate of human. ρ is the isolation rate of human. Multiplication via the transmissibility of A_p to I_p is δ . The recovery rate of symptomatic infectious human, isolation human, asymptomatic infectious human and quarantine human is denoted as ϕ_1, ϕ_2, ϕ_3 and ϕ_4 respectively.

The model explains the following nonlinear ordinary differential equations (ODEs) system with the help of the previously stated assumptions (A1-A3):

$$\frac{dS_b(t)}{dt} = \Lambda_b - \beta I_b S_b - \gamma S_b \tag{1}$$

$$\frac{dE_b(t)}{dt} = \beta I_b S_b - \omega E_b - \gamma E_b \tag{2}$$

$$\frac{dI_b(t)}{dt} = \omega E_b - \nu I_b - \gamma I_b \tag{3}$$

$$\frac{dR_b(t)}{dt} = \nu I_b - \gamma R_b \tag{4}$$

$$\frac{dM(t)}{dt} = \lambda M I_b - \varepsilon M \tag{5}$$

$$\frac{dS_p(t)}{dt} = \Lambda_p - \alpha(A_p + \delta I_p)S_p - \eta S_p M - \mu S_p \tag{6}$$

$$\frac{dE_p(t)}{dt} = \alpha(A_p + \delta I_p)S_p + \eta S_p M - (1 - \kappa)\xi E_p - \kappa\xi E_p - \mu E_p \tag{7}$$

$$\frac{dQ_p(t)}{dt} = \kappa\xi E_p - \theta\chi Q_p - (1 - \theta)\chi Q_p - \phi_4 Q_p - \mu Q_p \tag{8}$$

$$\frac{dI_p(t)}{dt} = (1-\kappa)\xi E_p + (1-\theta)\chi Q_p - \rho I_p - \phi_1 I_p - (\mu + \sigma)I_p \quad (9)$$

$$\frac{dI_{sp}(t)}{dt} = \rho I_p - \phi_2 I_{sp} - (\mu + \sigma)I_{sp} \quad (10)$$

$$\frac{dA_p(t)}{dt} = \theta\chi Q_p - \phi_3 A_p - (\mu + \sigma)A_p \quad (11)$$

$$\frac{dR_p(t)}{dt} = \phi_1 I_p + \phi_2 I_{sp} + \phi_3 A_p + \phi_4 Q_p - \mu R_p \quad (12)$$

Considering the initial conditions;

$$S_b(0) = S_{b0} \geq 0, E_b(0) = E_{b0} \geq 0, I_b(0) = I_{b0} \geq 0, R_b(0) = R_{b0} \geq 0, M(0) = M_0 \geq 0, S_p(0) = S_{p0} \geq 0, \\ I_{sp}(0) = E_{p0} \geq 0, Q_p(0) = Q_{p0} \geq 0, I_p(0) = I_{p0} \geq 0, I_{sp}(0) = I_{sp0} \geq 0, A_p(0) = A_{p0} \geq 0 \text{ and } R_p(0) = R_{p0} \geq 0$$

Mathematical investigation of non-negative solution

The non-negative solution of each compartment is studied. We must possess non-negative values for these compartments of these biological model (Khatun & Biswas, 2020).

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 $R_p(0) \geq 0$. Consequently, all of the existing solutions to our system of model nonlinear equations are non-negative. From (1) we acquire that,

$$\frac{dS_b(t)}{dt} = \Lambda_b - \beta I_b S_b - \gamma S_b \quad (13)$$

In order to reach the non-negative solution, from (13) we have obtained;

$$\frac{dS_b(t)}{dt} \geq \Lambda_b - \gamma S_b \quad (14)$$

$$\text{or, } \frac{dS_b(t)}{dt} + \gamma S_b \geq \Lambda_b \quad (15)$$

Hence the integrating factor is $I.F = e^{\int \gamma dt} = e^{\gamma t}$. Multiplying by $e^{\gamma t}$, both side of (15) equation we get,

$$e^{\gamma t} \cdot \frac{dS_b(t)}{dt} + e^{\gamma t} \cdot \gamma S_b \geq e^{\gamma t} \cdot \Lambda_b \text{ or, } \frac{d}{dt}(S_b e^{\gamma t}) \geq e^{\gamma t} \cdot \Lambda_b \text{ or, } d(S_b e^{\gamma t}) \geq e^{\gamma t} \cdot \Lambda_b dt \quad (16)$$

Integrating both sides of (16) we obtain,

$$S_b e^{\gamma t} \geq \frac{e^{\gamma t} \cdot \Lambda_b}{\gamma} + c_1 \quad (17)$$

where c_1 is a constant value.

Utilizing the initial value condition at $t = 0, S_b(t) \geq S_b(0)$

$$S_b(0) \geq \frac{e^{\gamma t} \cdot \Lambda_b}{\gamma} + c_1 \Rightarrow S_b(0) - \frac{\Lambda_b}{\gamma} \geq c_1 \quad (18)$$

Substituting c_1 into (18) equation, we have

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

At the point $t=0$ and $t \rightarrow \infty$ then we get $S_b(0) > 0$. Likewise, we may evaluate the non-negative solution that of $E_b, I_b, R_b, M, S_p, E_p, Q_p, I_p, I_{sp}, A_p$ and R_p . Hence, 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 $R_p(0) \geq 0$.

Equilibrium Point

The equilibrium point of the model of COVID-19 transmission network (1)-(12) obtainable by

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

Disease free equilibrium point (Khatun & Biswas, 2020)

Therefore, the disease free equilibrium point of the system of the model is

$$E_0 = \left(\frac{\Lambda_b}{\gamma}, 0, 0, 0, 0, \frac{\Lambda_p}{\mu}, 0, 0, 0, 0, 0, 0 \right).$$

Endemic equilibrium point (Khatun & Biswas, 2020)

Solving the following equations (1)-(12). We obtain,

$$S_b^* = \frac{(v + \gamma)(\gamma + \omega)}{\beta\omega}; E_b^* = \frac{\Lambda_b}{\gamma + \omega} - \frac{\gamma^2}{\beta\omega} - \frac{v\gamma}{\beta\omega}; I_b^* = \frac{\Lambda_b\omega}{(v + \gamma)(\gamma + \omega)} - \frac{\gamma}{\beta}; R_b^* = \frac{v(\beta\Lambda_b\omega - v\gamma^2 + \omega\gamma^2 + \gamma^3 + v\gamma\omega)}{\beta\gamma(v + \gamma)(\gamma + \omega)};$$

$$M^* = 0; S_p^* = \frac{x_3 x_5 x_7 (x_4 + \theta\xi)}{\alpha\chi(\theta x_4 x_7 - \theta\kappa x_4 x_7 + \delta\kappa x_7 \xi + \delta\theta x_7 \xi + \kappa\theta x_5 \xi - 2\delta\kappa\theta x_7 \xi)};$$

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

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

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

$$I_{sp}^* = \frac{-\left(\rho(x_4 - \kappa x_4 + \kappa\xi + \theta\xi - 2\kappa\theta\xi) \left(\mu x_3 x_4 x_5 x_7 + \mu\theta x_3 x_5 x_7 \xi - \alpha\Lambda_p \chi \delta x_4 x_7 + \alpha\Lambda_p \chi \delta \kappa x_4 x_7 - \alpha\Lambda_p \chi \delta \kappa x_7 \xi - \alpha\Lambda_p \chi \delta \theta x_7 \xi - \alpha\Lambda_p \chi \kappa \theta x_5 \xi + 2\alpha\Lambda_p \chi \delta \kappa \theta x_7 \xi\right)\right)}{(\alpha x_3 x_5 x_6 (x_4 + \theta\xi) (\delta x_4 x_7 - \delta\kappa x_4 x_7 + \delta\kappa x_7 \xi + \delta\theta x_7 \xi + \kappa\theta x_5 \xi - 2\kappa\theta x_7 \xi))};$$

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

$$R_p^* = -\frac{\left(\begin{aligned} & \left(\mu x_3 x_4 x_5 x_7 + \mu\theta x_3 x_5 x_7 \xi - \alpha\Lambda_p \chi \delta x_4 x_7 + 2\alpha\Lambda_p \chi \delta\kappa x_4 x_7 - \right. \\ & \left. \alpha\Lambda_p \chi \delta\kappa x_7 \xi - \alpha\Lambda_p \chi \delta\theta x_7 \xi - \alpha\Lambda_p \chi \kappa\theta x_5 \xi + 2\alpha\Lambda_p \chi \delta\kappa\theta x_7 \xi \right) \\ & \left(\phi_2 \rho x_4 x_7 + \phi_1 x_4 x_6 x_7 - \kappa\phi_2 \rho x_4 x_7 + \kappa\phi_2 \rho x_7 \xi - \kappa\phi_1 x_4 x_6 x_7 + \right. \\ & \left. \kappa\phi_4 x_3 x_6 x_7 + \kappa\phi_1 x_6 x_7 \xi + \phi_2 \rho\theta x_7 \xi + \phi_1 \theta x_6 x_7 \xi - 2\kappa\phi_2 \rho\theta x_7 \xi - 2\kappa\phi_1 \theta x_6 x_7 \xi + \kappa\phi_3 \theta x_5 x_6 \xi \right) \end{aligned} \right)}{\alpha\mu x_3 x_5 x_6 x_7 (x_4 + \theta\xi) (\delta x_4 x_7 - \delta\kappa x_4 x_7 + \delta\kappa x_7 \xi + \delta\theta x_7 \xi + \kappa\theta x_5 \xi - 2\delta\kappa\theta x_7 \xi)};$$

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

Therefore, the endemic equilibrium point of the system of the model is $E^* = (S_b^*, E_b^*, I_b^*, R_b^*, M^*, S_p^*, E_p^*, Q_p^*, I_p^*, I_{sp}^*, A_p^*, R_p^*)$.

Basic reproduction number investigation

In order to examine the basic reproductive number R_0 , we have approximated the Next Generation Matrix technique in this study. The rate of basic reproduction number is the average number of secondary cases generated by an infected animal or human when all susceptible individuals are present. It merges the biology of viral infections with the social and behavioral aspects that influence contact rate. The basic reproduction rate indicates the amount of secondary issues a single infectious population will generate in a community of just susceptible individuals (Khatun & Biswas, 2020).

$$R_b = \frac{\beta\omega S_b}{(\nu + \gamma)(\omega + \gamma)} \tag{20}$$

which is the fundamental reproduction number of bat population.

$$R_p = \frac{\alpha\xi(\delta x_2 x_5 - \delta x_2 x_3 \kappa + \chi x_3 \kappa\theta + \chi\delta x_3 \kappa - \chi\delta x_5 \kappa\theta)}{x_1 x_2 x_3 x_5} \tag{21}$$

which is the fundamental reproduction number of human population.

Total amount of reproduction number of the model is,

$$R_0 = \max(R_b, R_p) = \max\left(\frac{\beta\omega S_b}{(\nu + \gamma)(\omega + \gamma)}, \frac{\alpha\xi(\delta x_2 x_5 - \delta x_2 x_3 \kappa + \chi x_3 \kappa\theta + \chi\delta x_3 \kappa - \chi\delta x_5 \kappa\theta)}{x_1 x_2 x_3 x_5} \right)$$

$$\therefore R_0 = \frac{\alpha\xi(\delta x_2 x_5 - \delta x_2 x_3 \kappa + \chi x_3 \kappa\theta + \chi\delta x_3 \kappa - \chi\delta x_5 \kappa\theta)}{x_1 x_2 x_3 x_5} \tag{22}$$

where, $x_1 = \kappa\xi + (1 - \kappa) + \mu$; $x_2 = \theta\chi + (1 - \theta)\chi + \phi_4 + \mu$; $x_3 = \rho + \phi_1 + \mu + \sigma$; $x_4 = \phi_2 + \mu + \sigma$; and $x_5 = \phi_3 + \mu + \sigma$.

Stability analysis

The disease-free equilibrium point E_0 is unstable in the case of $R_0 > 1$ and it is also stable in the case of $R_0 < 1$. Therefore, the disease free equilibrium E_0 is locally asymptotically stable if $R_0 < 1$ and otherwise

unstable. The endemic equilibrium point E^* is unstable in the case of $R_0 < 1$ and it is also locally asymptotically stable in the case of $R_0 > 1$. Therefore, the endemic equilibrium E^* is the locally asymptotically stable if $R_0 > 1$ and otherwise unstable (Khatun & Biswas, 2020).

Results

Computational investigation of sensitivity analysis

In this context, the COVID-19 disease is quickly spreading over worldwide and poses a danger to human civilization. Therefore, prevention and therapy of this infectious disease are essential at this time. First, we must identify the important and significant model parameters. The sensitivity index of the fundamental reproduction number with regard to various parameters was determined. We have developed a sensitivity index using the normalized forward sensitivity approach;

$$S_\alpha = \frac{dR_0}{d\alpha} \cdot \frac{\alpha}{R_0} \tag{23}$$

where, the characteristic parameter is α whose sensitivity on R_0 is calculated. In the last column of each table, the calculated sensitivity indices for each model parameter utilizing sets of parametric values are shown. These indicators may be used to assess and determine the efficiency of control and prevention strategies.

$$\therefore R_0 = \frac{\alpha\xi(\delta x_2 x_5 - \delta x_2 x_5 \kappa + \chi x_3 \kappa \theta + \chi \delta x_3 \kappa - \chi \delta x_5 \kappa \theta)}{x_1 x_2 x_3 x_5}$$

$$S_\alpha = \frac{d}{d\alpha} \left(\frac{\alpha\xi(\delta x_2 x_5 - \delta x_2 x_5 \kappa + \chi x_3 \kappa \theta + \chi \delta x_3 \kappa - \chi \delta x_5 \kappa \theta)}{x_1 x_2 x_3 x_5} \right) \times \frac{\alpha x_1 x_2 x_3 x_5}{\alpha\xi(\delta x_2 x_5 - \delta x_2 x_5 \kappa + \chi x_3 \kappa \theta + \chi \delta x_3 \kappa - \chi \delta x_5 \kappa \theta)}$$

where, $x_1 = \kappa\xi + (1 - \kappa) + \mu$; $x_2 = \theta\chi + (1 - \theta)\chi + \phi_4 + \mu$; $x_3 = \rho + \phi_1 + \mu + \sigma$; $x_4 = \phi_2 + \mu + \sigma$ and $x_5 = \phi_3 + \mu + \sigma$. The sensitivity of all parameters describing the reservoir-mediator-human network transmission of COVID-19 model is summarized in Table 1.

Table 1. Sensitivity indices of parameters

Notation	Description of parameters	Parameter Values	Sensitivity values, S_α	Sensitivity indices (+ve/-ve)
Λ_b	Rate of Recruitment for bat population	0.02	0	+ve
γ	The rate of natural death of bat population	0.088	0	+ve
β	The rate of transmission from S_b to E_b	0.3016	0	+ve
ω	The rate of transmission from E_b to I_b	0.7	0	+ve
ν	Rate of recovered bat	0.2857	0	+ve
λ	The rate of purchasing or consuming of reservoir	1.5	0	+ve

ε	Rate of viral longevity	0.1	0	+ve
η	The rate of transmission from M to S_p	1.5	0	+ve
Λ_p	Recruitment rate of human	0.0181	0	+ve
μ	The rate of natural death of human population	0.0000391	-0.000257	-ve
σ	The death rate due to disease	0.0200	-0.0840	-ve
α	The rate of transmission from S_p to E_p	1.5	1.0000	+ve
κ	Type-1 infection rate of human	0.26556	-0.2260	-ve
χ	Type-2 infection rate of human	0.19230	-0.9003	-ve
ξ	The proportion of quarantine infection rate of human population	0.24754	0.9673	+ve
θ	The proportion of asymptomatic infected rate of human population	0.5	0.0166	+ve
ρ	Rate of isolation of human	0.26190	-0.2937	-ve
δ	Multiplication via the transmissibility of A_p to I_p	1	0.9419	+ve
ϕ_1	The recovery rate of symptomatic infected human	0.05090	-0.5709	-ve
ϕ_2	The recovery rate of isolated human	0.07048	0	+ve
ϕ_3	The recovery rate of asymptomatic infected human	0.05311	-0.0514	-ve
ϕ_4	The recovery rate of quarantine human	0.06667	-0.0669	-ve

In Figure 3, Sensitivity of all parameter depicting the reservoir-mediator-human network transmission of the COVID-19 disease model is displayed with tornadograph.

The real impact of this dataset will be that the index with the greatest effective magnitude is more sensitive to parameters influencing R_0 . The real impact of the positive or negative sign of the sensitivity index is that R_0 increases or decreases as the parameter α increases.

Computational Investigation of Numerical Analysis

Using the built-in function, we conducted numerical simulations of our model shown in (1)–(12) employing MATLAB programming (ODE45-Solver). To demonstrate the analytical results, we have made use of hypothetical data. The real valued parameters of the dynamical model are derived from observations made in the current world. Our primary objective is to show the findings using numerical simulations that are viewed qualitatively rather than quantitatively. Here we have conducted numerical computations for time from $t=0$ to $t=10$ months. The result of the individual compartments are presented in Figure 4.

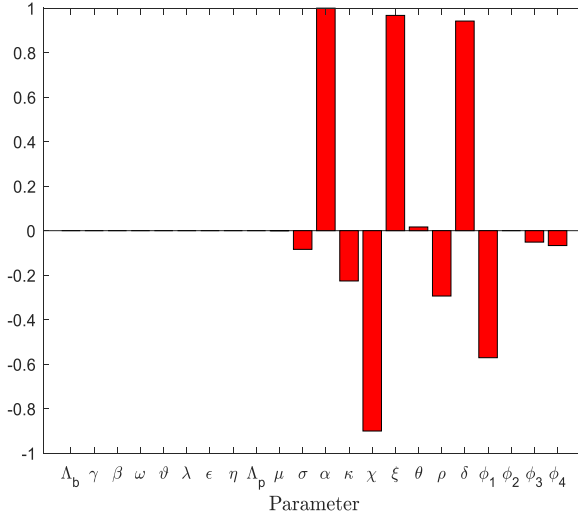


Figure 3. Sensitivity of all parameters depicting the reservoir-mediator-human network transmission of the COVID-19 disease model.

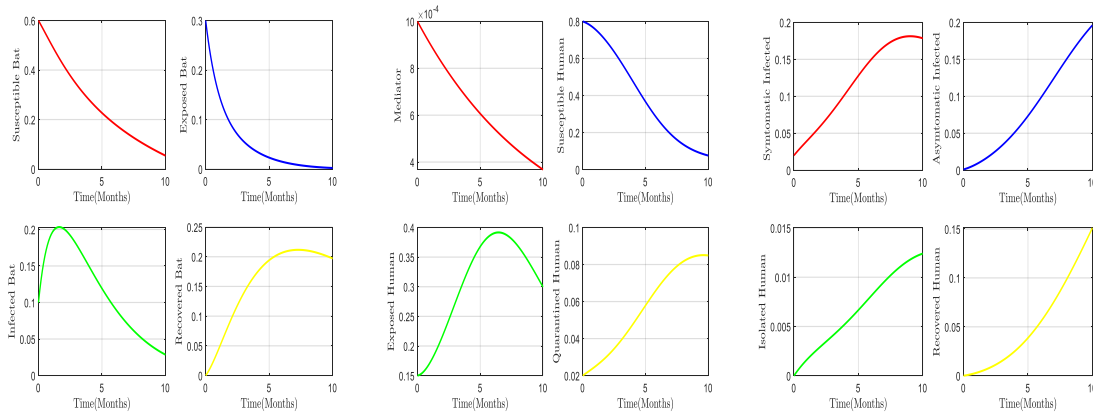


Figure 4. Individual compartments of reservoir-mediator-human network transmission of COVID-19 in our model (1)-(12) where time span 0 to 10 months.

A phase portrait is a visual representation of certain aspects of specific types of differential equations; a coordinate plane with the values of the three state variables as the axes.

Here, we formulated phase portrait by numerical simulations of the equation of model (1)-(12) by using the value of parameters where the time span 0 to 10 months. Figure 5 represents the phase portrait, a geometric depiction of the trajectories of a dynamical system in the phase plane.

In Figure 6, it is shown the variation of quarantined humans, symptomatic infected humans, isolated humans, asymptomatic infected humans, and recovered humans with time for the various kinds of type-1 infection rate of human. Figure 6 demonstrates that quarantined humans and asymptomatic infected humans

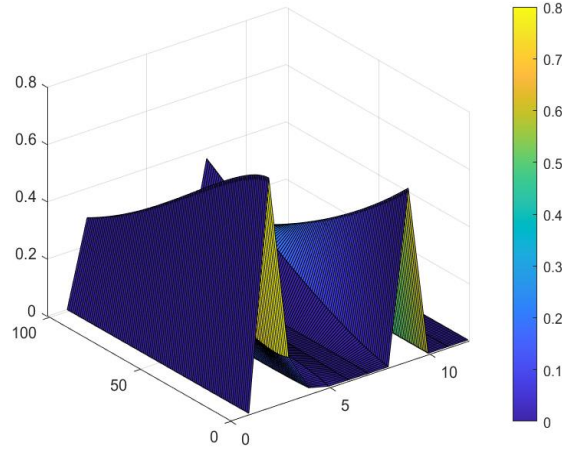


Figure 5. Phase portrait where the time range is 0 to 10 months of COVID-19 transmission network for reservoir-mediator-human in our model (1)-(12).

are on the increase as the type-1 infection rate of human increases globally. The number of quarantined humans and asymptomatic infected humans has decreased as the global infection rate of humans has decreased, while the number of the symptomatic infected humans and the isolated humans has grown.

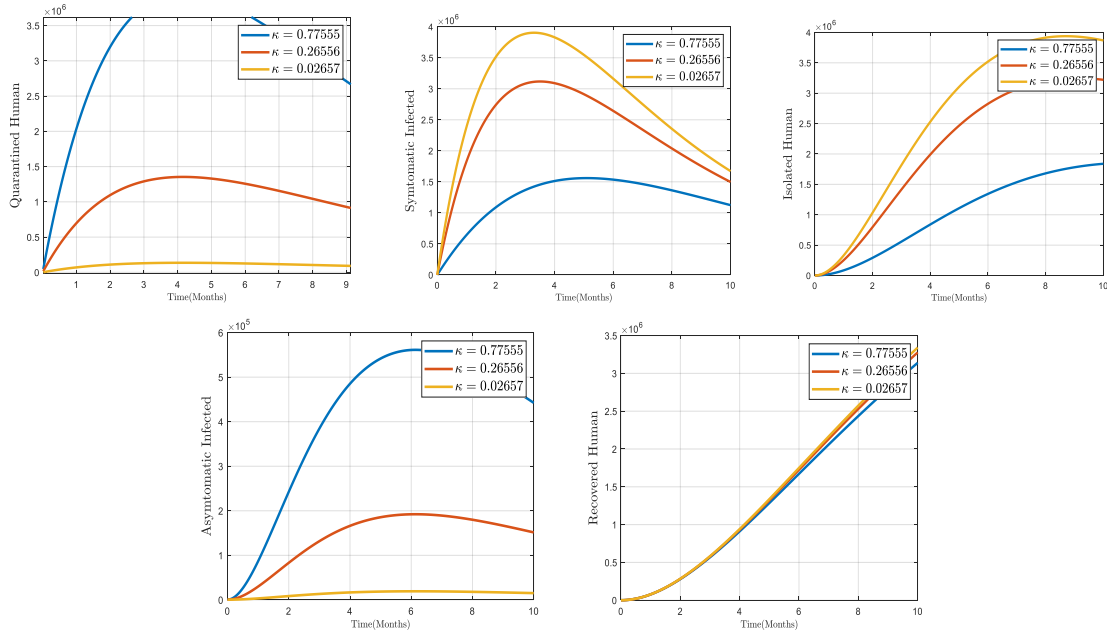


Figure 6. Variations of the type-1 rate of infection human for our model (1)-(12) of COVID-19 transmission network where $\kappa_1 = 0.7755$; $\kappa_2 = 0.26556$; $\kappa_3 = 0.02657$ and the time range 0 to 10 months.

In Figure 7, it is shown the variation of quarantined humans, symptomatic infected humans, isolated humans, asymptomatic infected humans, and recovered humans with time for the various kinds of type-2 infection rate of human.

Figure 7 demonstrates that, the number of quarantined people is decreasing as the type-2 infection rate of humans increases globally. Due to the decrease in the global, the type-2 infection rate of humans and the number of asymptomatic infected humans has also decreased, while the number of symptomatic infected humans and the isolated humans has increased.

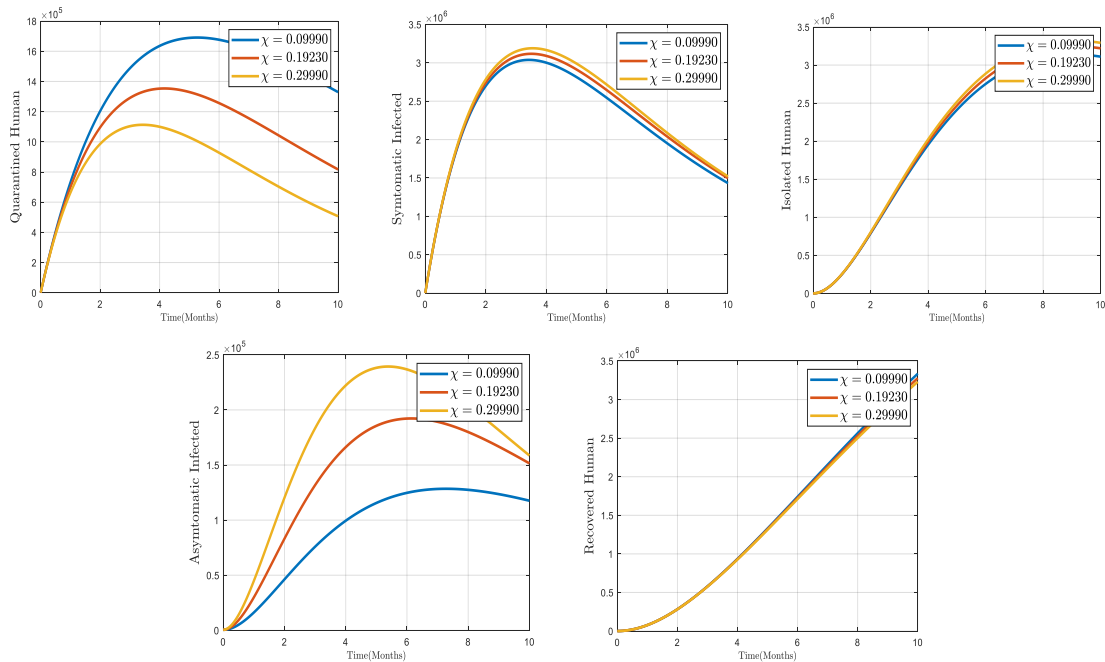


Figure 7. Variations of the type-II rate of infection for our model of human COVID-19 transmission network (1)-(12) where $\chi_1 = 0.09990$; $\chi_2 = 0.19230$; $\chi_3 = 0.29990$ and the time range 0 to 10 months.

In Figure 8, it is shown the variation of symptomatic infected humans, isolated humans, asymptomatic infected humans, quarantined humans, and recovered humans with time for the various kinds of quarantine infection rates of the human population.

Figure 8 demonstrates that the number of symptomatic infected humans, isolated humans, asymptomatic infected humans, quarantined humans, and recovered humans is decreasing globally as the quarantine infection rate of humans has decreased. Due to an increase in the global "human quarantine rate and quarantined humans, the numbers of symptomatic infected humans, isolated humans, asymptomatic infected people, and recovered humans has decreased.

In Figure 9, it is shown the variation of symptomatic infected humans, isolated humans, asymptomatic infected humans, quarantined humans, and recovered humans with time for the various kinds of quarantine recovery rate for COVID-19 transmission network.

Figure 9 demonstrates that the rate of quarantined and asymptomatic infected humans is decreasing as the quarantined recovery rate of humans grows globally. Due to the global increase in the quarantine recovery rate of people, the number of recovered individuals has increased. There is little effect on the

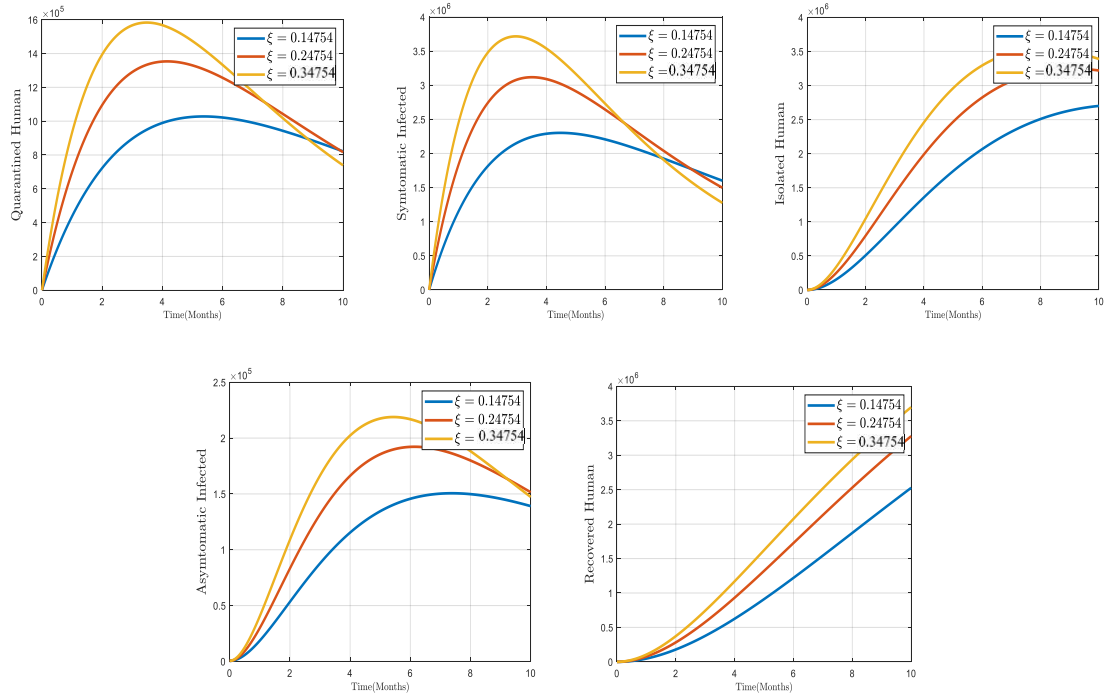


Figure 8. Variations of the quarantine infection rate of human for our model (1)-(12) of COVID-19 transmission network where $\xi_1 = 0.14754$; $\xi_2 = 0.24754$; $\xi_3 = 0.34754$ and the time range 0 to 10 months.

quarantined recovery rate of humans for symptomatic infected persons and isolated infected humans.

Discussion

All governments have implemented measures aimed at minimizing the destructive nature of this epidemic. After World-War-II, the COVID-19 epidemic is the second-worst calamity in the world. Initially, a dynamic computational and mathematical model of the reservoir, the mediator, and the humans are presented. This analysis supports the utilization of a system of nonlinear ordinary differential equations (ODEs), including the effective parameters of the COVID-19 transmission network for the reservoir, mediator, and human population. The equilibrium points of the mentioned model have been calculated. A stability study was conducted at the equilibrium points for the validity of the model. It was determined that whenever the equilibrium point is stable or unstable, analytical analysis is performed alongside the positivity test, equilibrium points, stability at the disease-free equilibrium point and the endemic equilibrium point and sensitivity analysis. We have utilized twelve compartments in the schematic network diagram. The compartments are referred to as variables. In addition, we have performed against objectives, the features of symptomatic infected, separated, asymptomatic and confined individuals throughout the COVID-19 epidemic. All of the parameters are mutually dependent and linked. We have provided the computational and numerical findings with their explanations, which demonstrate that as viral transmission increases, COVID-19 illnesses will rise as well. In addition, the findings say that people who have COVID-19 infections now need to be found quickly so that the virus doesn't spread to other people.

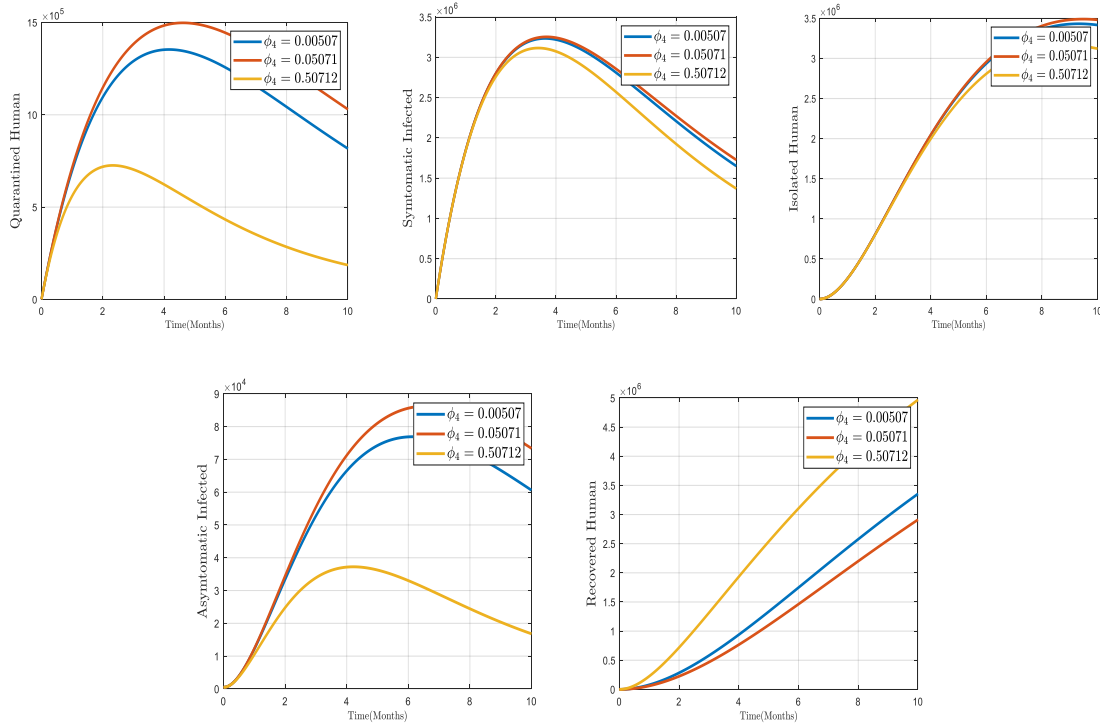


Figure 9. Variations of the quarantine recovery rate human for our model (1)-(12) of COVID-19 transmission network where $\phi_4 = 0.00507$; $\phi_4 = 0.05071$; $\phi_4 = 0.50712$ and the time range 0 to 10 months.

Conclusion

We are able to establish how the COVID-19 virus transmission network among individuals in our model. The model demonstrated unequivocally that disease propagation is strongly reliant on transmission rates among infected individuals who are unwell, isolated, asymptomatic, or quarantined. This is due to the conclusion of model.COVID-19 transmission may be decreased by early detection, which implies that new cases must be identified as soon as possible to allow for timely treatment. More people must be informed in order to improve public awareness about the virus's spread in society. We must assist individuals who have been impacted in order to recover and get the illness under control. A healthcare provider must take preventative actions that are both appropriate and proactive. We are aware that a few vaccines have reached the market. Despite their greatest efforts, they are unable to eradicate the most devastating variants virus. We may believe that increasing social awareness, such as wearing a mask and hand sanitizer, as well as social distancing and treatment for people who have been exposed to or infected with COVID-19, can help us reduce COVID-19 infections throughout our whole nation and regions.As a result, we recommend that our future research should focus on how to control COVID-19 sickness through the development and investigation of an effective vaccine that can detect and treat all of the most serious COVID-19 diseases.

References

Biswas, M. H., Khatun, M. S., Paul, A. K., Khatun, M. R., Islam, M. A., Samad, S. A., & Ghosh, U. (2020). Modeling the effective control strategy for the transmission dynamics of global pandemic covid-19. <https://doi.org/10.1101/2020.04.22.20076158>

- Biswas, M. H., Paul, A. K., Khatun, M. S., Mandal, S., Akter, S., Islam, M. A., Khatun, M. R., & Samad, S. A. (2021). Modeling the spread of covid-19 among doctors from the asymptomatic individuals. *Mathematical Analysis for Transmission of COVID-19*, 39–60. https://doi.org/10.1007/978-981-33-6264-2_3
- Coronavirus cases: Worldometer. (n.d.). Retrieved July 19, 2021, from <https://www.worldometers.info/coronavirus/>
- Disease Control and Corona Info. IEDCR. (n.d.). Retrieved May 3, 2022, from <https://iedcr.gov.bd/>
- Dym, C. L. (2008). *Principles of Mathematical Modeling*. Elsevier Academic Press.
- Kermack, W., & McKendrick, A. (1991). Contributions to the mathematical theory of epidemics—III. further studies of the problem of endemicity. *Bulletin of Mathematical Biology*, 53(1-2), 89–118. [https://doi.org/10.1016/s0092-8240\(05\)80042-4](https://doi.org/10.1016/s0092-8240(05)80042-4)
- Khatun, M. S., & Biswas, M. H. (2020). Modeling the effect of adoptive T cell therapy for the treatment of leukemia. *Computational and Mathematical Methods*, 2(2). <https://doi.org/10.1002/cmm4.1069>
- Maron, D. F. (2021, May 3). 'wet markets' launched the coronavirus. here's what you need to know. *Animals*. Retrieved May 19, 2022, from <https://www.nationalgeographic.com/animals/article/coronavirus-linked-to-chinese-wet-markets>
- Last, J. M. (1988). *A dictionary of epidemiology*. Oxford University Press.
- Rothan, H. A., & Byrareddy, S. N. (2020). The epidemiology and pathogenesis of coronavirus disease (COVID-19) outbreak. *Journal of Autoimmunity*, 109, 102433. <https://doi.org/10.1016/j.jaut.2020.102433>
- World Health Organization. (n.d.). *Report of the WHO-china joint mission on coronavirus disease 2019 (covid-19)*. World Health Organization. Retrieved May 19, 2022, from [https://www.who.int/publications-detail-redirect/report-of-the-who-china-joint-mission-on-coronavirus-disease-2019-\(covid-19\)](https://www.who.int/publications-detail-redirect/report-of-the-who-china-joint-mission-on-coronavirus-disease-2019-(covid-19))