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Research Article

Fuzzy SEIR Modeling and Analysis of COVID-19 Spread and Control

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Abstract: The main objective of the paper is to construct an susceptible-exposed-infected-recovered (SEIR) mathematical model by considering the transmission rate, death rate, and recovery rate as fuzzy parameters since we assumed heterogeneity in the population. We have examined the domain of the solutions and discussed the uniqueness of the constructed SEIR model. A qualitative analysis has been carried out to determine the stability of COVID-19 using Routh-Hurwitz criteria. The basic reproduction number is obtained using the next-generation matrix method. Fuzzy basic reproduction numbers with respect to various virus loads have been calculated to know how fast the disease spreads at different levels of virus loads. One of the main aims is to perform sensitivity analysis, which is essential for determining the controlling parameter and helps the government and other policymakers develop regulations for the prevention and control of the spread. The numerical simulation, which has been calculated using the homotopy perturbation method and illustrated graphically, shows the importance of getting vaccinated, which is important in controlling the spread of COVID-19.

Keywords: uniqueness, stability, fuzzy basic reproduction number, sensitivity analysis

MSC: 93A30, 03B52, 34K20, 74G55

1. Introduction

All individuals around the world have undergone a significant transformation as a result of COVID-19, one of the largest groups of RNA viruses and the primary cause of the deadly disease. The sickness not only had a significant negative influence on people's health, but it also had long-term financial and economic effects on everyone's lives. The disease's societal disruption is so severe that it leads to crises like acute poverty, unemployment, and child labor. Three years have passed since COVID shook the world, and individuals are still struggling to recover from the difficulties they faced. The disease was originally discovered in Wuhan, China, according to the World Health Organization (WHO), and the first case was reported on 31 December 2019. WHO proclaimed the illness a pandemic in March 2020 as it began to spread like wildfire. Although almost all of the governments established curfews, they took steps to ensure that this would not have an influence on children's education. The illness is contagious, and symptoms include coughing, sneezing, loss of taste and smell, decreased oxygen levels, and sore throats. As the disease's fatality rate rose rapidly, researchers and scientists around the world began working round-the-clock to produce a vaccine in the hope that it would help to stop the pandemic and save lives. Vaccines are typically used to increase the generation of antibodies

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against a disease. As of May 2022, nearly all of the high-income countries had vaccinated 70% of their populace.

In terms of understanding, spreading, and controlling the disease in a systematic way, mathematical models are essential. It is simple to use modern computing capabilities to get the desired results. This is used to resolve issues across a number of fields. A mathematical model is crucial to understanding the various dynamics of a disease and thereby overcoming it early on. To explain how disease spreads in the Indian desert region of Bhilwara, the scientists used a compartmental model. They discovered a substantial difference in the number of infected cases, recovered cases, and case fatality rates over all four lockdown phases, with 95% and 99% confidence intervals [1]. The analysis of COVID-19's spread across a specific time period was suggested using an improved susceptible-infected-recovered (SIR). They determined that during that time, the cure rate was 0.05 and the reproduction rate was 0.4490. Their study's findings suggested that the illness had been under control in China [2]. Tomchin and Fradkov [3] compared the anticipated outcomes for the SIR and susceptible-exposed-infected-recovered (SEIR) models, and they came to the conclusion that the data may be used to assess the effectiveness of lockdown protocols and choose the best strategy for quarantine measures. The authors of this study emphasized how the best method to cure this pandemic was to keep infected people away from healthy people and that migration should be rigorously prohibited in order to save human lives [4]. The authors of this article used a SIR model to analyze the spread of COVID-19 in a number of communities, including China, South Korea, India, Australia, the United States, Italy, and the state of Texas in the USA [5]. The authors built a COVID-19 infection model based on the SIR model that considered the potential effects of temperature, humidity, urban population density, and the rigor of control efforts. They then displayed the graphical results with time series for the daily number of fresh victims in six different nations [6]. The authors devised a new mathematical framework for COVID-19 and looked into elements including the invariant region, equilibrium state, and number. Additionally, a numerical simulation applying the least squares estimation method is provided, which leads to the conclusion that an increase in the pandemic will have greater effectiveness [7]. By using various fractional values associated with uncertainty, the authors examined fractional-order fuzzy dynamical systems and provided numerical approximations to illustrate the suggested strategy [8]. In this study, the model was examined using both fractional and ordinary differential equations. They concluded by saying that government officials must exert great effort to guarantee that interaction between those who are exposed and those who are susceptible is kept to a minimum [9]. Laplace transform and a few decomposition techniques were utilized by Shah et al. [10] to compute series-type solutions under fuzzy concepts. The authors of this article developed an algorithm based on the homotopy perturbation method that computes the results in series form and is rapidly convergent to the exact solution [11]. The authors investigated fuzzy fractional Volterrra-Fredholm integro-differential equations under Caputo's derivative and then displayed 2D and 3D graphs to examine the behavior of solutions for numerical instances at different levels of uncertainty [12]. An eight-compartment mathematical model was created by Ndaïrou et al. [13]. It differs from previous COVID-19-based models in that it includes the super spreaders class. Fanelli and Piazza [14] created a susceptible-infected-recovered-death (SIRD) model by categorizing people into classes for susceptibility, infection, recovery, and death. Using actual data, they ran simulations of the model for France, Italy, and mainland China. They also predicted the spread of COVID-19 in these three nations [14]. The researchers calculated the r0 value for COVID-19 at Hubei, China, and came to the conclusion that if the problem is not effectively solved, the disease will last for a very long time [15]. Laplace and decomposition fechniques (LADM) have been shown graphically by Din et al. to be a reliable and effective way of dealing with nonlinear problems [16]. An analysis of a noninteger-order model for Hepatitis B (HBV) under a singular-type Caputo fractional-order derivative has been compared with real data, which gives a better result as compared to an integer-order simulation [17]. Noises play a crucial role in controlling the spread of an epidemic, as demonstrated by the simulation [18]. This research will offer a solid foundation for researching the behavior and mechanisms of chronic infections. Extremely complex and realistic models are created by Tagliazucchi et al. [19], varying from straightforward and homogeneous models that calculate local reproduction rates to fully coupled inhomogeneous models that take into account migration predictions from mobile phone location data.

2. Preliminaries

2.1 *Fuzzy set*

Let X be a non-empty, crisp set. A fuzzy subset F of X is indicated as $\widetilde{F}$ and is defined as [20]

$$\widetilde{F} = \left\{\left(x, \mu_{F(x)}\right) : x \in X\right\}$$

where μ_F: $X \rightarrow [0,1]$ is a membership function in view with a fuzzy set $\widetilde{F}$, which describes the degree of belongingness of x with X.

Here, we use the membership function $\mu(x)$ to denote the fuzzy subsets $\tilde{S}$. Also, $\mu(x)$ is called a fuzzy number if X is the set of real numbers.

2.2 *Membership function*

Membership function $\mu_A(X)$ is a mapping from the universe X to the interval [0, 1] given as μ: $(X) \longrightarrow [0, 1]$ [20].

2.3 *Triangular fuzzy number*

The equation given below is the triangular fuzzy number for three parameters, $F(x: a, b, c)$

$$F(x:u,v,w) = \begin{cases} 0, & \text{if } x < u, \\ \dfrac{x-u}{v-u} & \text{if } a \le x < v, \\ \dfrac{w-x}{w-v} & \text{if } u < x \le v, \\ 0, & \text{if } x > v, \end{cases} \tag{1}$$

2.4 *Fuzzy measure*

Let φ be a non-empty set, and $M(\varphi)$ denote the set of all subsets of φ. Then, μ: $\varphi \rightarrow [0, 1]$ is a fuzzy measure if [21].

1) $\mu(\phi) = 0$ and $\mu(\varphi) = 1$
2) for X, $Y \in M(\varphi)$, $\mu(X) \le \mu(Y)$ if $X \subset Y$

Let μ: $\varphi \rightarrow [0, 1]$ be a fuzzy variable, i.e., μ is a fuzzy subset and μ a fuzzy measure on φ. Then, the fuzzy expected value (FEV) of μ is the real number, defined by the Sugeno measure

$$FEV(\mu) = \int \mu d\mu = \sup\left\{\min(\alpha, k(\alpha))\right\}, 0 \le \alpha \le 1$$

where $k(\alpha) = \mu\{\omega \in \varphi: \mu(\omega) \ge \alpha\}$.

2.5 *Sensitivity index*

The normalized forward sensitivity index [22, 23] of R_0, which is differentiable with respect to a given parameter, p, is defined by

$$S_p^{R_0} = \frac{\partial R_0}{\partial p} * \frac{p}{R_0}.$$

3. Method

We take the transmission rate, recovery rate, and death due to COVID-19 as fuzzy parameters for the mathematical

model in this research. The next-generation matrix approach is used to determine the basic reproduction number. We apply the Routh-Hurwitz criteria to determine the disease's stability. The most sensitive parameter has been calculated to reduce the spread using the normalized forward-sensitive index definition. The homotopy perturbation method has been used to perform the numerical simulation. We apply the MATLAB program to graphically represent the numerical simulation.

3.1 *Fuzzy SEIR mathematical model*

In this paper, we propose SEIR, a four-compartment model, where S is the number of susceptible population, E is the number of exposed population, who are in the state of not knowing if they are infected or not, I is the number of infected population, whose body is affected by the virus, R is the number of recovered population, who have been recovered from the virus infection, and N is the total number of population. Using non-linear ordinary differential equations, the proposed model depicts how all compartments interact with one another [24].

$$\begin{aligned}
\frac{dS}{dt} &= \varepsilon - (\sigma(v)I + \varepsilon + \vartheta)S \\
\frac{dE}{dt} &= \sigma(v)IS - (\alpha + \varepsilon)E \\
\frac{dI}{dt} &= \alpha E - \left(\alpha_i + \mu(v) + \varepsilon\right)I \\
\frac{dR}{dt} &= \mu(v)I + \vartheta S - \varepsilon R
\end{aligned} \tag{2}$$

where $N = S + E + I + R$.

Table 1. Description of parameters

Parameters	Description
ε	Rate of birth/death
σ	Transmission rate
α	Number of days taken to probably change from E to I
α_i	Rate of death population due to COVID-19
μ	Recovery rate
ϑ	Vaccination for susceptible population
v	Virus load

3.2 *Schematic diagram*

The following Figure 1 is the schematic representation of considered SEIR model along with the parameters.

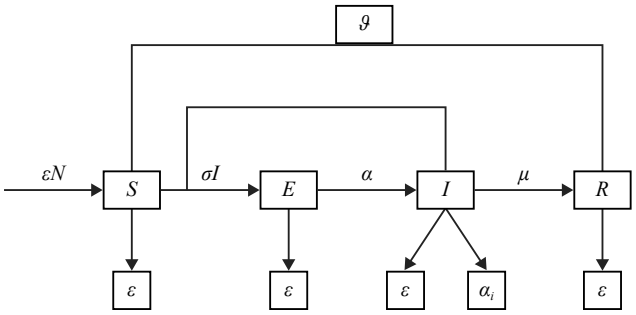

Figure 1. Schematic representation of the model

3.3 *Analysis of fuzzy system*

Let $\sigma = \sigma(v)$ be the chance of transmission, which is most likely shifting from susceptible to exposed. The transmission of the diseases varies depending on the virus load. The fuzzy membership function for the transmission parameter can be seen in the following equation. The membership function of transmission rate is depicted in Figure 2 below.

$$\sigma(v) = \begin{cases} 0, & \text{if } v < v_m, \\ \dfrac{v - v_m}{v_0 - v_m}, & \text{if } v_m \le v \le v_0, \\ 1, & \text{if } v_0 < v < v_M, \end{cases}$$

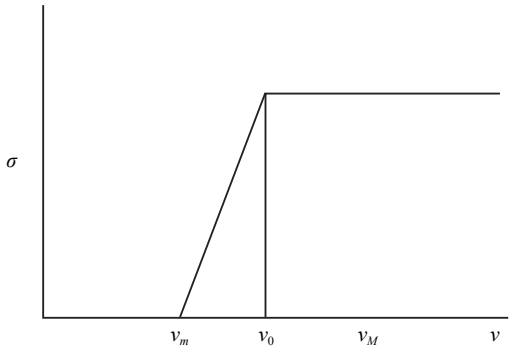

Figure 2. Membership function of $\sigma(v)$

The equation clearly demonstrates that there is almost no likelihood of virus transmission when the amount of virus load is minimal (v_m). There must be a certain amount of virus for transmission to occur (v_0). The amount of virus for each disease is always constrained by v_M.

Let $\alpha_i = \alpha_i(v)$ be the fuzzy membership function for the COVID-19 death rate. When the virus load is minimal, there will be no disease transmission, say γ_0, and the death rate will grow as the virus load increases. The death rate is considered to have a maximum value of $(1 - \eta)$, when $\eta \ge 0$.

$$\alpha_i(v) = \begin{cases} \dfrac{((1-\eta) - \alpha_{i0})}{v_0} v + \alpha_{i0}, & \text{if } 0 \le v \le v_0 \\ 1 - \eta, & \text{if } v_0 < v \end{cases}$$

The lowest death rate is $0 < \alpha_{i0} < 1$.

The recovery rate is also considered a fuzzy parameter. It is a decreasing function because the longer it takes to recover from infection, the higher the virus load. The equation below is the representation of the membership function of $\mu = \mu(v)$.

$$\mu(v) = \begin{cases} \dfrac{(\mu_0 - 1)}{v_M} v + 1, & \text{if } 0 \le v \le v_M \end{cases}$$

where $\mu_0 > 1$ is the lowest recovery rate.

Figures 3 and 4 represent the membership functions of $\alpha_i(v)$ and $\mu(v)$, respectively.

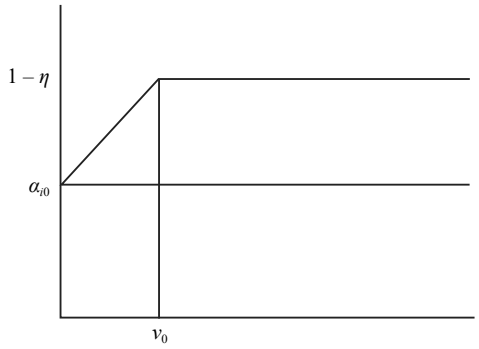

Figure 3. Membership function of $\alpha_i(v)$

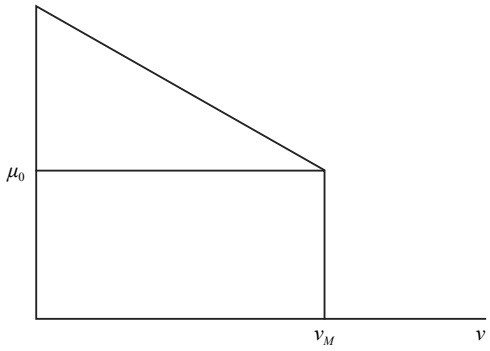

Figure 4. Membership function $\mu(v)$

Additionally, we take into account that various people have different viral loads because virus load is considered a linguistic variable. Following is a list of the members of the linguistic variable [9]. From (1),

$$\Gamma(y) = \begin{cases} 0, & \text{if } v - \overline{v} + \delta \\ \dfrac{v - \overline{v} + \delta}{\delta}, & \text{if } \overline{v} - \delta \le v \le \overline{v} \\ \dfrac{-(v - \overline{v} + \delta)}{\delta}, & \text{if } \overline{v} \le v \le \overline{v} + \delta \\ 0, & \text{if } v > \overline{v} + \delta \end{cases}$$

The center value and the dispersion of each fuzzy set assumed are denoted by the symbols $\overline{v}$ and δ. The linguistic variable [25] is categorized as weak, medium, and high. Every categorization can be visualized as a fuzzy number with a triangular form. The membership function $\Gamma(v)$ is depicted diagrammatically in Figure 5.

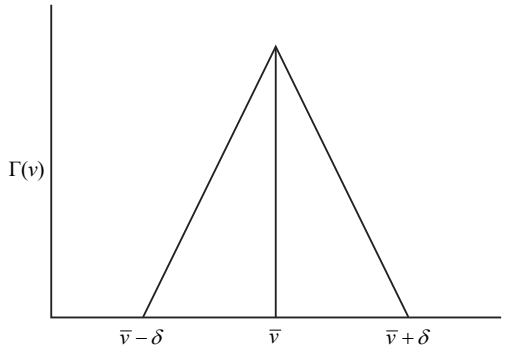

Figure 5. Membership function $\Gamma(v)$

3.4 *Well-posedness and boundedness*

Theorem 1. The solutions of the system are well-posed for all $t > 0$.

Proof. Let $P = \{(S, E, I, R)\} \in \mathbb{R}^4$: $0 \leq S, E, I, R\}$.

We need to show that P is a positive invariant, to do so we look at the behavior of the state variables at the boundedness of P.

i) On the boundary $S = 0$,

$$S' = \varepsilon > 0.$$

The solution cannot exit P by stepping over this limit.

ii) On the boundary $E = 0$,

$$E' = \sigma IS.$$

Case 1:
$E = 0, S > 0, I > 0$, then $E' > 0$.
Case 2:
$E = 0, S > 0, I = 0$, then $E' = 0$.
Case 3:
$E = 0, S = 0, I > 0$, then $E' = 0$.
Therefore, in all the cases E', the solution cannot exit P by stepping over this limit.

iii) On the boundary $I = 0$,

$$I' = \alpha E.$$

Case 1:
$I = 0, E > 0$, then $I' > 0$.
Case 2:
$I = 0, E = 0$, then $I' = 0$.
Thus, the solution cannot exit P by stepping over this limit.

iv) On the boundary $R = 0$,

$$R' = \mu I + \vartheta S.$$

Case 1:
$R = 0$, $S > 0$, $I > 0$, then $R' > 0$
Case 2:
$R = 0$, $S > 0$, $I = 0$, then $R' > 0$.
Case 3:
$R = 0$, S = 0, $I > 0$, then $R' > 0$.
Case 4:
$R = 0$, $S = 0$, $I = 0$, then $R' = 0$.
Thus, the solution cannot exit P by stepping over this limit.

Theorem 2. The system's solution is bounded on [0, b) for some $b > 0$.

Proof. We know that $N = S + E + I + R$. Therefore,

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dE}{dt} + \frac{dI}{dt} + \frac{dR}{dt},$$

which implies

$$\frac{dN}{dt} = \mu - \mu N$$
$$N = 1 - (1 - N(0))e^{-\mu t}$$
$$\limsup_{t \to \infty} N \leq 1.$$

Hence, $S(t)$, $E(t)$, $I(t)$, and $R(t)$ are all bounded above by 1 on [0, b) for some $b > 0$. Therefore, we conclude that the system's solution is bounded on [0, b) for some $b > 0$.

3.5 *Existence and uniqueness*

Theorem 3. The solutions of the system with non-negative initial conditions exist and are unique.

Proof. Let $u(t) = (S(t), E(t), I(t), R(t))$ $\mathbb{R}^4$.

Let

$$V_1 = \varepsilon - (\sigma I + \varepsilon + \vartheta)\, S$$
$$V_2 = \sigma IS\, (\alpha + \varepsilon)E$$
$$V_3 = \alpha E - (\alpha_i + \mu + \varepsilon)I$$
$$V_4 = \mu I + \vartheta S - \varepsilon R$$

where the system of equation is in the form $u' = V(u)$, V_i, i = 1, 2, 3, 4, represent the components of the vector field. This field is composed of algebraic polynomials of state variables. Thus, V_i is a continuous function on $\mathbb{R}^4$ and $\frac{\partial V_i}{\partial S}, \frac{\partial V_i}{\partial E}, \frac{\partial V_i}{\partial I}, \frac{\partial V_i}{\partial R}$ are the partial derivatives, which exist and are continuous. Thus, there exist a unique solution $u' = V(u)$ for any initial condition, $x(0) \in \mathbb{R}^4$ [26] using existence and uniqueness theorem.

3.6 *Equilibrium points*

There exist two equilibrium points, namely the disease-free equilibrium point and the endemic equilibrium point.

3.6.1 *Disease-free equilibrium point*

$$E_d = \left(\frac{\varepsilon}{\varepsilon + \vartheta}, 0, 0, 0 \right)$$

3.6.2 *Endemic equilibrium point*

$$S_1 \frac{(\alpha+\varepsilon)(\alpha_i+\mu+\varepsilon)}{\sigma\alpha}$$

$$E_1 \frac{\sigma\varepsilon\alpha - (\alpha_i+\mu+\varepsilon)(\varepsilon+\vartheta)(\alpha+\varepsilon)}{\sigma\alpha(\alpha+\varepsilon)}$$

$$I_1 = \frac{\varepsilon\sigma\alpha - (\varepsilon+\vartheta)(\alpha+\varepsilon)(\alpha_i+\mu+\varepsilon)}{\sigma(\alpha_i+\mu+\varepsilon)(\alpha+\varepsilon)}$$

$$R_1 = \frac{\mu\varepsilon\sigma\alpha^2 - \mu\alpha(\varepsilon+\vartheta)(\alpha+\varepsilon)(\alpha_i+\mu+\varepsilon) + \vartheta\left((\alpha+\varepsilon)(\alpha_i+\mu+\varepsilon)\right)^2}{\mu\varepsilon\sigma\alpha(\alpha+\varepsilon)(\alpha_i+\mu+\varepsilon)}$$

$$E_e = (S_1, E_1, I_1, R_1) = \left(\begin{array}{c} \frac{(\alpha+\varepsilon)(\alpha_i+\mu+\varepsilon)}{\sigma\alpha}, \frac{\sigma\varepsilon\alpha - (\alpha_i+\mu+\varepsilon)(\varepsilon+\vartheta)(\alpha+\varepsilon)}{\sigma\alpha(\alpha+\varepsilon)}, \frac{\varepsilon\sigma\alpha - (\varepsilon+\vartheta)(\alpha+\varepsilon)(\alpha_i+\mu+\varepsilon)}{\sigma(\alpha_i+\mu+\varepsilon)(\alpha+\varepsilon)}, \\ \frac{\mu\varepsilon\sigma\alpha^2 - \mu\alpha(\varepsilon+\vartheta)(\alpha+\varepsilon)(\alpha_i+\mu+\varepsilon) + \vartheta\left((\alpha+\varepsilon)(\alpha_i+\mu+\varepsilon)\right)^2}{\varepsilon\sigma\alpha(\alpha+\varepsilon)(\alpha_i+\mu+\varepsilon)} \end{array} \right).$$

4. Qualitative analysis of the model

4.1 *Basic reproduction number*

The average number of secondary infections that a single infected person causes over the course of their whole contagious lifetime is known as the basic reproduction number.

Theorem 4. The basic reproduction number is $R_0 = \frac{\alpha\sigma\varepsilon}{(\alpha+\varepsilon)(\alpha_i+\mu+\varepsilon)(\varepsilon+\vartheta)}$.

Proof. Consider the following system of equation (2):

$$\frac{dS}{dt} = \varepsilon - (\sigma I + \varepsilon + \vartheta)S$$

$$\frac{dE}{dt} = \sigma IS - (\alpha+\varepsilon)E$$

$$\frac{dI}{dt} = \alpha E - (\alpha_i+\mu+\varepsilon)I$$

$$\frac{dR}{dt} = \mu I + \vartheta S - \varepsilon R$$

$$\mathcal{F} = \begin{bmatrix} 0 & \sigma S \\ \alpha & 0 \end{bmatrix} \upsilon = \begin{bmatrix} \alpha+\varepsilon & 0 \\ 0 & \alpha_i+\delta+\mu \end{bmatrix}$$

$$\rho = \mathcal{F}\upsilon^{-1} = \begin{bmatrix} 0 & \frac{\sigma S}{\alpha_i+\mu+\varepsilon} \\ \frac{\alpha}{\alpha+\varepsilon} & 0 \end{bmatrix}$$

$$\rho = \frac{\alpha\sigma\varepsilon}{(\alpha+\varepsilon)(\alpha_i+\mu+\varepsilon)(\varepsilon+\vartheta)}$$

Thus,

$$R_0 = \frac{\alpha\sigma\varepsilon}{(\alpha+\varepsilon)(\alpha_i+\mu+\varepsilon)(\varepsilon+\vartheta)}. \tag{3}$$

4.2 *Stability analysis*

4.2.1 *Disease-free equilibrium*

Theorem 5. If R_0 <1, then at the disease-free equilibrium point, the system is locally asymptotically stable; otherwise. it is unstable.

Proof. The Jacobian matrix at $\left(\frac{\varepsilon}{\varepsilon+\vartheta},0,0,0\right)$

$$J = \begin{bmatrix} -(\varepsilon+\vartheta) & 0 & \frac{-\sigma\varepsilon}{\varepsilon+\vartheta} & 0 \\ 0 & -(\alpha+\varepsilon) & \frac{\sigma\varepsilon}{\varepsilon+\vartheta} & 0 \\ 0 & \alpha & -(\alpha_i+\mu+\varepsilon) & 0 \\ \vartheta & 0 & \mu & -\varepsilon \end{bmatrix}$$

$$|J-\lambda I| = \lambda^4 + \lambda^3(A+B+C+D) + \lambda^2(AB+(A+B)(C+D)+CD-E)$$
$$+\lambda((A+B)(CD-E)+AB(C+D))+ABCD-ABE=0.$$

Where

$$A = \varepsilon$$
$$B = \varepsilon+\vartheta$$
$$C = \alpha+\varepsilon$$
$$D = (\alpha_i+\mu+\varepsilon)$$
$$E = \frac{\sigma\alpha\varepsilon}{\varepsilon+\vartheta}$$

$$A_1\lambda^4 + A_2\lambda^3 + A_3\lambda^2 + A_4\lambda + A_5 = 0.$$

Where

$$A_1 = 1$$
$$A_2 = A+B+C+D$$
$$A_3 = (AB+(A+B)(C+D)+CD-E)$$
$$A_4 = (A+B)(CD-E)+AB(C+D)$$
$$A_5 = ABCD-ABE.$$

Hence, the system is stable at disease-free equilibrium by Routh-Hurwitz criteria (refer to Appendix).

4.3 *Fuzzy basic reproduction number*

The basic reproduction number is $R_0(v) = \dfrac{\alpha\sigma(v)\varepsilon}{(\alpha+\varepsilon)(\alpha_i(v)+\mu(v)+\varepsilon)(\varepsilon+\vartheta)}$, which rises with an increase in virus load, cannot be a fuzzy set because it can be larger than 1. Thus, $0 \le \mu_0 R_0(v) \le 1$ where $\mu_0 R_0(v)$ is a fuzzy set, hence, $FEV[\mu_0 R_0(v)]$ is well defined. We introduce the fuzzy basic reproduction number in this approach.

The fuzzy basic reproduction number [27] is given by

$$R_0^f = \frac{1}{\mu_0} FEV\left(\mu_0 R_0(v)\right) \tag{4}$$

where $FEV(\mu_0 R_0(v)) = \sup\{\inf(\alpha, k(\alpha))\}$, $0 \le \alpha \le 1$, $k(\alpha) = \mu\{v : \mu_0 R_0(v) \ge \alpha\} = \mu(X)$, which is a fuzzy measure [21]. To get $FEV(\mu_0 R_0(v))$, we define fuzzy measure μ.

$\mu(X) = \sup \Gamma(v)$, $\forall\ \sigma \in X$, $X \subset R$, which is a possibility measure.

From $FEV(\mu_0 R_0(v))$, it is clear that $R_0(v)$ is not decreasing with v, where the set, $X = [\overline{v}, v_M]$ and $\overline{v}$ are the solutions of the equation given below.

$$\mu_0 \frac{\alpha\sigma(v)\varepsilon}{(\alpha+\varepsilon)(\alpha_i(v)+\mu(v)+\varepsilon)(\varepsilon+\vartheta)} = \alpha$$

Thus, $k(\alpha) = \mu[v', v_M] = \sup \Gamma(v)$ with $v' \le v \le v_M$, here $k(0) = 1$ and $k(1) = \Gamma(v_M)$.

The amount of virus v in the population, which was assumed to have a linguistic meaning is classified into three cases, and all of them have fuzzy behavior. They are weak virus load (v_M), medium virus load (v_0), and strong virus load (v_M).

Case 1: Weak virus load (v_M) (i.e.) when $\overline{v} + \delta < v_m$, we have

$$FEV\left(\mu_0 R_0(v)\right) = 0 < \mu_0 \Leftrightarrow R_0^f < 1$$

Thus, we can conclude that the disease will be extinct.

Case 2: Medium virus load (v_0) (i.e.) when $\overline{v} - \delta < v_m$ and $\overline{v} + \delta < v_0$. Therefore,

$$k(\alpha) = \begin{cases} 1, & \text{if } 0 < \alpha \le \mu_0 R_0(\overline{v}), \\ \Gamma(v'), & \text{if } \mu_0 R_0(\overline{v}) < \alpha \le \mu_0 R_0(\overline{v}+\delta), \\ 0, & \text{if } \mu_0 R_0(\overline{v}+\delta) < \alpha \le 1 \end{cases}$$

if $\delta > 0$, $k(\alpha)$ is continuous and decreasing function with $k(0) = 1$ and $k(1) = 0$. Hence, $FEV(\mu_0 R_0(v))$ is the fixed point of k and

$$\mu_0 R_0(\overline{v}) \le FEV\left(\mu_0 R_0(v)\right) \le \mu_0 R_0(\overline{v}+\delta)$$
$$R_0(\overline{v}) \le R_0^f \le R_0(\overline{v}+\delta).$$

As the function $R_0(\overline{v})$ is increasing and continuous, then by the intermediate value theorem, there exists v with $\overline{v} < v < \overline{v} + \delta$

$$R_0^f = R_0(v) > R_0(\overline{v}).$$

R_0^f and $R_0(v)$ coincide as there exist virus load. Since a medium amount of virus load is present, the average number of secondary cases R_0^f is higher than the number of secondary cases $R_0(\overline{v})$.

Case 3: Strong virus load (v_M) (i.e.) $\overline{v}-\delta > v_0$ and $\overline{v}+\delta < v_M$, then

$$k(\alpha)=\begin{cases}1, & \text{if } 0<\alpha\le \mu_0 R_0(\overline{v}),\\ \Gamma(v'), & \text{if } \mu_0 R_0(\overline{v})<\alpha\le \mu_0 R_0(\overline{v}+\delta),\\ 0, & \text{if } \mu_0 R_0(\overline{v}+\delta)<\alpha\le 1\end{cases}$$

similar to case 2, we have

$$\mu_0 R_0(\overline{v}) \le FEV\left(\mu_0 R_0(v)\right) \le \mu_0 R_0(\overline{v}+\delta)$$
$$R_0(\overline{v}) \le R_0^f \le R_0(\overline{v}+\delta).$$

Thus, $R_0^f > 1$, we can conclude that the disease will spread further.

4.4 *Sensitivity analysis*

Epidemiology may benefit greatly from sensitivity analysis. In sensitivity analysis, a model's results are examined for robustness. Sensitivity analysis is used to examine the elements that contribute to the spread and persistence of the disease in the community. We focus on the parameters that cause a greater variance in the value of the basic reproduction number. Early disease transmission is directly correlated with reproduction numbers. A sensitive parameter should be carefully estimated because even a slight change in this parameter can result in significant quantitative changes.

Table 2. Sensitive index values of the parameters

Parameters	Sensitivity index
α	0.00207
σ	1
ε	-0.290
α_i	-0.000106
μ	-0.096
ϑ	-0.6153

Figure 6 is a graphical illustration of the sensitivity index.

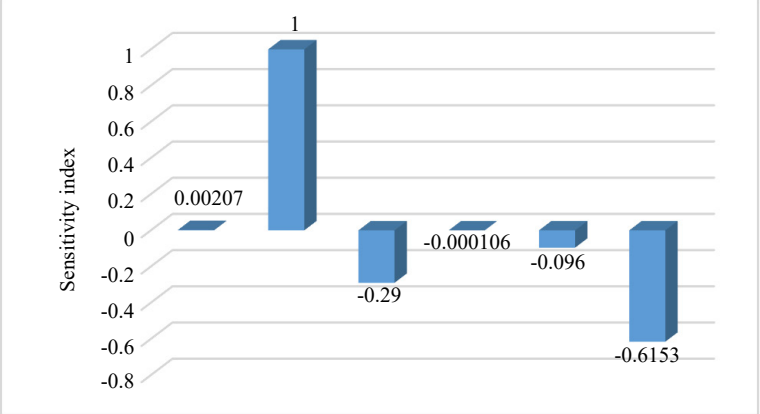

Figure 6. Sensitivity index

The sensitivity index has been calculated by considering $\alpha = 3$ and $\vartheta = 0.01$. The table makes it quite evident that as the birth rate rises, so do the rates of secondary infections. And the transmission rate will be at its highest during the phase where $\vartheta = 0.01$. The use of vaccinations is crucial in preventing the spread of disease. There will be a drop in the reproduction number as ϑ increases.

4.5 *Controlling parameters*

As was already noted, the main objective of this research is to determine the COVID-19 model's governing parameters in order to assist policymakers in considering various approaches for controlling the pandemic. Controlling parameters are those model parameters that have the greatest impact on output uncertainty. As an example, the governing parameter is ϑ. Therefore, based on this finding, policymakers could implement measures to regulate and prevent the spread of COVID-19.

4.6 *Bifurcation point*

At the disease-free equilibrium point, when $R_0(v) < 1$, the system is stable, and when it is greater than 1, it is unstable. Let v^* be the bifurcation value, which is given in the following equation:

$$v^* = \frac{\varepsilon\alpha v_m v_0 v_M + \left[\left(v_M v_0\left(\alpha_{i0}+\varepsilon\right)\right)\left(v_0 - v_m\right)\left(\alpha+\varepsilon\right)\left(\varepsilon+\vartheta\right)\right]}{\varepsilon\alpha v_0 v_M - \left[\left(v_M\left(1-\eta-\alpha_{i0}\right)\right)+v_0\left(\mu_0-1\right)\right]\left(v_0 - v_m\right)\left(\alpha+\varepsilon\right)\left(\varepsilon+\vartheta\right)}$$

where $v_m \le v^* \le v_0$.

We can think of v^* as a parameter connected to coronavirus control in the sense that it should be observed that v is not higher than v^* if a coronavirus is transmitted to a certain number of people.

Corollary. The disease-free equilibrium is locally asymptotically stable if $v < v^*$.

4.7 *Numerical simulation*

The data in Tables 3, 4, and 5 were collected from [24].

Table 3. Initial parameter values for SEIR model

Parameters	Estimated value
$N(0)$	269.6 juta
$S(0)$	37,538
$E(0)$	13,923
$I(0)$	23,191
$R(0)$	13,213

Table 4. Parameter values for SEIR model

Parameters	Estimated value
ε	$6.25^* 10^{-3}$
σ	$0.62^* 10^{-8}$ / person /day
α_i	$7.344 * 10^{-7}$
μ	0.0006667 per day

Table 5. Assumed parameter values for SEIR model

Parameters	Simulation 1	Simulation 2	Simulation 3
ϑ	1%	50%	100%
α	3 days	7 days	14 days

Figures 7, 8, and 9 represent the susceptible population with varying vaccination loads on varying days.

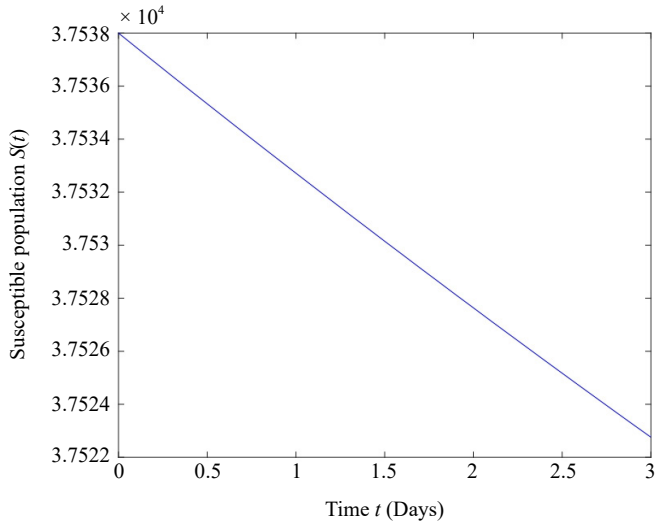

Figure 7. Susceptible population for $\vartheta = 0.01$, $\alpha = 3$ days

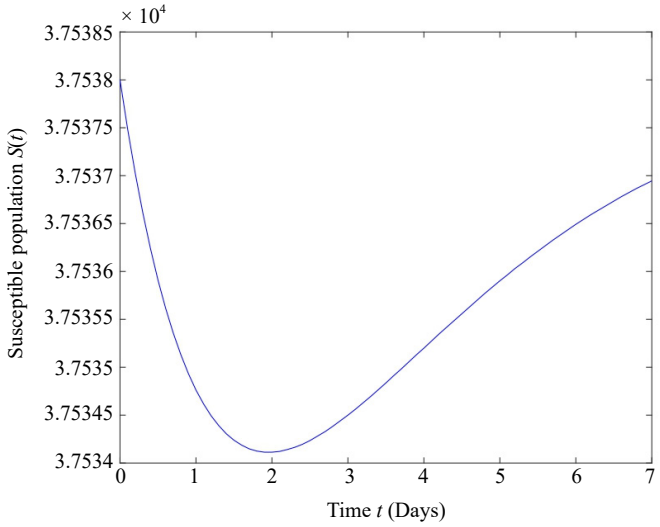

Figure 8. Susceptible population for $\vartheta = 0.5$, $\alpha = 7$ days

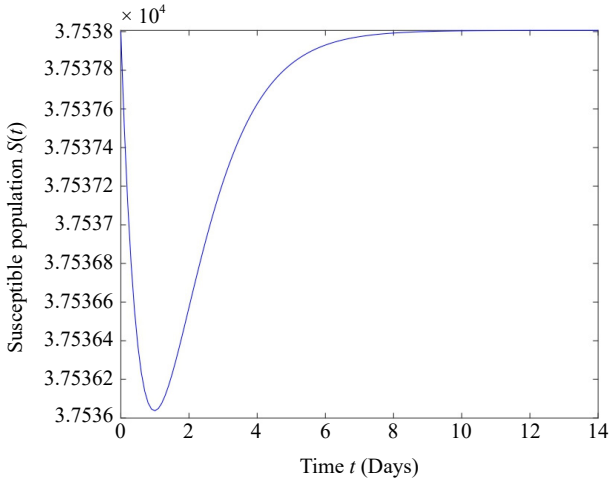

Figure 9. Susceptible population for $\vartheta = 1$, $\alpha = 14$ days

Similarly, Figures 10, 11, and 12 represent the exposed population, and Figures 13, 14, and 15 represent the recovered population with different vaccinations during various time periods.

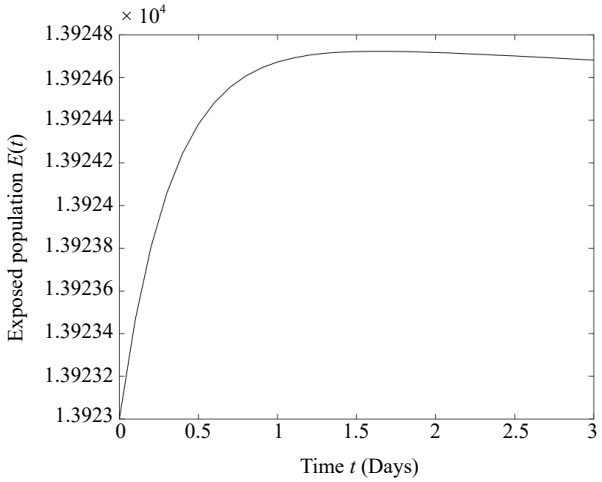

Figure 10. Exposed population for $\vartheta = 0.1$, $\alpha = 3$ days

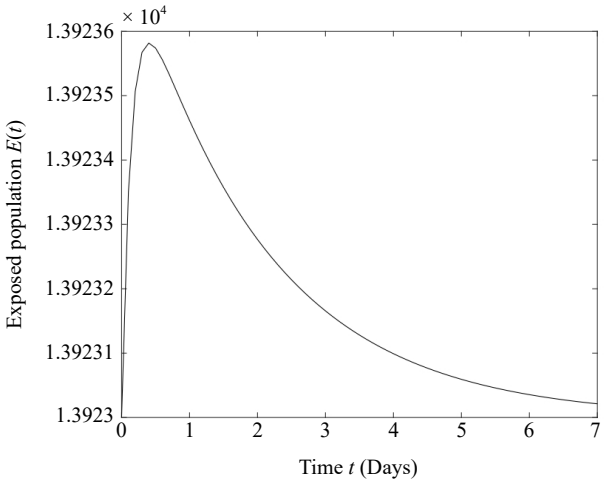

Figure 11. Exposed population for $\vartheta = 0.5$, $\alpha = 7$ days

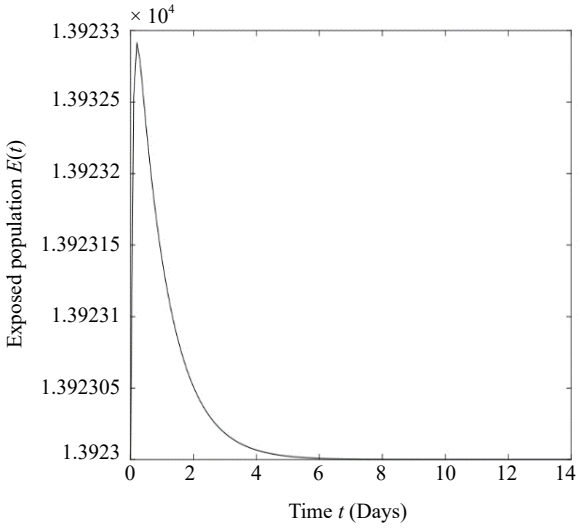

Figure 12. Exposed population for $\vartheta = 1$, $\alpha = 14$ days

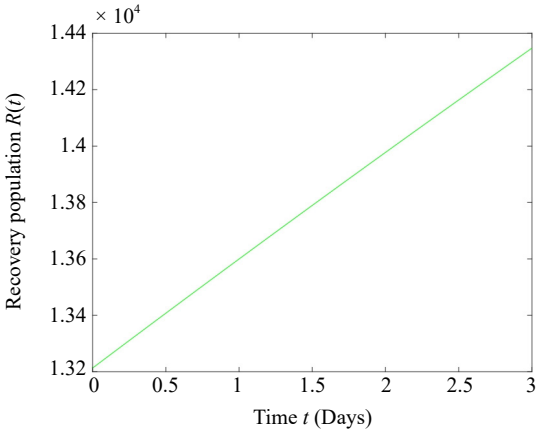

Figure 13. Recovered population for $\vartheta = 0.01$, $\alpha = 3$ days

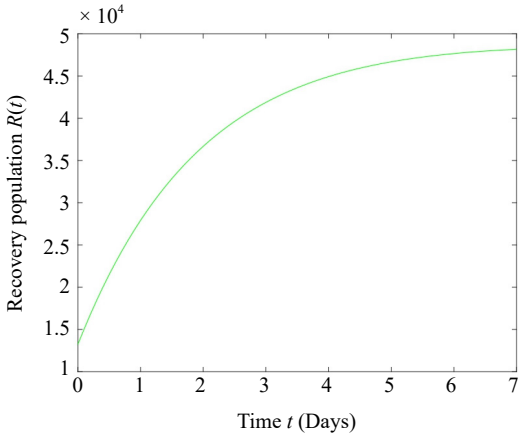

Figure 14. Recovered population for $\vartheta = 0.5$, $\alpha = 7$ days

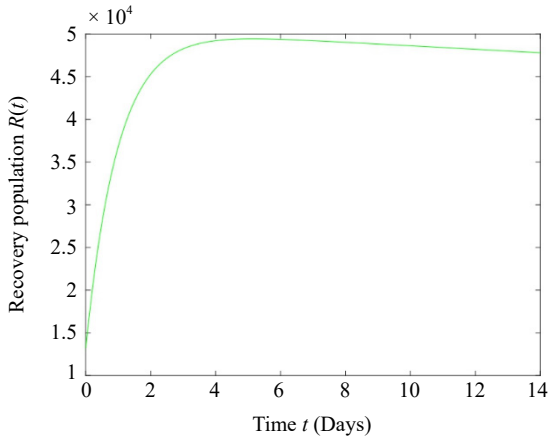

Figure 15. Recovered population for $\vartheta = 1$, $\alpha = 14$ days

5. Results and discussion

The figures make it abundantly evident that vaccination has a significant impact on the disease's spread and management. We could observe that the disease spreads more quickly if vaccination loads are lower. Similar to how the rate of vaccination increases the rate of recovery. This provides a clear image for government officials and policymakers to use when developing campaigns to educate the public about the benefits of getting vaccinated.

6. Conclusion

Our SEIR model offers a conceptual framework for studying the COVID-19 virus spread. The dynamics of COVID-19 in humans have been studied using a fuzzy modeling strategy. A vital role in disease transmission is played by the uncertain model parameters, such as the transmission rate, death rate, and recovery rate. COVID-19 cannot spread in the population when the virus load is low, and it will be endemic if the virus load is higher. The stability of the disease-free equilibrium suggests that COVID-19 can be controlled if $R_0 < 1$. Since vaccination is seen as a controlling factor, it can speed healing, while the COVID-19 isolation period can stop the virus transmission. To minimize and stop the spread of the disease, strict and sufficient safeguards must be set up. The findings of the research can be used as a guide for early disease prevention in any future outbreaks.

Conflict of interest

There is no conflict of interest in this study.

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Appendix

We verify the conditions for Routh-Hurwitz criteria

$$A_1\lambda^4 + A_2\lambda^3 + A_3\lambda^2 + A_4\,\lambda + A_5 = 0$$
$$A_1 = 1$$
$$A_2 = A + B + C + D = 3.035667434$$
$$A_3 = \left(AB + (A+B)(C+D) + CD - E\right) = 0.08869$$
$$A_4 = (A+B)(CD-E) + AB(C+D) = 0.0007738956$$
$$A_5 = ABCD - ABE = 0.0007738956$$

Condition: $A_2 > 0, A_2A_3 - A_1A_4 > 0, A_2A_3 - A_1A_4)A_4 - A_2^2A_5 > 0, A_5 > 0$

$$A_2 = 3.035667434 > 0$$
$$A_2A_3 - A_1A_4 = 0.268459448 > 0$$
$$A_2A_3 - A_1A_4)A_4 - A_2{}^2A_5 = 0.0001882970 > 0$$
$$A_5 = 0.00000211199 > 0$$

Since all the above conditions of the Routh-Hurwitz criteria are satisfied, the system is stable at disease-free equilibrium.