The Impact of Vaccination on COVID-19 Pandemic in the Kurdistan Region of Iraq: A Mathematical Modelling

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Abstract The spreading of COVID-19 became a global issue that had a significant impact on health, life, and economic sectors. Efforts from all over the world are focused on discussing a variety of healthcare approaches to reduce the effect of COVID-19 among individuals. Mathematical tools with numerical simulations are important approaches that help international efforts to determine critical transmission factors as well as controlling the virus spread. In this paper, we develop a mathematical model that considers a vaccination compartment in terms of ordinary differential equations. This study focuses on the real data of confirmed cases in Kurdistan Region of Iraq from July 17^{th} , 2021 to January 1^{st} , 2022. Model results and real data for the total number of infected people were compared using computational tools in MATLAB. Additionally, non-normalization, half-normalization, and full-normalization methods are used to determine the local sensitivities between model variables and parameters. Interestingly, computational results show that the dynamics of model results and real confirmed cases are very close to each other. Accordingly, the elasticity coefficients provide a great understanding of the impact of vaccination on transmissions. The model results here can also help international efforts for further suggestions and improvements to control this disease more effectively.

1 Introduction

In December of 2019, the COVID-19 pandemic appeared in Wuhan, China, where the majority of the first cases were recorded [1]. Since then, it has quickly expanded from Wuhan to other provinces in China and almost every other country worldwide [2]. Inside the affected countries, there are millions of reported cases globally [3]. The global spread of COVID-19 has become a problem; this virus became a threat to public health and spread easily from person to person [4, 5]. Global efforts are focused on addressed many healthcare solutions for limiting the effect of the novel coronavirus on communities around the world. According to a study given in [6], as May 26, 2022 there have been 524,878,064 confirmed cases of COVID-19, including 6,283,119, deaths around the world have been recorded. As of May 24, 2022, a total of 11,811,627,599 vaccine doses have been administered [7]. For the first time the COVID-19 was recorded in Kurdistan region of Iraq on March 1, 2020 [8, 9].

Modeling new coronavirus has recently become very important, and numerous mathematical and computational studies have been presented to predict disease dynamics [4]. Mathematical modelling has a great role in predicting and analyzing this disease, it includes some effective tools for understanding and interpreting the spreading of this disease. Although there were some mathematical approaches, computer simulations, and clinical tests for controlling this disease but there are still several aspects of this topic that may be addressed [10]. Spreading of the COVID-19 continues including a new round of epidemic of the COVID- 19 such as Delta and Omega [11]. Therefore, the COVID-19 virus should be studied further, including its vaccination impact and transmission mechanisms [12]. There were different mathematical models including the well-known standard SIR model and its improvements have been used to build model extensions [9, 10, 13, 14].

Several authors modified SIR model for studying the transmission of pathogens. The applications of optimal control are used to SIR model in [15]. The basic reproduction number,

sometimes called R_0 , is one of the most well-known terms in the field of epidemiology [16]. Estimating basic reproductive numbers is challenging, especially when the processes of data collection is difficult. For this reason, mathematical models are treated with caution [17]. In [8, 14] for the COVID-19, the concept of sensitivity of R_0 to model parameters has been presented. According to a study presented in [18], local sensitivity results show the model parameters may have a role in the virus's transmission within susceptible individuals. In particular, the contact rate of person-to-person, the exposure rate during quarantine, and the transfer rate of exposed persons all have a significant role in the transmission of this virus.

As part of our investigation, we looked at some previously published studies on mathematical modeling for COVID -19 disease. The goal of this work is to extend our previous studies on the COVID-19 transmission model [10, 14]. A topic that has received little attention is the use of different local sensitivity analysis approaches in COVID-19 computational simulations. The issue that remains is how successfully vaccination against COVID-19 might limit the spread of COVID-19. What is the most essential factor in deciding COVID-19's existence? Based on mathematical model analysis, this paper will answer the above mentioned questions. The idea is coming from vaccination term. Vaccination influence on epidemiology has been researched using mathematical models [19]. Daniel Bernolli, for example, assessed the projected influence of cowpox vaccination on the life expectancy of the vaccinated population in 1760 [20]. The model we offer here is a mathematical model with six compartments, which includes Susceptible people S(t), Vaccinated people V(t), Infected people I(t), Reported infected people W(t), Unreported infected people U(t), and Recovered people R(t), this is called SVIUWR model.

In this work, we develop and improve our previously published studies given in [10, 14]. The main improvement here is the vaccination compartment. This component is added to the model with all its interactions. The vaccination strategy to control this disease is significant in several ways. Firstly, vaccinated individuals are less likely to get infected than unvaccinated individuals. Secondly, even if vaccinated individuals get the virus, their mortality rate will be lower than that of unvaccinated individuals [4]. After introducing a vaccination for COVID-19, to study how to predict model dynamics, you need to understand and study model equations. Here, we suggest the *SVIUWR* model of COVID-19 vaccination. More details about the suggested model given in the next section.

This work includes some main contributions. Firstly, we develop a model to describe the spreading of COVID-19 in Kurdistan Region of Iraq, from July 17th, 2021 to January 1st, 2022. The suggested model here is defined based on mass action law using nonlinear ordinary differential equations with constant rates. Another contribution is related to basic reproduction number. This quantity helps us to identify critical model parameters and control strategies. Accordingly, the key model parameters are identified using the techniques of local sensitivity and elasticity. Finally, the model computational results and the real confirmed data are compared using the computational simulations. This provides that the suggested model can be used for the future predications in this region and suggestion further control strategies.

2 Model Transmissions of COVID-19 Pandemic

Mathematical models based on the classical theory of chemical kinetics can help to explain biological processes. This provides an important tool for identifying the infectious disease transmissions in terms of mathematical model equations [20]. To construct such models, three primary sets should be considered: a set of species $x = (x_1, x_2, \ldots, x_m)$, a vector of reaction rates $v = (v_1, v_2, \ldots, v_n)$ and a vector of reaction constants $k = (k_1, k_2, \ldots, k_n)$.

In order to define a system of differential equations from biochemical reactions, we assume n irreversible biochemical reactions and m chemical components, with the following stoichiometric equation:

$$\sum_{i=1}^{m} \delta_{ij} x_i \xrightarrow{k_j} \sum_{i=1}^{m} \mu_{ij} x_i, \quad j = 1, 2, \dots, n$$
(2.1)

where *n* is the number of reactions, δ_{ij} and μ_{ij} are non-negative integers, and they are called stoichiometric coefficients, x_i for i = 1, 2, ..., m are chemical components. The standard mass

action law is used to determine the model reaction rates. This is given below:

$$v_j = k_j \prod_{i=1}^m x_i^{\delta_{ij}}(t), \quad j = 1, 2, \dots, n.$$
 (2.2)

The chemical mechanisms can be expressed as a system of equations with initial states. The model equations here are given as follows:

$$\frac{dx}{dt} = \sum_{j \in J \subset \mathbb{R}} \gamma_j \, v_j \,, \quad j = 1, 2, \dots, n \tag{2.3}$$

where J is a set of reactions, $x \in \mathbb{R}^m$, $\gamma_i = \mu_{ij} - \delta_{ij}$ for i = 1, 2, ..., m and j = 1, 2, ..., n. In a given model, the differential equation for a specific component x^* can be expressed as:

$$\frac{d[x^*]}{dt} = \sum_{j \in J \subset \mathbb{R}} \mu v_{x^*} - \sum_{j \in J \subset \mathbb{R}} \delta v_{x^*}.$$
(2.4)

This means that rate of change of $[x^*] = (\text{concentration of } x^* \text{ generated in all reactions}) - (\text{concentration of } x^* \text{ eliminated in all reactions}). Equation (2.3) can be also shown as follows:$

$$\frac{dx_i}{dt} = f_i\left(x,k\right),\tag{2.5}$$

where f_i , for i = 1, 2, ..., m are commonly non-linear function, and the model equations (2.5) occasionally cannot be solved analytically. Thus, numerical approaches with computational simulations can be used to solve such systems and to understand their model dynamics and predictions. More information and explanations of chemical reactions including their differential equations and applications in different areas on systems biology can be found in [21, 22].

Classical epidemic disease models usually include compartments (individuals) and their interactions. This means Classical epidemic disease models usually include compartments (individuals) and their interactions. This means that nodes are persons in an epidemic network model, and edges represent contacts between individuals [23]. Accordingly, we suggest the transmission model of COVID-19 called SVIUWR model. The model states are susceptible people S(t), vaccinated people V(t), infected people I(t), unreported symptomatic infected people U(t), reported symptomatic infected people W(t), recovered people R(t); see Figure 1. The model parameters with their biological interpretations are shown in Table 1.



Figure 1: The SVIUWR model transmissions of the COVID-19 pandemics.

The chemical reactions of the developed model are given below:

$$\begin{array}{lll} null \xrightarrow{\lambda} S, & S \xrightarrow{d_1S} null, & S \xrightarrow{\beta S(I+U)} I, \\ S \xrightarrow{u_1S} V, & V \xrightarrow{u_2V} S, & R \xrightarrow{\alpha_3R} S, \\ I^{(d_1+d_2)I} null, & I \xrightarrow{\gamma I} U, & I \xrightarrow{\delta I} W, \\ I \xrightarrow{\alpha_4I} R, & V \xrightarrow{u_3V} I, & V \xrightarrow{d_1V} null, \\ U \xrightarrow{\eta_2 U} R, & U^{(d_1+\alpha_2)U} null, & W \xrightarrow{\eta_1 W} R, \\ W \xrightarrow{(d_1+\alpha_1)W} null, & R \xrightarrow{d_1R} null. \end{array}$$

The COVID-19 transmissions shown in Figure 1 can be expressed as a system of differential equations. By applying mass action law based on the above chemical reactions, the model equations are given:

$$\frac{dS}{dt} = \lambda - \frac{\beta S (I+U)}{N} - (d_1+u_1) S + u_2 V + \alpha_3 R,$$

$$\frac{dV}{dt} = \mathbf{u}_1 \mathbf{S} - (\mathbf{u}_2 + \mathbf{u}_3 + \mathbf{d}_1) \mathbf{V},$$

$$\frac{dI}{dt} = \frac{\beta S (I+U)}{N} - (\gamma + \delta + d_1 + d_2 + \alpha_4) I + u_3 V,$$

$$\frac{dU}{dt} = \gamma I - (\eta_2 + \alpha_2 + d_1) U,$$

$$\frac{dW}{dt} = \delta I - (\eta_1 + \alpha_1 + d_1) W,$$

$$\frac{dR}{dt} = \eta_1 W + \eta_2 U + \alpha_4 I - (\alpha_3 + d_1) R.$$
(2.6)

The model non-negative initial conditions are defined to the system as below: S(0) > 0, V(0) > 0, $I(0) \ge (0)$, $U(0) \ge 0$, $W(0) \ge 0$, $R(0) \ge 0$. The model parameters and their definitions explained in Table 1.

Symbols	Biological descriptions	Estimated values	Sources
S(0)	Initial susceptible individuals	5900000	Appendix A
V(0)	Initial vaccinated individuals	10000	Appendix A
I(0)	Initial infected individuals	1190	Appendix A
U(0)	Initial unreported symptomatic infected individuals	350	Appendix A
W(0)	Initial reported symptomatic infected individuals	840	Appendix A
R(0)	Initial recovered individuals	765	Appendix A
N	Total population	6000000	Assumed
λ	Recruitment rate	$\frac{6000000}{365*70} = 234.83$	Estimated
β	The rate of transmission between susceptible and asymptomatic infected persons	0.42	Estimated
γ	The rate of transition between asymptomatic and re- ported symptomatic infection	0.0281	[10]
δ	The rate of transition between asymptomatic and un- reported symptomatic infection	0.018	Estimated
η_1	Transition rate between symptomatic infected and recovered people	0.79	Estimated
η_2	The rate of transition between unreported symp- tomatic infected and recovered people	0.83	Estimated
u_1	Vaccination rate	0.0045	Assumed
u_2	Duration of vaccine still valid	0.009	Estimated
u_3	The rate at which people get infected after being vac- cinated.	0.0015	Estimated
d_1	Natural death rate	0.019	Estimated
d_2	The asymptomatic infected death rate	0.36	Estimated
α_1	The unreported symptomatic death rate	0.005	Estimated
α_2	The reported symptomatic death rate	0.002	Estimated
α ₃	The immunity loss rate	0.03	[14]
α_4	Transition rate between infected persons who are asymptomatic and those who have recovered	0.0005	Estimated

Table	1:	The	model	initial	individuals	and	parameters	with	their	biological	meaning	and	esti-
mated	va	lues.											

3 Basic Reproduction Number

The basic reproduction number called R_0 is an important ratio to discuss spreading of the diseases such as COVID-19 pandemics. This quantity characterizes the number of secondary infections induced by a single primary infection in the area when everybody is susceptible [24]. The idea of the next-generation matrix method was used to compute the basic reproduction number R_0 for a compartmental model. Recently, this is the most popular way for computing this threshold parameter. This technique was discussed in more details in [17, 25].

According to some recently published studies, R_0 may play an important role in discovering the model essential parameters and explaining the dynamical behavior of infectious disease models [10]. If there are infected persons in a compartment, it is known as an infected compartment. Individuals in this compartment are both asymptomatic and symptomatic. Assume you have an infectious disease model with m compartments (x_1, x_2, \ldots, x_m) . We consider the

model equations as below:

$$\frac{dx_i}{dt} = f_i(x), \text{ for } i = 1, 2, \dots, m.$$
 (3.1)

The compartments may be divided into n disease groups (infected individuals) and r non-disease groups (non-infected individuals) as follows:

$$(x_1, x_2, \ldots, x_m) = \left(\underbrace{x_1, x_2, \ldots, x_n}_{n-\text{infected}}, \underbrace{x_{n+1}, x_{n+2}, \ldots, x_m}_{r-\text{noninfected}}\right)$$

Let $Y_i(x)$ be the new infection rate appearing in i_th compartment and the transfer rate be as follows:

$$v_i(x) = v_i^-(x) - v_i^+(x),$$

where v_i^+ indicates the rate of individual transfer into the *i*_th compartment and v_i^- represents the rate of individual transfer out of the *i*_th compartment, they are shown in Figure 2:

Figure 2: Entering and leaving fluxes for a given compartment x_i^I .

In addition, the subpopulations are denoted by by $x^I \in \mathbb{R}^n$ and $x^N \in \mathbb{R}^r$. It is critical to clustering new infections from all other model compartments. It guides in calculating the basic reproduction number R_0 . Equation (3.1) for the compartmental model may be written as below:

$$\begin{cases} \frac{dx_i^{I}}{dt} = Y_i(x^{I}, x^{N}) - v_i(x^{I}, x^{N}), & i = 1, 2, \dots, n\\ \frac{dx_j^{N}}{dt} = M_j(x^{I}, x^{N}), & j = 1, 2, \dots, r \end{cases}$$
(3.2)

The Jacobian matrices H and W are now defined as follows:

$$H = \begin{bmatrix} \frac{\partial Y_i(E_0)}{\partial x_j^I} \end{bmatrix} \quad \text{and} \quad W = \begin{bmatrix} \frac{\partial v_i(E_0)}{\partial x_j^I} \end{bmatrix}, \quad 1 \le i, j \le n \quad (3.3)$$

Equation (3.1)'s free equilibrium is E_0 , H is non-negative, and W is a non-singular matrix. The basic reproduction number R_0 is produced from the spectral radius (dominant eigenvalue) of the next generation matrix HW^{-1} as shown in the following expression:

$$R_0 = \rho \left(H W^{-1} \right), \tag{3.4}$$

where ρ represents the spectral radius. More information on the next generation matrix and the basic reproduction number, as well as its applications in infectious disease models can be found in [16].

Some models of infectious diseases include many components (variables and parameters). Model equations (3.1) are generally nonlinear differential equations. Therefore, to find the model equilibrium points putting the right-hand side of system (2.6) equal to zero. The disease-free equilibrium of the system is:

$$E_0 = \left(\frac{\lambda(u_2 + u_3 + d_1)}{d_1^2 + d_1(u_1 + u_2 + u_3) + u_1u_3}, \frac{\lambda u_1}{d_1^2 + d_1(u_1 + u_2 + u_3) + u_1u_3}, 0, 0, 0, 0\right)$$
(3.5)



In addition, the proposed model is divided into two subcompartments, the infected compartments X^{I} , and non-infected compartments X^{N} as defined below:

$$X^{I} = \begin{bmatrix} I \\ U \\ W \end{bmatrix}, \qquad X^{N} = \begin{bmatrix} S \\ V \\ R \end{bmatrix}.$$

The model equations for the infected compartments are defined here:

$$\frac{d}{dt} \begin{bmatrix} I\\ U\\ W \end{bmatrix} = \begin{bmatrix} \frac{\beta S(I+U)}{N} + u_3 V\\ 0\\ 0 \end{bmatrix} - \begin{bmatrix} (\gamma+\delta+d_1+d_2+\alpha_4) I\\ (\eta_2+\alpha_2+d_1) U - \gamma I\\ (\eta_1+\alpha_1+d_1) W - \delta I \end{bmatrix}.$$
 (3.6)

For the subsystem (3.6), the matrices Y and V are defined below:

$$Y = \begin{bmatrix} \frac{\beta S(I+U)}{N} + u_3 V \\ 0 \\ 0 \end{bmatrix} \quad and \quad V = \begin{bmatrix} (\gamma + \delta + d_1 + d_2 + \alpha_4) I \\ (\eta_2 + \alpha_2 + d_1) U - \gamma I \\ (\eta_1 + \alpha_1 + d_1) W - \delta I \end{bmatrix}$$

$$\begin{split} H &= \left[\frac{\partial Y}{\partial \left(I, U, W \right)} \right]_{\begin{pmatrix} \frac{\lambda \left(u_{2} + u_{3} + d_{1} \right)}{d_{1}^{2} + d_{1} \left(u_{1} + u_{2} + u_{3} \right) + u_{1} u_{3}}, \frac{\lambda u_{1}}{d_{1}^{2} + d_{1} \left(u_{1} + u_{2} + u_{3} \right) + u_{1} u_{3}}, 0, 0, 0, 0 \end{pmatrix} = \\ \begin{bmatrix} \frac{\beta \lambda \left(u_{2} + u_{3} + d_{1} \right)}{N \left(d_{1}^{2} + d_{1} \left(u_{1} + u_{2} + u_{3} \right) + u_{1} u_{3} \right)} & \frac{\beta \lambda \left(u_{2} + u_{3} + d_{1} \right)}{N \left(d_{1}^{2} + d_{1} \left(u_{1} + u_{2} + u_{3} \right) + u_{1} u_{3} \right)} & 0 \\ 0 & 0 & 0 \\ \end{bmatrix} \text{ and } \\ W &= \left[\frac{\partial V}{\partial \left(I, U, W \right)} \right]_{\begin{pmatrix} \frac{\lambda \left(u_{2} + u_{3} + d_{1} \right)}{d_{1}^{2} + d_{1} \left(u_{1} + u_{2} + u_{3} \right) + u_{1} u_{3}}, \frac{\lambda u_{1}}{d_{1}^{2} + d_{1} \left(u_{1} + u_{2} + u_{3} \right) + u_{1} u_{3}}, 0, 0, 0, 0 \end{pmatrix} = \\ \begin{bmatrix} \left(\gamma + \delta + d_{1} + d_{2} + \alpha_{4} \right) & 0 & 0 \\ \left(-\gamma \right) & \left(\eta_{2} + \alpha_{2} + d_{1} \right) & 0 \\ \left(-\delta \right) & 0 & \left(\eta_{1} + \alpha_{1} + d_{1} \right) \end{bmatrix} \end{split}$$

Thus, the next generation matrix can be given below:

$$HW^{-1} = \begin{bmatrix} \frac{\beta\lambda(u_2+u_3+d_1)(\eta_1+\alpha_1+d_1+\delta)}{N(d_1^2+d_1(u_1+u_2+u_3)+u_1u_3)(\gamma+\delta+d_1+d_2+\alpha_4)(\eta_1+\alpha_1+d_1)} & 0 & \frac{\beta\lambda(u_2+u_3+d_1)}{N(d_1^2+d_1(u_1+u_2+u_3)+u_1u_3)(\eta_1+\alpha_1+d_1)} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

There is only one dominant eigenvalue for HW^{-1} . The equation of the basic reproduction number for system (2.6) is given below:

$$R_0 = \frac{\beta\lambda (u_2 + u_3 + d_1) (\eta_1 + \alpha_1 + d_1 + \delta)}{N (d_1^2 + d_1 (u_1 + u_2 + u_3) + u_1 u_3) (\gamma + \delta + d_1 + d_2 + \alpha_4) (\eta_1 + \alpha_1 + d_1)}.$$
 (3.7)

Interestingly, we use the real collected data for infected cases in Kurdistan region of Iraq and we use the suggested estimator given in [26], the curve of reproduction number is shown in the Figure 3.



Figure 3: Curve of reproduction number in Kurdistan region from June 17^{th} , 2021 to January 1^{st} , 2022.

The Figure 3 shows that this quantity is high than one until August 10th, 2022. It means that this disease was spread during this period. After that it was over all less than one, this means the disease under control and fewer people getting infected by COVID-19. Based on this quantity, more preventions and control strategies can be noticeably proposed as a local policy to control this pandemic.

4 Elasticity of R_0

The idea of basic reproduction number for infectious diseases plays an important role in COVID-19 transmissions. Consequently, in a complex modeling scenario such as the dynamics of novel coronaviruses, it is vital to pay more attention to sensitivity analysis [14]. In infectious disease models, the idea of elasticity plays a significant role in defining the sensitivity between R_0 and the model parameters. The normalized sensitivity analysis of parameter ω regard to R_0 , represented by $\Gamma_{\omega^0}^{R_0}$, as defined by:

$$\Gamma_{\omega}^{R_0} = \frac{\partial R_0}{\partial \omega} \; \frac{\omega}{R_0}.$$
(4.1)

The elasticity index for each model parameter can be calculated, where ω is the set of model parameters. They are as follows:

$$\begin{split} &\Gamma_{\lambda}^{R_{0}} = \frac{\partial R_{0}}{\partial \lambda} * \frac{R_{0}}{R_{0}} = 1, \\ &\Gamma_{\beta}^{R_{0}} = \frac{\partial R_{0}}{\partial \gamma} * \frac{\beta}{R_{0}} = 1, \\ &\Gamma_{\gamma}^{R_{0}} = \frac{\partial R_{0}}{\partial \gamma} * \frac{\beta}{R_{0}} = -\frac{\gamma}{\gamma + \delta + d_{1} + d_{2} + \alpha_{4}} , \\ &\Gamma_{\gamma}^{R_{0}} = \frac{\partial R_{0}}{\partial \gamma} * \frac{\beta}{R_{0}} = -\frac{\gamma}{\gamma + \delta + d_{1} + d_{2} + \alpha_{4}} , \\ &\Gamma_{\beta}^{R_{0}} = \frac{\partial R_{0}}{\partial \gamma} * \frac{\beta}{R_{0}} = \frac{-\frac{\gamma}{\gamma + \delta + d_{1} + d_{2} + \alpha_{4}} + \eta_{1} - \alpha_{1}}{(\eta_{1} + \alpha_{1} + d_{1} + \delta)(\gamma_{1} + \alpha_{1} + d_{2} + \alpha_{4})} , \\ &\Gamma_{\eta_{1}}^{R_{0}} = \frac{\partial R_{0}}{\partial \eta_{2}} * \frac{\eta_{1}}{R_{0}} = 0, \\ &\Gamma_{\eta_{1}}^{R_{0}} = \frac{\partial R_{0}}{\partial \eta_{2}} * \frac{\eta_{2}}{R_{0}} = \frac{u_{2}}{(\eta_{1} + \alpha_{1} + d_{1} + \delta)(\eta_{1} + \alpha_{1} + d_{1})} , \\ &\Gamma_{\eta_{1}}^{R_{0}} = \frac{\partial R_{0}}{\partial \eta_{2}} * \frac{\eta_{2}}{R_{0}} = \frac{u_{2}}{u_{2} + u_{3} + d_{1}}, \\ &\Gamma_{\eta_{1}}^{R_{0}} = \frac{\partial R_{0}}{\partial \eta_{3}} * \frac{\eta_{3}}{R_{0}} = \frac{u_{2}}{u_{2} + u_{3} + d_{1}}, \\ &\Gamma_{\eta_{1}}^{R_{0}} = \frac{\partial R_{0}}{\partial d_{0}} * \frac{d_{1}}{R_{0}} = \frac{-(\gamma + \gamma + \eta_{1} + \alpha_{1})\delta^{2} - (2d_{1} + d_{2} + \eta_{1} + \gamma + \alpha_{1} + \alpha_{4})(u_{2} + u_{3} - \eta_{1} - \alpha_{1})\delta}{(\eta_{1} + \alpha_{1} + d_{1} + \delta)(u_{2} + u_{3} + \eta_{1} + \alpha_{1})\delta} , \\ &\Gamma_{\eta_{1}}^{R_{0}} = \frac{\partial R_{0}}{\partial d_{0}} * \frac{d_{2}}{R_{0}} = \frac{-d_{2}}{\gamma + \delta + d_{1} + d_{2} + \alpha_{4}} , \\ &\Gamma_{\eta_{1}}^{R_{0}} = \frac{\partial R_{0}}{\partial \alpha_{1}} * \frac{\alpha_{1}}{R_{0}} = \frac{-\delta}{(\eta_{1} + \alpha_{1} + d_{1} + \delta)(\eta_{1} + \alpha_{1} + d_{1})} , \\ &\Gamma_{\eta_{2}}^{R_{0}} = \frac{\partial R_{0}}{\partial \alpha_{3}} * \frac{\alpha_{3}}{R_{0}} = 0, \\ &\Gamma_{\eta_{1}}^{R_{0}} = \frac{\partial R_{0}}{\partial \alpha_{3}} * \frac{\alpha_{3}}{R_{0}} = 0, \\ &\Gamma_{\eta_{1}}^{R_{0}} = \frac{\partial R_{0}}{\partial \alpha_{3}} * \frac{\alpha_{3}}{R_{0}} = 0, \\ &\Gamma_{\eta_{1}}^{R_{0}} = \frac{\partial R_{0}}{\partial \alpha_{3}} * \frac{\alpha_{3}}{R_{0}} = 0, \\ &\Gamma_{\eta_{1}}^{R_{0}} = \frac{\partial R_{0}}{\partial \alpha_{0}} * \frac{\alpha_{3}}{R_{0}} = \frac{-\delta}{\gamma + \delta + d_{1} + d_{2} + \alpha_{4}} . \end{split}$$

We can calculate the model elasticity using the estimated parameters given in Table 1. As a result, the model elasticity values are given in Table 2.

Parameters	$\Gamma^{R_0}_{\omega}$
λ	1
β	1
γ	-0.9983101466
δ	-0.02065861770
η_1	-0.02099673974
η_2	0
u_1	0
<i>u</i> ₂	0.3050847458
<i>u</i> ₃	0.05084745763
d_1	0.5989199545
d_2	-0.8458646616
α_1	-0.0001328907579
α_2	0
α_3	0
α_4	-0.001174812030

Table 2: Elasticity values of R_0 regarding to model parameters.

Accordingly, we illustrate the impact of each parameter on the reproduction number for our suggested COVID-19 model. The positive and negative signs for model elasticity are shown in Table 2. These show us if R_0 and the model parameters have a direct or indirect relationship. For instance, this coefficient is positive for this set of parameters $\{\lambda, \beta, u_2, u_3, d_1\}$. This means that when these parameters are increased then the value of R_0 increases, and the virus spreads faster. In addition, for the given parameters here $\{\lambda, \beta\}$, there is a strong positive relation, that means R_0 very sensitive to recruitment rate and transmission rate between susceptible and infected individuals. Furthermore, the sign of each parameter given in this set $\{\gamma, \delta, \eta_1, d_1, \alpha_1, \alpha_1, \alpha_4\}$ is negative. It shows that the value of basic reproduction number can be reduced by increasing such parameters. Finally, we may say the set of parameters $\{\eta_2, u_1, \alpha_2, \alpha_3\}$ has not much effect on the virus spread.

5 Sensitivity Analysis

The purpose of sensitivity analysis in mathematical modeling is to identify the variables or parameters that are most affected by a certain condition. In systems biology, there are two forms of sensitivity analysis. The first form is called local sensitivity, while the second technique is known by global sensitivity. Networks of biochemical reactions and cell signaling pathways as well as metabolic networks are all examples of biological processes [18]. They were studied using both approaches. Assume that there are m compartments x_i for i = 1, 2, ..., m and nparameters k_j for j = 1, 2, ..., n in a given infectious disease model. As seen below, the model balanced equations are written as a system of differential equations:

$$\frac{dx_i}{dt} = f_i\left(x,k\right),\tag{5.1}$$

where $x \in \mathbb{R}^m$ and $k \in \mathbb{R}^n$. The local sensitivity can be calculated using three well-known techniques called non-normalization, half-normalization, and full-normalization techniques. The following are the non-normalization sensitivities:

$$S_{k_j}^{x_i} = \left(\frac{\partial x_i}{\partial k_j}\right) \,. \tag{5.2}$$

The following are the half-normalization sensitivities:

$$S_{k_j}^{x_i} = \left(\frac{1}{x_i}\right) \left(\frac{\partial x_i}{\partial k_j}\right) \,. \tag{5.3}$$

The following are the full -normalization sensitivities:

$$S_{k_j}^{x_i} = \left(\frac{k_j}{x_i}\right) \left(\frac{\partial x_i}{\partial k_j}\right) \quad , \tag{5.4}$$

where $S_{k_j}^{x_i}$ represents the sensitivity coefficient of each x_i to each parameter k_j . In simulations, this approach may be used to estimate the local sensitivities for non-normalization, half-normalization, and full-normalization. Also, this may be calculated using SimBiology Toolbox in MATLAB. Further details, improvements, and sensitivity analysis applications analysis in the area of systems biology are available in [10, 18].

As stated before, our aim in this section is to understand the sensitivity of compartments to the parameters of the COVID-19 model. This technique was used recently in [8, 10]. In order to calculate all local sensitivities for the model compartments with regard to model parameters, we analyze the coronavirus equations provided in system (2.6). This technique helps us to understand coronavirus dynamics more accurately and widely. The model sensitivities can be calculated using MATLAB tools with the following techniques: non normalization, half normalization and, full normalization. For the Figure 4a, we will show the non-normalization technique, which is interestingly demonstrate some crucial aspects. First, the model compartments: Susceptible, and Vaccinated individuals are very sensitive to u_1 (vaccination rate). Consequently, susceptible individuals are very sensitive to d_1 (natural death rate) see Figure 4a. As indicated by computational simulations, local sensitivity analysis using half normalizations discovered that a set of individuals I, U, and W are very sensitive to the parameter (u_3) , that is transition rate between vaccination and infected individuals; see Figure 4b. This method shows that vaccinated, infected, unreported infected, and reported infected individuals have sensitivity to u_1 (vaccination rate) in different levels. This is well shown in our computational simulation, as seen in Figure 4b. Therefore, computational findings based on local sensitivity for full-normalizations demonstrate that the majority of the factors play a significant role in model variable sensitivities, as seen in Figure 4c. Interestingly, it may be determined that the transmission rate between (susceptible and infected individuals), transition rate between (reported infected and recovered individuals), transition rate between (unreported infected and recovered individuals), transition rate between (asymptomatic infected and unreported infected individuals), and transition rate between (asymptomatic infected and reported infected individuals) are the most important factor in coronavirus transmission. As a result, identifying the key model factors is an effective way to understand the model transmissions both practically and theoretically. It may also help us for further improvements including vaccination programs, interventions, and disease control.



⁽c) Full normalization

Figure 4: Computational simulations for the COVID-19 model using MATLAB, local sensitivity analysis using (a) non-normalizations, (b) half-normalizations, and (c) full-normalizations.

6 Computational Simulations and Discussions

The data for this research came from the ministry of health in Kurdistan region of Iraq. Period under study is from July 17^{th} , 2021 to January 1^{st} , 2022. In a summary, the COVID-19 pandemic data under analysis are death on a daily, recovered on a daily, and those who are in the hospital on a daily (patients with different COVID-19 symptoms and patients). From all cities of Kurdistan region, the population of the studied region is approximately 6000000. All the data that used are available in Appendix A.

As part of efforts around the world to limit the effects of the new COVID-19, a number of healthcare interventions and preventions have been studied and proposed. The proposed mathematical models are useful tools that provide estimates and recommendations for more effective viral strategy and future preventions in the issue of COVID-19. In this section, we deal with two

questions. The first question is, how is the dynamics of the model compartments change over the time and comparing with the collected real data of Kurdistan region from July, 17^{th} 2021 to January, 1^{st} 2022. All the confirmed cases are given in the Appendix A. The second question is, which model compartments are sensitive to the model parameters? Thus, we run a simulation to analyze the answer of these questions. The current study's findings represent a significant improvement to predict future model dynamics for development programs, interventions, and health care strategies.

Using the System Biology Toolbox known by SBedit for MATLAB, we can calculate the numerical approximate solutions of the model equations (2.6) using the model initial populations and parameter values. Two dimensional planes are used to perform computational numerical simulations. Figure 5 demonstrates the model dynamics of susceptible, vaccinated, infected, unreported symptomatic infected, reported symptomatic infected, and recovered people. In addition, Figure 6a shows the total number of infected cases in Kurdistan region using the real data given in Appendix A. The confirmed infected cases and model results are compared in Figure 6c shows the total number of recovered individuals in Kurdistan region using real data given in Appendix A. The confirmed recovered cases and model results are compared in Figure 6c shows the total number of recovered cases and model results are compared in Figure 6d. As a result, the suggested SVIWUR model of COVID-19 can be effectively applied for future model predictions and parameter estimations.

The computational results shown here may provide more biological interpretations and descriptions. Interestingly, the model results may help global efforts for controlling this pandemic with different strategies. Results can also show dynamics of each compartment with time intervals, they provide a great understanding about future predictions of this virus. For example, the total number of infected people, unreported infected people, and reported infected people are clearly shown in Figure 5c, Figure 5d, and Figure 5e. Accordingly, the results show that the total number of infected people in Kurdistan region has been slightly decreased for the months of August to the end of December. Obviously, the total number of infected people in this region was significantly decreased at the end of 2021.



Figure 5: The model computational simulations given here are (a) Susceptible individuals, (b) Vaccinated individuals, (c) Infected individuals, (d) Unreported infected individuals, (e) Reported infected individuals, (f) Recovered individuals . They are calculated using MATLAB for the COVID–19 model states and estimated parameters given in Table 1.



(a) The real confirmed infected cases in Kurdistan

(b) The model results and the confirmed infected cases in Kurdistan



(c) The real data for recovered individuals in Kurdistan

(d) The model results and the real data for recovered individuals in Kurdistan

Figure 6: The number of people that have been infected; (a) The real confirmed cases in Kurdistan, (b) The model results and the confirmed cases in Kurdistan. The number of people who have been recovered; (c) The real data for recovered individuals in Kurdistan, (d) The model results and the real data for recovered individuals in Kurdistan.

7 Conclusions

A number of healthcare interventions and preventions have been considered and proposed to minimize the effect of the new COVID-19 virus. The mathematical simulation that represents the worldwide COVID-19 pandemic was suggested after reviewing some recent research on the disease. Computational simulations combined with mathematical modeling gives estimates and predictions regarding the dynamics of model states and parameters. However, the daily confirmed cases and death cases from 17^{th} July, 2021 to 1^{st} January, 2022 were collected and used to assume the model parameters. Comparing model predictions with observed confirmed cases reported in Kurdistan region, we found that the model predicted results were in a good level.

In addition, the basic reproduction number R_0 was obtained. This is an important step forward to identify the model critical parameters. Some computational simulations are calculated to discuss the dynamics of model states. We compared the model results and the real confirmed data. As a result, there are a good agreement between both results. Accordingly, the concept of local sensitivity to compute the sensitivity of each model state to model parameters using three basic techniques: non normalizations, half normalizations, and full normalizations has been discussed and studied. The sensitivity analysis results showed that practically all model parameters may have a role in the transmission of this virus among individuals. Therefore, some model critical factors were highlighted in spreading this disease in the region. The findings of this study will be useful in discussing various COVID-19 intervention programs to control this virus in the Finally, the suggested mathematical model here for spreading COVID-19 plays an essential role to discuss this pandemic more widely and accurately. Although, collecting the real data for this pandemic in the region becomes a difficult task to study this model more widely, but the suggested model can be further developed, and more parameters will be added to discuss all critical factors. Interestingly, the model results here can also help local government and heath care strategies in the region for further suggestions and improvements to control this disease more effectively. For example, educational awareness through social media campaigns and community leaders may have a great role in reducing this spreading. Another possibility to reduce this pandemic in the future is testing for those who seem to be infected along with their contacts soon. Accordingly, these findings suggest to increase the vaccination rate in the community that provides a good immune response across all individuals in the region.

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Appendix A: Real Confirmed data of Kurdistan Region of Iraq, from July 17th, 2021 to January 1st, 2022.

Dates	Infection	Recovery	Deaths	Hospitalized
July 17, 2021	942	838	6	11973
July 18, 2021	1456	651	6	12772
July 19, 2021	1985	1032	19	13706
July 20, 2021	1347	787	16	14250
July 21, 2021	1078	723	11	14594
July 22, 2021	1220	701	22	15091
July 23, 2021	1598	911	12	15766
July 24, 2021	1010	902	15	15859
July 25, 2021	2178	1057	14	16966
July 26, 2021	3559	1041	13	19471
July 27, 2021	3250	1076	19	21626
July 28, 2021	3468	1277	19	23798
July 29, 2021	3056	1436	10	25408
July 30, 2021	2924	1276	20	27036
July 31, 2021	1695	1230	16	27518
August 1, 2021	2422	814	19	29107
August 2, 2021	3350	716	13	31728
August 3, 2021	3149	797	16	34065
August 4, 2021	3172	749	24	36464
August 5, 2021	3220	755	14	38915
August 6, 2021	2755	777	28	40865
August 7, 2021	1052	614	11	41292
August 8, 2021	2380	615	21	43036
August 9, 2021	2543	736	19	44824
August 10, 2021	2069	967	19	45907
August 11, 2021	1632	1204	14	46321

August 12, 2021	1925	1421	16	46809
August 13, 2021	2348	1682	20	47455
August 14, 2021	827	2010	19	46253
August 15, 2021	2020	1869	19	46358
August 16, 2021	2362	1923	20	46777
August 17, 2021	2189	1995	20	46951
August 18, 2021	1938	1987	21	46881
August 19, 2021	1823	2235	25	46444
August 20, 2021	1449	2160	23	45710
August 21, 2021	722	2044	33	44355
August 22, 2021	1531	2181	20	43685
August 23, 2021	2024	2239	20	43350
August 24, 2021	1869	2351	22	42846
August 25, 2021	1921	2440	21	42306
August 26, 2021	1626	2234	19	41679
August 27, 2021	1546	2246	25	40954
August 28, 2021	704	2123	18	39517
August 29, 2021	1513	2129	17	38884
August 30, 2021	2010	2259	16	38619
August 31, 2021	1573	2277	16	37899
September 1, 2021	1994	2390	11	37492
September 2, 2021	1871	2222	14	37127
September 3, 2021	1406	2155	22	36356
September 4, 2021	442	2128	12	34658
September 5, 2021	1618	2249	21	33541
September 6, 2021	1448	2026	16	33564
September 7, 2021	1764	2239	11	33055
September 8, 2021	1463	2138	20	32360
September 9, 2021	1491	2116	16	31719
September 10, 2021	1380	1870	22	31207
September 11, 2021	1291	1725	16	31380
September 12, 2021	1214	1380	17	30149
September 13, 2021	1339	1627	17	29844
September 14, 2021	1235	1487	16	29576
September 15, 2021	1178	1430	11	29313
September 16, 2021	1253	1547	22	28997
September 17, 2021	1378	1567	19	28789
September 18, 2021	634	1412	13	27998
September 19, 2021	1253	1476	17	37758
September 20, 2021	1285	1175	12	27856
September 21, 2021	1254	1076	8	28026
September 22, 2021	1117	1036	13	28094
September 23, 2021	1236	1063	19	28248
September 24, 2021	1360	1180	20	28408
September 25, 2021	360	1002	11	27755

September 26, 2021	1265	1085	14	27921
September 27, 2021	1421	1215	10	28117
September 28, 2021	1401	1290	19	28209
September 29, 2021	1349	1246	17	28295
September 30, 2021	1353	1218	18	28412
October 1, 2021	1372	1453	19	28312
October 2, 2021	438	1414	19	27317
October 3, 2021	1532	1388	13	27448
October 4, 2021	1049	1428	13	27056
October 5, 2021	1360	1504	9	26903
October 6, 2021	1318	1539	9	26273
October 7, 2021	1305	1574	13	26291
October 8, 2021	1115	1650	18	25738
October 9, 2021	524	1856	18	24388
October 10, 2021	1096	1866	15	23603
October 11, 2021	401	1655	19	22330
October 12, 2021	1114	1883	16	21545
October 13, 2021	1099	1805	26	20813
October 14, 2021	1409	1534	9	20679
October 15, 2021	1331	1554	15	20441
October 16, 2021	464	1608	20	19277
October 17, 2021	1147	1517	12	18895
October 18, 2021	792	1321	23	18343
October 19, 2021	1154	1475	17	18005
October 20, 2021	688	1367	12	17314
October 21, 2021	1076	1313	28	17049
October 22, 2021	1076	1406	21	16698
October 23, 2021	560	1211	28	16019
October 24, 2021	770	1208	20	15561
October 25, 2021	1002	1393	23	15147
October 26, 2021	787	1500	23	14411
October 27, 2021	802	1259	25	13929
October 28, 2021	844	1296	18	13459
October 29, 2021	849	1358	21	12929
October 30, 2021	358	1009	21	12257
October 31, 2021	643	1035	25	11840
November 1, 2021	655	946	17	11532
November 2, 2021	722	1028	23	11203
November 3, 2021	688	957	11	10923
November 4, 2021	591	960	15	10539
November 5, 2021	657	1052	11	10133
November 6, 2021	400	916	17	9600
November 7, 2021	447	551	16	9480
November 8, 2021	621	630	15	9456
November 9, 2021	628	770	18	9296

November 10, 2021	442	852	11	8875
November 11, 2021	427	813	25	8464
November 12, 2021	502	744	19	8203
November 13, 2021	322	706	12	7807
November 14, 2021	567	643	16	7715
November 15, 2021	475	566	18	7606
November 16, 2021	444	456	17	7579
November 17, 2021	465	513	11	7520
November 18, 2021	464	685	16	7283
November 19, 2021	362	632	17	6996
November 20, 2021	355	592	11	6748
November 21, 2021	293	315	17	6709
November 22, 2021	480	558	15	6616
November 23, 2021	358	539	15	6420
November 24, 2021	372	478	8	6306
November 25, 2021	364	322	16	6332
November 26, 2021	468	529	12	6259
November 27, 2021	241	551	3	5946
November 28, 2021	268	404	14	5796
November 29, 2021	423	478	8	5733
November 30, 2021	311	488	10	5546
December 1, 2021	435	412	19	5550
December 2, 2021	282	410	12	5410
December 3, 2021	369	456	5	5309
December 4, 2021	162	401	3	5076
December 5, 2021	210	403	12	4871
December 6, 2021	278	327	14	4808
December 7, 2021	258	423	10	4633
December 8, 2021	255	242	8	4639
December 9, 2021	212	296	8	4546
December 10, 2021	267	317	10	4486
December 11, 2021	81	351	5	4211
December 12, 2021	157	370	9	3989
December 13, 2021	269	416	10	3832
December 14, 2021	215	313	12	3722
December 15, 2021	195	351	9	3557
December 16, 2021	173	468	9	3253
December 17, 2021	115	407	11	2950
December 18, 2021	61	227	4	2780
December 19, 2021	104	134	9	2741
December 20, 2021	147	226	6	2656
December 21, 2021	119	220	9	2546
December 22, 2021	141	187	6	2494
December 23, 2021	102	214	8	2374
December 24, 2021	112	234	3	2249

December 25, 2021	47	220	2	2074
December 26, 2021	99	162	5	2006
December 27, 2021	76	211	6	1865
December 28, 2021	89	173	4	1777
December 29, 2021	98	197	2	1676
December 30, 2021	102	201	3	1574
December 31, 2021	103	169	2	1506
January 1, 2022	64	104	3	1463

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