



## Modeling The Effect of Contaminated Object, Vaccination and Treatment on The Diseases Epidemiology

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### ABSTRACT

In this paper, the effect of contaminated objects on a SIRS Model with vaccination and hospitalization compartments is modeled. Positivity and boundedness properties of the solutions of model are proved, basic reproduction number of the model is founded through criteria which make the eigenvalues of the Jacobean matrix at the disease-free equilibrium point, negative. Globally stability analysis of the disease-free equilibrium point is proved when the basic reproduction number is less than unity. The existence, uniqueness of the endemic equilibrium point is investigated when the basic reproduction number is greater than unity. Parameter values regarding to spreading covid-19 in Kurdistan region are estimated. Finally, sensitivity analysis of the reproduction number is carried out.

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*Keywords:* Epidemic model, Basic reproduction number, Stability analysis, Sensitivity analysis.

### 1. Introduction

In day-to-day life, humans interact with different infectious virus such as Covid 19, measles, tuberculosis .et, those viruses are a massive threat for humans and also for national economies, as a result humanity has developed techniques, weapons and sophisticated technological instruments to help reduce the threat. This humanity effort to prevent the spreading infectious disease cannot be well done only by biological and healthcare. Mathematical modeling of the infectious diseases is one of the key tools in order to handle these efforts<sup>[7-10]</sup>.

Most recently new strain coronavirus SARS-COV-19, have spread in the Wuhan city, China in December 2019<sup>[13]</sup>, many epidemic models based on the SIR model have been modified to predicate the dynamics of Covid-19 transmission; for example, B.Tang.Wang, O.Li.and et, Estimated the transmission risk of covid2019 and its implication for public health intervention<sup>[11]</sup>. And S.H.Khoshnaw, M.Shahzad, et studies the quantitative and qualitative analysis of covid-19 pandemic model<sup>[12]</sup>.

Vaccination and treatment including hospitalization or quarantine, are important intervention strategy, to decrease

spreading of infectious disease among people. Therefore, many mathematicians studied the effect of vaccination and treatment on reducing the spreading of infectious disease. Z. Qiu and Z. Feng, studied the Transmission dynamics of an influenza model with vaccination and antiviral treatment<sup>[10]</sup>. In<sup>[9-11, 14-18]</sup>, the author considered a modified SEIR model to study the effect of detected infection, isolation, and quarantine, their proposed model was analyzed to determine all possible equilibrium points and the basic reproduction number.

Infectious Viruses are one such threat, Invisible to the human eye, they live in the air, soil, and water and on material surfaces. Therefore, the transmission of epidemic disease can occur, from infected individuals to susceptible individuals directly as well as from contaminated object to susceptible individual, in<sup>[5]</sup> the author proposed an epidemic model for the transmission dynamics of Coronavirus diseases (Covid-19) their proposed model incorporating the effect of contaminated objects on SEIR model only but effect f intervention strategy like Vaccination and hospitalization are important factor for modeling the dynamics spreading of infectious disease in humanity. Therefore, in this paper, an epidemic model is formulated for studying the effect of each of vaccination, hospitalization and contaminated object on spreading infectious.

According to published works given in<sup>[12, 19]</sup>, the concept of sensitivity analysis has been present to detect model sensitivity parameter, in<sup>[19]</sup> the authors used the data of infected peoples the Covid-19 virus. In this work, together with studying the dynamics

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behaviors, parameter sensitivity analysis for the proposed model is also studied.

This work is arranged as follows: In the second section, details are given about formulation of the model. In section three, positivity and boundedness of model solutions is proved. In the fourth section, the threshold parameter (basic reproduction number) is founded and locally as well as global stable of the disease free equilibrium point is done. In section five, existence and uniqueness of the endemic equilibrium point is carried out. In section six the model parameters regarding to spreading of covid-19, in Kurdistan region of Iraq are estimated. Finally, in section six, sensitivity analysis the basic reproduction number for the model parameters relative to vaccination, hospitalization and contaminated object is done.

**2. The Model Formulation**

The classical epidemiology model consists of three compartments, namely Susceptible S (t), Infected (t) and Recovered (t). The main idea for modifying the classical epidemiological models based on the transmission dynamics<sup>[5]</sup> and intervention measures like vaccination and hospitalization<sup>[9-11, 14-18]</sup>. Accordingly, both of transmissions; dynamics and intervention compartments are taken into account for formulate a new epidemic model, in our new proposed model; we assume that the epidemic disease is transmitted through two dynamic ways.

- 1-Direct disease transmission, which means the disease, is transmitted from infected individuals to uninfected individuals by direct contact.
- 2-Indirect disease transmission, transmission from infected person to susceptible person through contaminated surfaces.

Also, the proposed model combined with intervention compartment such as hospitalization and vaccination. The model state variable is given in table (1), and the diagram of the model and interaction components shown in figure-(1).

**Table 1:** The compartment and their description.

Symbol	biological description of the state variable
S	Susceptible population numbers
V	Vaccinated population numbers
I	Infected population numbers
H	hospitalization individuals
R	Recovered population numbers
C	Contaminate object or surface in the environment

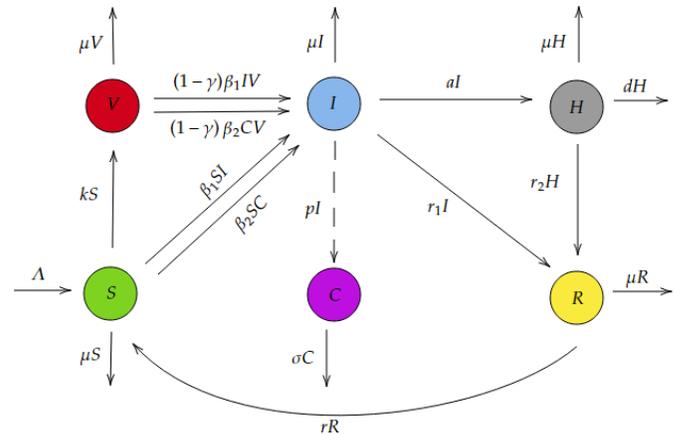
According to our assumptions and model diagram, the model can be written as the following set of non-linear ordinary differential equations

$$\begin{aligned} \frac{dS}{dt} &= \Lambda + rR - (\mu + K)S - (\beta_1 I + \beta_2 C)S \\ \frac{dV}{dt} &= kS - \mu V - (1 - \gamma) (\beta_1 I + \beta_2 C)V \\ \frac{dI}{dt} &= (\beta_1 I + \beta_2 C)(S + (1 - \gamma)V) - \mu I - r_1 I - aI \end{aligned} \tag{1}$$

$$\frac{dH}{dt} = aI - (\mu + r_2 + d)H$$

$$\frac{dR}{dt} = r_1 I + r_2 H - (\mu + r)R$$

$$\frac{dC}{dt} = \rho I - \sigma C$$



**Figure 1:** Model diagram and interaction of individuals.

With the following initial conditions

$$S(0) > 0, I(0) \geq 0, V(0) \geq 0, H(0) \geq 0, R(0) \geq 0, \text{ and } C(0) \geq 0, \tag{2}$$

and all the model parameters is positive and described in table2.

**Table 2:** biological description of model parameters.

Parameters	biological description
$\Lambda$	Recruitment rate of the susceptible population
$\beta_1$	Rate of directly disease transmission from populations
$\beta_2$	Rate of indirectly disease transmission from (contaminate object)
$\gamma$	Vaccination efficacy
$R$	Rate of being susceptible from recovery individual
$\mu$	Natural death rate of the individual
$r_1$	rate of recovery of infected population from infectious disease
$r_2$	rate of recovery of individuals from treatable individuals
$\rho$	Rate of shedding of the virus from infected population to the environment
$\sigma$	Decay rate of the virus from the environment
$D$	Rate of death due to the virus
$k$	Vaccination rate
$a$	Hospitalization rate

**3. Positivity and Boundedness**

In this section, the positivity of the model solution is proved in theorem (1) and an invariant and attractor simplex set is found in theorem (2), which quarantines that system (1) is bounded

**Theorem 1** Every trajectory  $(S(t), V(t), I(t), H(t), R(t), C(t))$  of system (1) with condition (2) is unique and will remain non negative.

**Proof** The right side of system (1) is completely continues and locally Lipchizion, therefore every trajectory of system (1) with initial conditions (2) exist and unique, and furthermore the following inequalities are obtained from system (2)

$$\begin{aligned} \frac{dS}{dt} &> 0 \text{ at every point } (0, V(t), I(t), H(t), R(t), C(t)) \text{ in } \{0\} \times R_+^5. \\ \frac{dV}{dt} &> 0 \text{ at every point } (S(t), 0, I(t), H(t), R(t), C(t)) \text{ in } R_+ \times \{0\} \times R_+^4. \\ \frac{dI}{dt} &= 0 \text{ at every point } (S(t), V(t), 0, H(t), R(t), C(t)) \text{ everywhere in } R_+^2 \times \{0\} \times R_+^3. \\ \frac{dH}{dt} &\geq 0 \text{ at every point } (S(t), V(t), I(t), 0, R(t), C(t)) \text{ in } R_+^3 \times \{0\} \times R_+^2. \\ \frac{dR}{dt} &\geq 0 \text{ at every point } (S(t), V(t), I(t), H(t), 0, C(t)) \text{ in } R_+^4 \times \{0\} \times R_+. \\ \frac{dC}{dt} &\geq 0 \text{ at every point } (S(t), V(t), I(t), H(t), R(t), 0) \text{ in } R_+^5 \times \{0\}. \end{aligned}$$

Therefor for initial condition (2), each of compartments of the system (1) cannot cross zero, which completes the proof. In the following theorem the bounded of the solution of the system (1) is proved.

**Theorem 2** The simplex set

$$\Omega = \left\{ (S, V, I, H, R, C) \in R_+^6; S + V + I + H + R \leq \frac{\Lambda}{\mu}, C \leq \frac{\rho\Lambda}{\sigma\mu} \right\}$$

is forward invariant and attractor.

**Proof** Let  $N(t) = S(t) + V(t) + I(t) + H(t) + R(t)$ , then

$$\frac{dN}{dt} = \Lambda - \mu N - dH \leq \Lambda - \mu N$$

By solving above first order differential inequality, we get

$$N(t) \leq \frac{\Lambda + (N(0) - \Lambda)e^{-\mu t}}{\mu}; \forall t \geq 0$$

If the solution of system (1) initiate in  $\Omega$ , then

$$N(0) \leq \frac{\Lambda}{\mu} \text{ and } C(0) \leq \frac{\rho\Lambda}{\sigma\mu}, \text{ and hence the following inequality is get } N(t) \leq \frac{\Lambda}{\mu}; \forall t \geq 0 \tag{3}$$

Using (3) and last equation of system (1), it is obtained that

$$\frac{dC}{dt} \leq \frac{\rho\Lambda}{\mu} - \sigma C; \forall t \geq 0$$

Again, using comparison theorem, it is obtained that

$$C(t) \leq \frac{\frac{\rho\Lambda}{\mu} + (C(0) - \frac{\rho\Lambda}{\mu})e^{-\sigma t}}{\sigma}; \forall t \geq 0 \text{ and since } C(0) \leq \frac{\rho\Lambda}{\sigma\mu}, \text{ so}$$

$$C(t) \leq \frac{\rho\Lambda}{\sigma\mu}; \forall t \geq 0 \tag{4}$$

Inequalities (3) and (4) guarantee that  $\Omega$  is forward invariant.

If the trajectory of system initiate at exterior of  $\Omega$ , then

$$\lim_{t \rightarrow \infty} N(t) \leq \frac{\Lambda}{\mu} \text{ and } \lim_{t \rightarrow \infty} C(t) \leq \frac{\rho\Lambda}{\sigma\mu}$$

So,  $\Omega$  attract any solutions that initiated at any point.

And hence  $\Omega$  is attractor set.

### 4. Basic Reproduction Number

Basic reproduction number is one of the most useful threshold parameters in the studying of epidemic models, which is defined as the average number of secondary cases produced by one infections individual during infections period<sup>[1]</sup>. This threshold parameter is often defined to be maximal eigenvalue of the next generation matrix<sup>[2,3]</sup> or found through the study and computation of eigenvalues of Jacobean matrix at disease free equilibrium.

If  $R_0 = \frac{\Lambda(\mu + (1-\gamma)k)(\beta_1 + \frac{\rho}{\sigma}\beta_2)}{\mu(\mu+k)(\mu+r_1+a)}$ , then it will be shown in the next theorem that the disease free equilibrium point  $E_1 = (\frac{\Lambda}{\mu+k}, \frac{k\Lambda}{\mu(\mu+k)}, 0, 0, 0, 0)$ , is asymptotically stable when  $R_0 < 1$ , which means that, the disease will disappear, and also it will be seen that the disease free equilibrium point is unstable when  $R_0 > 1$ , that is the disease continuous to exist, therefore,  $R_0$  can be become the basic reproduction number for system(1).

**Theorem 3** The disease-free equilibrium point is asymptotically stable if  $R_0 < 1$ , otherwise it is unstable.

**Proof** The variational matrix at the disease equilibrium point is

$$J(E_1) = (a_{ij})_{6 \times 6} \text{ where,}$$

$$\begin{aligned} a_{11} &= -\mu - k, a_{12} = 0, a_{13} = \frac{-\beta_1\Lambda}{\mu+k}, a_{14} = 0, a_{15} = r, \\ a_{16} &= \frac{-\beta_2\Lambda}{\mu+k} \\ a_{21} &= k, a_{22} = -\mu, a_{23} = \frac{-(1-\gamma)\beta_1 k\Lambda}{\mu(\mu+k)}, a_{24} = a_{25} = 0, \\ a_{26} &= \frac{-(1-\gamma)\beta_2 k\Lambda}{\mu(\mu+k)}, \\ a_{31} &= a_{32} = 0, \\ a_{33} &= \frac{\Lambda(\mu + (1-\gamma)k)}{\mu(\mu+k)}\beta_1 - (\mu + r_1 + a), a_{34} = a_{35} = 0, \\ a_{36} &= \frac{\Lambda(\mu + (1-\gamma)k)}{\mu(\mu+k)}\beta_2, a_{41} = a_{42} = 0, a_{43} = a, a_{44} \\ &= -(\mu + r_2 + d), \\ a_{45} &= a_{46} = a_{51} = a_{52} = 0, a_{53} = r_1, a_{54} = r_2, \\ a_{55} &= -(\mu + r), \\ a_{56} &= a_{61} = a_{62} = 0, a_{63} = \rho, a_{64} = a_{65} = 0 \text{ and} \\ a_{66} &= -\sigma \end{aligned}$$

eigenvalues in S-direction, V-direction, H-direction and R-directions are

$\lambda_s = -\mu - k < 0$ ,  $\lambda_v = -\mu < 0$ ,  $\lambda_i = -(\mu + r_2 + d) < 0$  and  $\lambda_r = -(\mu + r) < 0$  respectively, while both eigenvalues in IC-plane satisfies the following equation

$\lambda^2 + B_1\lambda + B_2 = 0$  where

$$B_1 = \sigma + \frac{\Lambda\rho(\mu + (1-\gamma)K)}{\sigma\mu(\mu + K)}\beta_2 + \left( (\mu + r_1 + a) - \frac{\Lambda(\mu + (1-\gamma)k)\left(\beta_1 + \frac{\rho}{\sigma}\beta_2\right)}{\mu(\mu + k)} \right)$$

$$= \sigma + \frac{\Lambda\rho(\mu + (1-\gamma)K)}{\sigma\mu(\mu + K)}\beta_2 + (\mu + r_1 + a)(1 - R_0)$$

and  $B_2 = \sigma(\mu + r_1 + a) - \sigma \frac{\Lambda(\mu + (1-\gamma)k)\left(\beta_1 + \frac{\rho}{\sigma}\beta_2\right)}{\mu(\mu + k)}$

$$= \sigma(\mu + r_1 + a)(1 - R_0)$$

then, all Routh-Hurwitz criteria  $B_1 > 0$  and  $B_2 > 0$  if and only if  $R_0 < 1$ , and hence the disease-free equilibrium point is locally asymptotically stable if  $R_0 < 1$  otherwise it is unstable. In the following theorem the global stability of the disease equilibrium point is given.

**Theorem 4** Though the vaccination efficacy approaches zero, the disease-free equilibrium point is globally asymptotically stable if  $R_0 < 1$ .

**Proof** The third equation and final equation of system (1) can be written as

$$\frac{d}{dt} \begin{pmatrix} I(t) \\ C(t) \end{pmatrix} = D_x(E_1) \begin{pmatrix} I(t) \\ C(t) \end{pmatrix} - F(S(t), V(t), I(t), C(t)) \text{ where}$$

$$D_x(E_1) = \begin{pmatrix} \frac{\beta_1\Lambda}{\mu + k} + \frac{(1-\gamma)\beta_1 k\Lambda}{\mu(\mu + k)} - (\mu + r_1 + a) & \frac{\beta_2\Lambda}{\mu + k} + \frac{(1-\gamma)\beta_2 k\Lambda}{-\sigma} \\ 0 & 0 \end{pmatrix}$$

and

$$F(S(t), V(t), I(t), C(t)) = \begin{pmatrix} (\beta_1 I + \beta_2 C) \left( \frac{\Lambda(\mu + (1-\gamma)k)}{\mu(\mu + k)} - (S + (1-\gamma)V) \right) \\ 0 \end{pmatrix}$$

If  $(1-\gamma) \rightarrow 1$ , then  $S + (1-\gamma)V \leq \frac{\Lambda(\mu + (1-\gamma)k)}{\mu(\mu + k)}$  in simplex set  $\Omega$

So,  $F(S(t), V(t), I(t), C(t))$  is non-negative function in simplex set  $\Omega$ , therefore

$$\begin{pmatrix} I(t) \\ C(t) \end{pmatrix} = \begin{pmatrix} I(0) \\ C(0) \end{pmatrix} e^{D_x(E_1)t} - \int_0^t F(S(u), V(u), I(u), C(u)) du \leq \begin{pmatrix} I(0) \\ C(0) \end{pmatrix} e^{D_x(E_1)t}$$

It is clear that  $D_x(E_1)$  is Metzler-matrix and its dominant eigenvalue is negative if  $R_0 < 1$ , therefore,

$$\lim_{t \rightarrow \infty} \|e^{D_x(E_1)t}\| \rightarrow 0 \text{ and hence } \lim_{t \rightarrow \infty} \begin{pmatrix} I(t) \\ C(t) \end{pmatrix} = \begin{pmatrix} 0 \\ 0 \end{pmatrix}$$

Therefore, as  $t \rightarrow \infty$ , both  $\frac{dH}{dt}$  and  $\frac{dR}{dt}$  will be negative, therefore

$$\lim_{t \rightarrow \infty} H(t) = 0 \text{ and } \lim_{t \rightarrow \infty} R(t) = 0. \text{ So, system (1), become}$$

$$\frac{dS}{dt} = \Lambda - (\mu + k)S \quad (5)$$

$$\frac{dV}{dt} = kS - \mu V \quad (6)$$

$$\text{Solving eq (6), gives } S(t) = \frac{\Lambda + (S(0)(\mu + K) - \Lambda)e^{-(\mu + K)t}}{\mu + K}$$

$$\text{Thus } \lim_{t \rightarrow \infty} S(t) = \frac{\Lambda}{\mu + k} \text{ for } S(0) \geq 0 \quad (7)$$

Putting eq (7) in eq (6) and solving eq (6), we get

$$\text{and } \lim_{t \rightarrow \infty} V(t) = \frac{k\Lambda}{\mu(\mu + k)}$$

That is  $\lim_{t \rightarrow \infty} (S(t), V(t), I(t), H(t), R(t), C(t)) = E_1$ , consequently,  $E_1$  is globally stable.

## 5. Existence and Uniqueness of The Endemic Equilibrium Point

In this section, we investigate the existence and uniqueness the endemic equilibrium point when

$R_0 > 1$  as follows:

Let  $E_2 = (S_e, V_e, I_e, H_e, R_e, C_e)$  be the endemic equilibrium point of system (1), then

$$h_e = \frac{a}{r_2 + \mu + d} I_e, C_e = \frac{e}{\sigma} I_e, R_e = \frac{r_1 I_e + r_2 h_e}{\mu + r}, S_e = \frac{\Lambda + r R_e}{\mu + k(\beta_1 + \beta_2 \frac{e}{\sigma}) I_e},$$

$$V_e = \frac{k S_e}{\mu + (1-\gamma)(\beta_1 + \beta_2 \frac{e}{\sigma}) I_e}$$

and  $I_e$  is solution for the following equation

$$\varkappa_1 I^2 + \varkappa_2 I + \varkappa_3 = 0 \quad (8)$$

$$\varkappa_1 = (1-\gamma) \left( \beta_1 + \beta_2 \frac{e}{\sigma} \right) \left[ r \left( \frac{r_1}{(\mu+r)} + \frac{r_2 a}{(\mu+r)(r_2 + \mu + d)} \right) - (\mu + r_1 + a) \right]$$

$$\varkappa_2 = \frac{(\mu + (1-\gamma)k)\varkappa_1}{(1-\gamma)(\beta_1 + \beta_2 \frac{e}{\sigma})} + (1-\gamma) \left[ \Lambda \left( \beta_1 + \beta_2 \frac{e}{\sigma} \right) - \mu(\mu + r_1 + a) \right]$$

$$\kappa_3 = \frac{\mu(\mu+k)(\mu+r_1+a)}{(\beta_1 + \beta_2 \frac{e}{\sigma})} (R_0 - 1)$$

It is clear that

$$\kappa_1 \leq (1 - \gamma) \left( \beta_1 + \beta_2 \frac{e}{\sigma} \right) (r_1 + a - (\mu + r_1 + a)) = (\gamma - 1) \left( \beta_1 + \beta_2 \frac{e}{\sigma} \right) \mu < 0$$

Therefore, equ(8) has unique positive root  $I_e = \frac{-\kappa_2 - \sqrt{\kappa_2^2 - 4\kappa_1\kappa_3}}{2\kappa_1}$  if and only if  $\kappa_3 > 0$

Consequently, the endemic equilibrium point  $E_2$  exist uniquely in  $R_+^6$  if and only if  $R_0 > 1$ .

In theorem (3,4) it has been shown that condition for stable of free disease equilibrium point is  $R_0 < 1$  that is if  $R_0 > 1$ , the free equilibrium point is stable, in this section it is proved that the reproduction number  $R_0$  must be greater than one for existence of the endemic equilibrium point.

**6. Parameter estimation: case of covid -19 in Kurdistan region of Iraq**

To estimate parameters of epidemic models, various techniques are used, author in<sup>[5]</sup> collected the observed date and using least

square method. But System (1) contained compartment of contaminated object, which cannot be observed, therefor, according to the model parameter description, they formulated by the following rules.

$\Lambda$  = Average number of new daily born.

$\frac{1}{\mu}$  = Global median age of population  $\approx$  half average of individual's life span,

$\frac{1}{r_1}$  = Average period from detected to recovery,  $\frac{1}{r_2}$  = average length of hospital stay.

$\frac{1}{r}$  = average time of recovery period,

$\frac{1}{\sigma}$  = Average surface area contaminated objects washing out from virus per unite time.

$\rho$  = Average surface area of shading objects by virus by one infected person per unite time.

$\gamma$  = efficacy of the vaccine,  $k = \frac{V_a}{S_a}$ ,  $d = \frac{d_a}{r_1 - I_a(1 - (d + \mu))}$

**Table 3:** New cases of infected individuals and death caused due to covid19 in Kurdistan region of Iraq.

Date	New cases of infected	Number of Death	Date	New cases of infected	Number of Death
22/8/2021	1531	20	11/9/2021	1214	17
23/8/2021	2024	20	12/9/2021	1339	17
24/8/2021	1869	22	13/9/2021	1235	16
25/8/2021	1921	21	14/9/2021	1178	11
26/8/2021	1626	19	15/9/2021	1253	22
27/8/2021	1546	25	16/9/2021	1378	19
28/8/2021	704	18	17/9/2021	634	13
29/8/2021	1513	17	18/9/2021	1253	17
30/8/2021	2010	16	19/9/2021	1285	12
31/8/2021	1573	16	20/9/2021	1254	8
1/9/2021	1994	11	21/9/2021	1117	13
2/9/2021	1871	14	22/9/2021	1236	19
3/9/2021	1406	22	23/9/2021	1360	20
4/9/2021	442	12	24/9/2021	360	13
5/9/2021	1679	17	25/9/2021	1265	14
6/9/2021	1618	21	26/9/2021	1421	10
7/9/2021	1764	11	27/9/2021	1401	19
8/9/2021	1463	20	28/9/2021	1349	17
9/9/2021	1491	16	29/9/2021	1353	18
10/9/2021	1380	22	30/9/2021	1372	19

$\beta_1(\bar{S} + (1 - \gamma)V_n) \left( \frac{1}{r_1} I_a(1 - (d + \mu)) \right)$  = Average number of daily new infectious caused by c directed contact with infected individuals

$\beta_2(\bar{S} + (1 - \gamma)V_n)\rho \left( \frac{1}{r_1} I_a(1 - (d + \mu)) \right)$  = average number of daily new infectious person caused by contact with contaminated objects,

Where  $I_a$  = Average number of daily new cases of infected person.,  $V_d$  = Average number of daily vaccination.,  $d_a$  = Average number of daily death due virus,  $V_n$ = Total number of vaccinated individuals.  $\bar{S} = \frac{1}{n} \sum_{t=0}^n (1 - t\mu)S_0 + t(\Lambda - V_d - I_a)$ .

Note that the term  $\frac{1}{r_1} \times I_a(1 - (d + \mu))$  is daily average number of existence of infectious person

Now, estimation parameter values regarding to the spreading of covid-19 in Kurdistan region/Iraq, the data given by table 3, which is announced by Kurdistan regional Government/Ministry of Health, from (August 22, 2021) to (September 30, 2021), is used and the following assumption is assumed

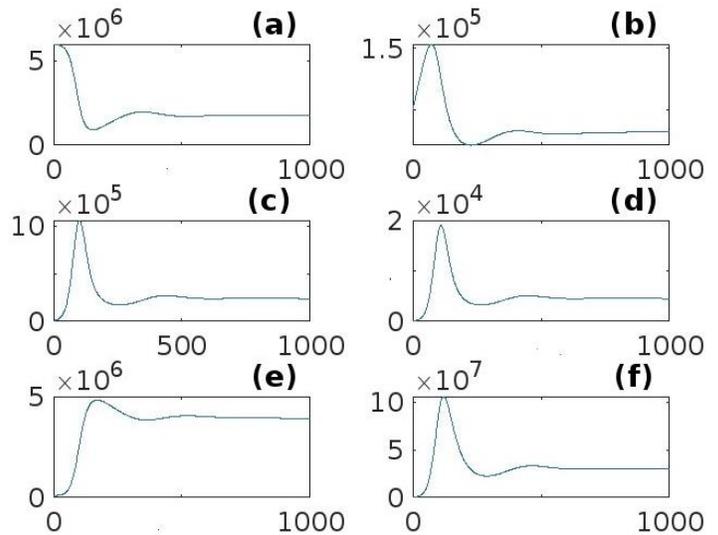
1.  $S(0) = 6 \times 10^6$ .
2. Every day 300 susceptible individuals will born.
3. The life span of individuals in Kurdistan is 70 years.
4. average time of hospitalizing period and Infectious period of individuals are 10 and 12 days respectively.
5. two percent of new case of infected need hospitalization.
6. average recovery period of individuals is 200 days
7. 5 object is shaded by virus by one infected person in a day.
8. four percent of contaminated objects is wished out in a unit time.
9. Every day 1000 susceptible individuals vaccinated.
10. The probability of infected vaccinated to be infectious is 0.3.
11. Ten percent of new cases of infected through contact with contaminated objects.

Therefore, the parameter values given in table 4, is obtained

Let us numerically solve the system (1) with parameters given in Table 4, and plotted the solution MATLAB see Fig.2

**Table 4:** Parameter model values for speeding covid 19 in Kurdistan region.

Parameters	Values
$\Lambda$	300
$\beta_1$	$1.2 \times 10^{-8}$
$\beta_2$	$2.7 \times 10^{-10}$
$\rho$	5
$\sigma$	0.04
$\mu$	0.00008
$r_1$	0.08
$r_2$	0.1
r	0.005
d	0.006
K	$1.6 \times 10^{-4}$
A	0.002
$\gamma$	0.7

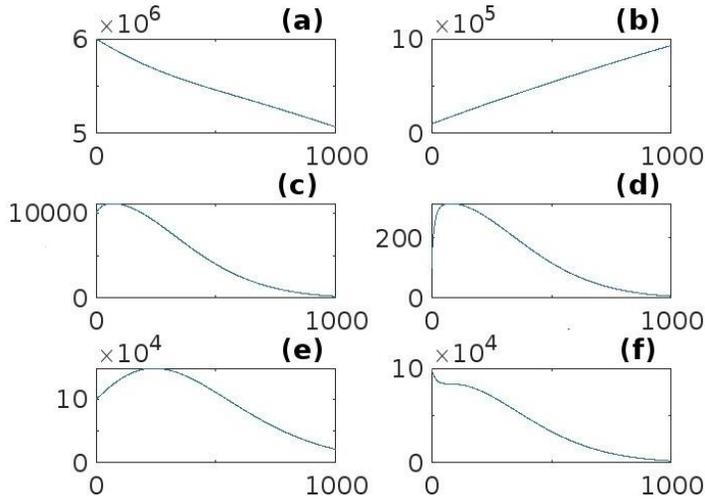


**Figure 2:** Time series for system (1) with parameter values in table4: (a) Susceptible individual density (b)Vaccinated individual density(c)Infected individual density (b) Hospitalized individual density (e)Recovered individual density (f) Contaminated objected density.

Note that for the parameters values in Table 4, the basic reproduction number is  $R_0 = 1.1148 > 1$ , by theorem 3, the disease free equilibrium is unstable, biologically it means that spreading of disease will continue and Fig.2 confirms that.

Again, we solved system (1) with parameters given in Table 4 and changing the values of parameters  $\sigma, \gamma$  and a to 0.3, 0.85 and 0.003 respectively, see Fig.3.

Note that for the used parameter values in above figure,  $R_0 = 0.361 < 1$ , by theorem 3, the disease-free equilibrium point is stable, biologically it means that spreading of disease will be stop, and Fig.3 confirms that.



**Figure 3:** Time series for system (1) with parameter values in table 4: (a) Susceptible individual density (b) Vaccinated individual density (c) Infected individual density (d) Hospitalized individual density (e) Recovered individual density (f) Contaminated object

## 7. Sensitivity Analysis

In section four, it has been shown that the basic reproduction number  $R_0$  has a great role on the local as well as global stability of the disease-free equilibrium point, therefore  $R_0$  is the most important threshold while studying infection. In this section, sensitive analysis for the basic reproduction number is done, such analysis is commonly used to determine the parameters that have impact on the basic reproduction number and must be targeted by intervention strategies. The formula

$$\gamma_p^{R_0} = \frac{p}{R_0} \frac{\partial R_0}{\partial p}$$

is normalized forward sensitivity index of  $R_0$  [4], which is the ratio of the relative change in  $R_0$  to relative change in the parameter  $p$ .

Note that when  $\gamma_p^{R_0} > 0$ , meaning that increasing (decreasing) value of parameter  $p$  by a given percentage increases (decreases) approximately  $R_0$  by the given percentage  $\times |\gamma_p^{R_0}|$ , but if  $\gamma_p^{R_0} < 0$ , meaning that increasing (decreasing) value of parameter  $p$  by a given percentage decrease (increases) approximately  $R_0$  by the given percentage  $\times |\gamma_p^{R_0}|$ .

The value of the sensitivity indices for the parameter values of table (4) are given in table (5).

Note that parameters with small value for sensitivity index is not necessary, because a small change in values of those parameters leads small change in the value of basic reproduction number, while the parameters with big value of forward sensitivity index requires much attention. role because its forward sensitivity index is positive.

**Table 5:** Sensitivity of  $R_0$  for the given parameter values in table 4.

Parameters	Sensitivity
$\rho$	0.7377
$\sigma$	-0.7377
$a$	-0.0244
K	-0.2917
$\gamma$	-0.875

In Table 5, model parameters relative to treatment, vaccination, washing out the contaminated object from virus and vaccination efficacy have negative forward sensitivity index, consequently, if those model parameters increase, the basic production will decrease, especially the vaccination efficacy has much more positive role on decreasing the spreading disease. While the model parameter relative to contaminated objects has positive forward sensitivity index, consequently, if this model parameter increases, also the basic production increases and hence, model parameter relative to contaminated objects has negative role on increasing the spreading disease

## 8. Conclusion

In this paper, an epidemic model is considered for effecting vaccination, treatment and contaminated object on the transmission dynamics of infectious disease, positivity of the model solution is proved, an invariant simplex set is founded for the model. The model basic reproduction number  $R_0$  is calculated through eigenvalues of variational matrix at the disease free equilibrium point, it can be seen that  $R_0$  decrease when the rates of vaccination and hospitalization increases and rate of infection through contaminated object decreases and decreasing of  $R_0$  is very important because locally stability analysis of the disease free equilibrium point is proved when the basic reproduction number is less than unity in theorem 3 and globally stability analysis of the disease free equilibrium point is proved when the basic reproduction number is less than unity and the vaccination efficacy approaches unity. The roles of parameters relative of vaccination and treatment and vaccination efficacy, regarding of spreading covid-19 in Kurdistan region of Iraq, under some assumption and the data's in Table 3, all parameters model are estimated and it is predicated that after 1000 days, the disease will continues to exist, see Figure-(1), but if we increase each of the vaccination efficacy to eighty five percent, rate of washing out the contaminated object to thirty five percent in a unit time and hospitalization rate to  $a=0.003$ , then after 1000 days the speeding will be stopped see figure-(2), and this confirms that vaccination and hospitalization have great positive role on decreasing the spreading of infectious disease especial the vaccination efficacy, while the contaminated object has negative role on spreading the infectious disease. Therefore, this analysis must be targeted by intervention strategy and population individuals.

## Conflict of interests

None.

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