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# The investigation of variant vaccination models in Iran

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**Abstract**

Kermack-McKendrick-type epidemic models are commonly used for modeling epidemic diseases. In this study, we have proposed a Kermack-McKendrick-based model to elucidate the impact of COVID-19 vaccination on the spread of the virus in Iran. This model serves as an endemic assessment tool, tailored to fit reported data in Iran, for gauging the potential population-level effects of the COVID-19 vaccine. It's important to note that COVID-19 vaccines do not guarantee complete protection against the disease. A vaccinated person may still become infected, highlighting the necessity of continuous vaccination while an individual is in the system. To address this, we considered two models—one with only one strain and the other containing two strains. We hypothesize that the vaccine results in complete immunization against one strain while conferring partial immunization against the other. To explore this, we consider two scenarios. In the first scenario, we assume that the vaccine does not provide complete immunity, and individuals may become infected again after vaccination. In the second scenario, a dual-strain model is considered, positing that individuals, when vaccinated, remain immune to the strain present in the vaccine, but are susceptible to another strain for which the vaccine provides partial protection. However, this other strain may still lead to infection in individuals. The analysis of the proposed models revealed that where the prevalence rate, or the basic reproduction number (R0) - an index measuring the spreading potential of a pathogenic agent and the average number of individuals each infected person can potentially transmit the infectious agent to susceptible individuals - has a direct correlation with vaccination. Therefore, to assess the extent of vaccine efficacy, this indicator is employed, with a lower prevalence rate being the targeted outcome.

Keywords: COVID-19, Corona virus, Mathematical modeling of infection disease, SEIRUS-model, Parameter Estimation, Vaccination
2020 MSC: Primary 26A33, 34D10; Secondary 45N05

## 1 Introduction

A novel coronavirus (nCoV), named "2019-nCoV", is causing the deadliest pandemic in late 2019 and early 2020, defined as the coronavirus disease 2019 (COVID-19) by the World Health Organization (WHO). It is also known as severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). The first cases that occurred in early December 2019, had been reported in China. In order to contain the spread of the virus, many countries and regions were locked down

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at that time and applied strict social distancing measures. From a strategic and health care management perspective, the propagation pattern of the disease and the prediction of its spread over time is of great importance, to save lives and minimize the social and economic consequences of the disease. Within the scientific community, the problem of interest has been studied in various communities including mathematical epidemiology [3], biological systems modeling [10, 24], signal processing [26] and control engineering [1]. Epidemiological mathematical models have been developed to help policymakers to make the right decisions.

A first tentative mathematical model of this pandemic (see [13]), is based on the Be-CoDiS model. For information on this model, see [14, 15].

Mathematical models of infectious diseases have been recognized as powerful tools that can provide important insights into our understanding of epidemiological processes, the course of infection within a host, the transmission dynamics in a host population, and the formulation or implementation of disease control programs [11, 21]. Compartmental mathematical models involving vaccination strategy for infectious disease control have been considered in [25, 27].
In this work, we developed a mathematical model based on the Susceptible-Infectious-Susceptible (SIS) model which is impacted by vaccines to explore how the vaccination rate can affect estimates of virus activity and forecast performance. This model consists of state variables (e.g., number of susceptible persons, S), which describe the evolution of conditions within the simulated population, and parameters (e.g., recovery rate, $\gamma$), which describe biological properties. on the other hand, Covid-19 Vaccines do not guarantee complete protection against the disease. In fact, it is possible that a vaccinated person becomes infected indicating the necessity of continuous vaccination while an individual is in the system. Moreover, we take into account the fact that vaccines do not have all pathogens. Hence, we consider two models, in the first scenario the SIS model with vaccination is assumed that the vaccine does not provide permanent immunity and the vaccinated person can become infected. In the second proposed model different variants of the coronavirus are examined.Coronavirus has different strains that may not all be included in the vaccine. We know that the immunity that the vaccine creates is specific to that strain included in the vaccine. The scenario requires a two-strain model, one for the vaccine strain and one for the strain with which the vaccine is partially safe in the case of vaccination.An accurate analysis depends not only on how accurately a dynamic model represents real-world transmission dynamics but also on the appropriate specification of model parameters and the accuracy of estimation of model state variables at the beginning of the simulation.

Susceptible-Exposed-Infected-Removed (SEIR) model is similar to SIR, with the variables ($S, I$, and $R$) representing the number of people in each compartment at a particular time, but the incubation period has been added in SEIR so that it is more applicable to infectious diseases with a certain incubation period ([16]). By considering the characteristics of SARS-CoV-2-its spread trends and local condition constraints and economic optimization, we aimed to develop mathematical models that would provide the optimal COVID-19 eradication plan that was sensible and feasible.

By using methods in [16, 8, 2] and KB, in [22], we consider the dynamics of COVID-19 epidemic in Iraan, and model it using a modified age-structured compartmental SEIR (susceptible, exposed, infected and recovered) framework. The modifications account for the presence of asymptomatic carriers, different types of clinical progression of the disease once someone becomes infected, the need for hospitalisation, as well as the severity of the hospital interventions. The model assumes that individuals who have recovered from COVID-19, subsequently have immunity against the virus for the remaining duration of the epidemic. Official data from the Ministry of Health of Iran regarding confirmed daily infected cases and deaths, as well as distributions of incubation and recovery times, are used to parameterise the model. We also provide a short-term forecast of further dynamics of COVID-19 in Iran and two states: Ardabil and Guilan.

In [20], authors collected publicly available information, interviewed experts, and used our diverse range of expertise to analyse and model the COVID-19 vaccine portfolio. In [19] authors studied aims to inform SARS-CoV-2 vaccine development/licensure/decision-making/implementation, using mathematical modeling, by determining key preferred vaccine product characteristics and associated population-level impacts of a vaccine eliciting long-term protection. In this paper by using [20] and [19], we consider the SEIRUS-model and present two senario for Iran.

and explore the impact of different types of lockdown on the number of cases and deaths. Consequently, it is important for the analysis that model parameters and initial conditions be well specified. The least-squares and MATLAB-embedded functions (such as $lsqcurvefit$ and $fminsearch$) methods are used, inconjunction with the SIS model and observations of Covid incidence, to estimate the state variable conditions and estimated the model parameters. The least-squares method minimizes the gap of confirmed cases between the actual data to train the model so that current conditions are better depicted and evolving outbreak characteristics (i.e. the trajectory of the epidemic

curve) are better matched. Also, analysis with inferred parameters and updated state variables was made to make it more accurate and reliable.

The paper is organized as follows: Section 2, gives an overview of the variety of vaccines in Iran. The model description is presented in Section 3. Also, in Section 4, an analysis of the model for two proposed scenarios is performed to investigate the existence of endemic equilibria, the local stability of the endemic equilibrium, and the reproduction number. Numerical simulations are presented in Section 5, and the reproduction numbers are derived by using the theory and compared for two scenarios, to illustrate the main theoretical results. A brief conclusion is given in Sec. 6.

## 2 Types of the vaccine in Iran

Iran received the first batch of COVID-19 vaccines on 9 February 2021 as shown in Figure 1. Until August 24, 2021, five types of vaccines have been approved for use in Iran such as Oxford / AstraZeneca, Sputnik V, Bharat Biotech, Sinopharm and Barakat according to the Iran health organization reports. Also currently, when we write this paper, two types of mRNA-based COVID- 19 vaccines have been authorized by the Iran health organization too.
According to the government's vaccination program, on February 9, 2021, Iran started the first doses of the vaccine. But, due to the global outbreak of Covid 19 disease and the need of all world countries to the vaccine, Asian countries like Iran had fewer opportunities for vaccination. Also, the political situation in this country and the problems of financial exchanges were other obstacles to vaccination. So, the Iranian government has not operated a regular vaccination schedule and at some point, the vaccination schedule was strained due to a lack of vaccines, as shown in Figure 2.

However the government program consisted of several stages:

In the first stage, the vaccine dose is limited and health care workers work in hospitals whose work is known to be high-risk jobs.

Then in the second stage, which started in the spring of 2021, the list of people who could be vaccinated was expanded further, in this stage adults separately by age were given priority. Also, some jobs such as those who worked in public transportation are vaccinated as well.

Finally, in stage III, teachers, the employee who works in universities, banks, educational departments and so wanted to become immunized received their dose of vaccine.

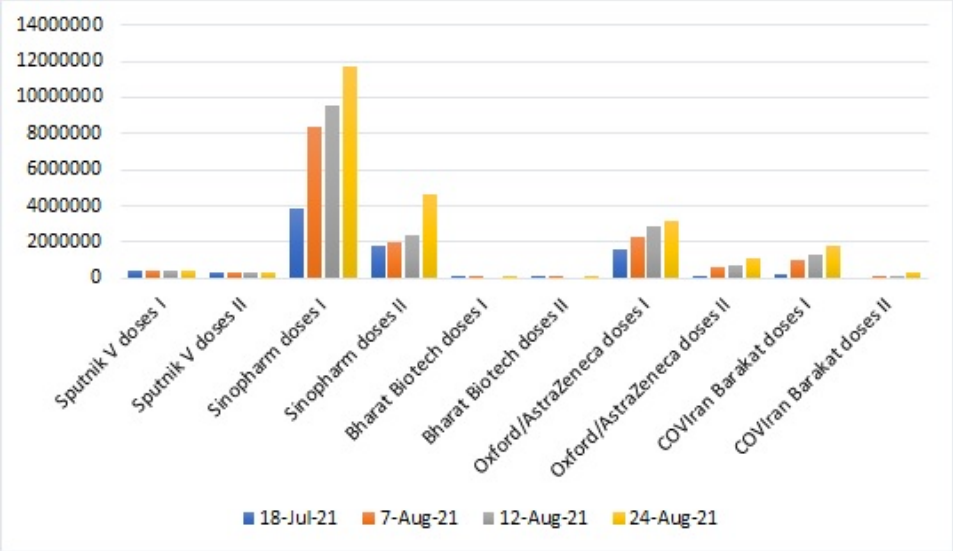


Figure 1: The Statistics on corona vaccination in Iran from the beginning of the vaccination program until August 24, 2021.

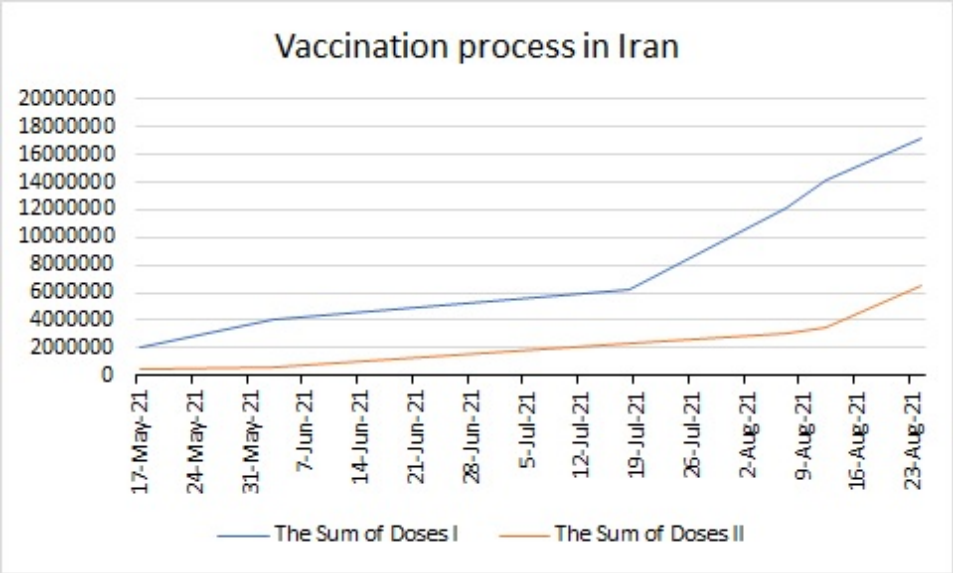


Figure 2: Corona Vaccination process in Iran from the beginning of the vaccination program until August 24, 2021.

## 3 The model description

In this section, we look into the impact of vaccines on the dynamics of the model. We developed a mathematical model using nonlinear differential equations. Our model captures the dynamics of COVID-19 infection coupled with the vaccination.

To gain some insights into the mathematical model of the disease, we have considered the following cases,
• All diseases for which vaccination is successful have an improved (immune) stage.
• In vaccination, behave the immune system is more or less like a disease. Also, according to the WHO reported, the immunity is temporary, improved individuals and vaccinated individuals can be reinfected by the coronavirus.
• Coronaviruses are RNA viruses that are phenotypically and genotypically diverse.
• Coronavirus is not a bacterial virus so it can't exist in the host without causing disease, there is no such thing as a carry scenario.

Therefore, for mathematical modeling, we consider two scenarios as follows:

### 3.1 First scenario: The SIS model with vaccination

In this section, we assume that the vaccine does not provide permanent immunity. Consequently, susceptible individuals do not acquire lasting immunity, and vaccinated individuals remain susceptible to infection. Therefore, an additional class, labeled $V$ is introduced to the SIR model for those who have received the vaccine. Thus, we have the following scenario.

$$\begin{aligned} \frac{dS}{dt} &= \Lambda - \frac{\beta SI}{N} - (\mu+\psi)S + \chi\gamma I \\ \frac{dI}{dt} &= \frac{\beta SI}{N} + \frac{\beta\delta VI}{N} - (\mu+\gamma)I \\ \frac{dV}{dt} &= \psi S - \frac{\beta\delta VI}{N} + (1-\chi)\gamma I - \mu V \end{aligned} \tag{3.1}$$

Also, vaccination should only be applied to healthy individuals, specifically to those who are susceptible. However, in reality, it does not distinguish between individuals who are sick or not. Although we overlook this error in our analysis, it's important to note that the available corona vaccines are not foolproof. Some vaccinated individuals can still become infected due to the transmission rate, denoted by "$\beta\delta$," even if they have received the vaccine (where $0 \leq \delta \leq 1$). If $\delta = 0$, it implies that vaccinated individuals cannot be infected, while $\delta = 1$ indicates that the vaccine

provides no protective effect. We have listed the parameters and variables in Table 1 The flowchart of the model is presented in Figure 3., illustrating the ongoing and repetitive nature of the vaccination process.

Table 1: List of parameters, variables, and their meanings

| | |
|---|---|
| $\Lambda$ | Birth/recruitment rate into the population |
| $\mu$ | Per capita natural death rate |
| $\beta$ | Per capita transmission rate |
| $\gamma$ | Per capita recovery rate |
| $\chi$ | Proportion of individuals who recover to the susceptible class |
| $1-\chi$ | Proportion of individuals who recover to the vaccinated class |
| $\psi$ | Per capita vaccination rate |
| $S(t)$ | Number of susceptible individuals |
| $I(t)$ | Number of infected individuals |
| $V(t)$ | Number of vaccinated individuals |
| $\varepsilon = 1-\delta$ | Vaccine efficacy |
| $I_1(t)$ | Number of infected individuals by the first strain |
| $I_2(t)$ | Number of infected individuals by the second strain |
| $\beta_1$ | Per capita transmission rate for $I_1$ |
| $\beta_1$ | Per capita transmission rate for $I_2$ |
| $\alpha$ | Per capita recovery rate for $I_2$ |

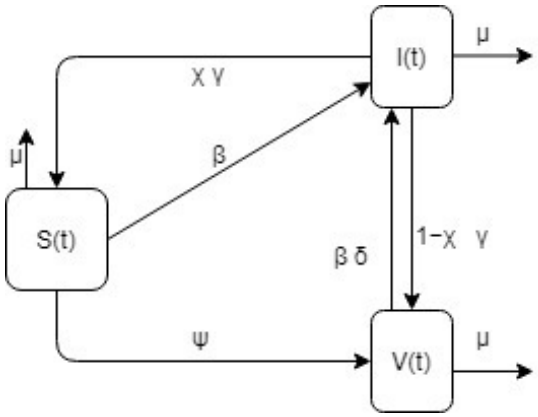


Figure 3: Flowchart of the model with vaccination.

### 3.2 Second scenario: Virus with diverse genetics and vaccination

In this section, various variants of the coronavirus are examined. According to medical reports, the coronavirus has different strains that may not all be covered by the vaccine. We understand that the immunity provided by the vaccine is specific to the targeted strain. To model this scenario, we must consider a two-strain model. One strain corresponds to the vaccine and, in the case of vaccination, susceptible individuals will not be infected with that strain. The other strain is only partially covered by the vaccine. The model with two strains and vaccination becomes:

$$\begin{aligned}
\frac{dS}{dt} &= \Lambda - \frac{\beta_1 S I_1}{N} - \frac{\beta_2 S I_2}{N} - (\mu+\psi)S + \chi\gamma I_1 + \alpha I_2 \\
\frac{dI_1}{dt} &= \frac{\beta_1 S I_1}{N} + \frac{\beta_1 \delta V I_1}{N} - (\mu+\gamma)I_1 \\
\frac{dI_2}{dt} &= \frac{\beta_2 S I_2}{N} - (\mu+\alpha)I_2 \\
\frac{dV}{dt} &= \psi S - \frac{\beta_1 \delta V I_1}{N} + (1-\chi)\gamma I_1 - \mu V
\end{aligned} \tag{3.2}$$

where the parameter $\alpha$ is the per capita recovery rate from the second strain and the parameter $\gamma$ is that from the first strain too. The $I_1$ and $I_2$ are the number infected with the first and second strain, respectively. The flowchart of the model is given in Figure 4.

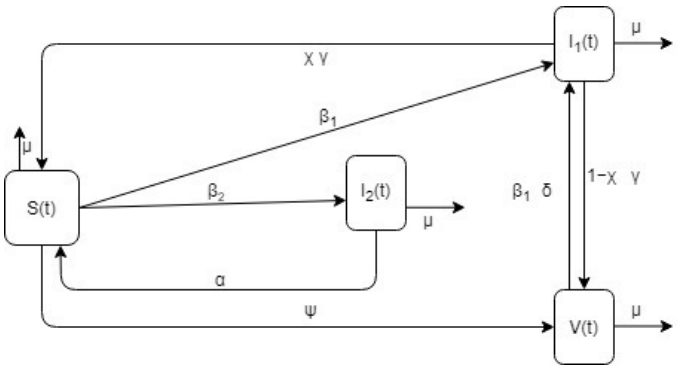


Figure 4: Flowchart of the model with two-Strain.

The following assumptions would help in the derivation of the above models:

1) There is no emigration from the total population and there is no immigration into the population. In fact, the current model is only suitable for countries or territories with a relevant number of people infected by COVID-19, where the local spread is very important.

2) Since there is no clear scientific evidence of the effect of the humidity and the temperature on SARS-CoV-2, we have not included these two factors in our model.

Our equations with initial conditions $S(t_0), I(t_0), V(t_0)$ are derived from observations of Covid-19 incidence in Iran at $t_0$, also the total population size is $N(t) = S(t) + I(t) + V(t)$.

## 4 Analysis of the model

### 4.1 First scenario

The equilibria of system (3.1) is obtained by setting the right-hand side of the equations to be equal to zero. The disease-free equilibrium $E_0$ is given by

$$(\tfrac{\Lambda}{\mu+\psi}, 0, \tfrac{\psi\Lambda}{(\mu+\psi)\mu}).$$

**Theorem 4.1.** There is a unique disease-free equilibrium $E_0$ for the model represented by system (3.1).

Proof. This theorem is proved by substituting $E_0$ into system (3.1). The results show that all the derivatives are equal to zero, hence the disease-free equilibrium.

To establish the linear stability of $E_0$, we use the next generation operator approach on system (3.1) to compute the basic reproduction number $R_0$. This is determined using the approach by van den Driessche and Watmough [5]. For the notation of the matrices $F$ and $V$, we have

$$V = \begin{bmatrix} -\frac{\beta\delta}{N} + \mu + \gamma & -\frac{\beta\delta}{N} \\ \frac{\beta\delta}{N} - (1-\chi)\gamma & \frac{\beta\delta}{N} + \mu \end{bmatrix}$$

Evaluating $F$ at the disease-free equilibrium, we obtain

$$F = \begin{bmatrix} \frac{\beta S}{N} & 0 \\ 0 & 0 \end{bmatrix}$$

and, thus

$$V^{-1} = \begin{bmatrix} \frac{\frac{\beta\delta}{N}+\mu}{\frac{\beta\delta\chi\gamma}{N}+\mu(\mu+\gamma)} & \frac{\frac{\beta\delta}{N}}{\frac{\beta\delta\chi\gamma}{N}+\mu(\mu+\gamma)} \\ \frac{-\frac{\beta\delta}{N}+(1-\chi)\gamma}{\frac{\beta\delta\chi\gamma}{N}+\mu(\mu+\gamma)} & \frac{-\frac{\beta\delta}{N}+\mu+\gamma}{\frac{\beta\delta\chi\gamma}{N}+\mu(\mu+\gamma)} \end{bmatrix}$$

Now we have

$$FV^{-1} = \begin{bmatrix} \frac{\beta\Lambda}{\mu+\psi}\frac{\frac{\beta\delta}{N}+\mu}{\frac{\beta\delta\chi\gamma}{N}+\mu(\mu+\gamma)} & \frac{\beta\Lambda}{\mu+\psi}\frac{\frac{\beta\delta}{N}}{\frac{\beta\delta\chi\gamma}{N}+\mu(\mu+\gamma)} \\ 0 & 0 \end{bmatrix}$$

The eigenvalues for the matrix $FV^{-1}$ are given by

$$\begin{vmatrix} x-\frac{\beta\Lambda}{\mu+\psi}\frac{\frac{\beta\delta}{N}+\mu}{\frac{\beta\delta\chi\gamma}{N}+\mu(\mu+\gamma)} & -\frac{\beta\Lambda}{\mu+\psi}\frac{\frac{\beta\delta}{N}}{\frac{\beta\delta\chi\gamma}{N}+\mu(\mu+\gamma)} \\ 0 & x \end{vmatrix}$$

So

$$x = 0, \quad x = \frac{\beta\Lambda(\frac{\beta\delta}{N}+\mu)}{(\mu+\psi)(\frac{\beta\delta\chi\gamma}{N}+\mu(\mu+\gamma))}$$

The spectral radius is given by

$$x = \frac{\beta\Lambda(\frac{\beta\delta}{N}+\mu)}{(\mu+\psi)(\frac{\beta\delta\chi\gamma}{N}+\mu(\mu+\gamma))}$$

which gives the effective reproduction number as

$$R_e = \frac{\beta\Lambda(\frac{\beta\delta}{N}+\mu)}{(\mu+\psi)(\frac{\beta\delta\chi\gamma}{N}+\mu(\mu+\gamma))}.$$

$R_e$ is referred to as the effective reproduction number rather than the basic reproduction number because vaccination and treatment have been included in the model (3.1). It is defined as the expected number of secondary cases caused by a typical infected individual entering an entirely susceptible population at equilibrium.

**Theorem 4.2.** The disease-free equilibrium $E_0$ of the Covid-19 model under treatment and vaccination interventions is locally asymptotically stable if $R_e < 1$ and unstable if $R_e \geq 1$.

A disease-free equilibrium is assumed to be stable if $R_e < 1$, while it is unstable if $R_e \geq 1$. Based on Theorem 2, of [5].

### 4.1.1 Existence of endemic equilibria

Consider system (3.1) with right-hand side equal to zero to obtain

$$\Lambda - \frac{\beta SI}{N} - (\mu+\psi)S + \chi\gamma I = 0 \tag{4.1}$$

$$\frac{\beta SI}{N} + \frac{\beta\delta VI}{N} - (\mu+\gamma)I = 0$$

$$\psi S - \frac{\beta SVI}{N} + (1-\chi)\gamma I - \mu V = 0$$

together with

$$\Lambda - \mu N - \sigma I = 0$$

Solving system (4.1) gives the endemic equilibrium $E_e = (S, I, V)$.

### 4.1.2 Local stability of the endemic equilibrium

The Jacobian matrix for system (3.1) is given by

$$J = \begin{bmatrix} -\frac{\beta}{N} - (\mu+\psi) & -\frac{\beta}{N} + \chi\gamma & 0 \\ \frac{\beta}{N} & \frac{\beta}{N} + \frac{\beta\delta}{N} - (\mu+\gamma) & \frac{\beta\delta}{N} \\ \psi & -\frac{\beta\delta}{N} + (1-\chi)\gamma & -\frac{\beta\delta}{N} - \mu \end{bmatrix}.$$

We now obtain the characteristic equation $P(x) = |I - J_{E_e}|$, where $I$ is a $3 \times 3$ unit matrix.

$$P(x) = \begin{vmatrix} x + \frac{\beta}{N} + (\mu+\psi) & 0 & 0 \\ 0 & x+\mu & 0 \\ 0 & 0 & x+\mu \end{vmatrix}$$

Thus the characteristic equation becomes

$$P(x) = x^3 + (2\mu + \tfrac{\beta}{N} + (\mu+\psi))x^2 + (\mu^2 + 2\tfrac{\beta}{N}\mu + 2\mu(\mu+\psi))x + \tfrac{\beta}{N}\mu^2 + (\mu+\psi)\mu^2$$

where

$$A_1 = (2\mu + \tfrac{\beta}{N} + (\mu+\psi)),$$

$$A_2 = (\mu^2 + 2\tfrac{\beta}{N}\mu + 2\mu(\mu+\psi))),$$

$$A_3 = 2\mu(\mu+\psi))x + \tfrac{\beta}{N}\mu^2 + (\mu+\psi)\mu^2.$$

The necessary and sufficient conditions for the local asymptotic stability of endemic equilibrium are that the Hurwitz determinants are all positive for the Routh-Hurwitz criteria. For more information see [18]. From which we can conclude that the endemic equilibrium is locally asymptotically stable.

### 4.2 Second scenario

Equilibrium of the system (3.2) is obtained by setting the right-hand side of the equations to be equal to zero. The disease-free equilibrium $E_0$ is given by

$$(\tfrac{\Lambda}{\mu+\psi}, 0, 0, \tfrac{\psi\Lambda}{(\mu+\psi)\mu}).$$

**Theorem 4.3.** There is a unique disease-free equilibrium $E_0$ for the model represented by system (3.2).

Proof. This theorem is proved by substituting $E_0$ into system (3.2). The results show that all the derivatives are equal to zero, hence the disease-free equilibrium.

To establish the linear stability of $E_0$, we use the next generation operator approach on system (3.2) to compute the basic reproduction number $R_0$. This is determined using the approach by van den Driessche and Watmough [5]. For the notation of the matrices $F$ and $V$, we have

$$V = \begin{bmatrix} -\frac{\beta_1\delta}{N} + \mu + \gamma & 0 & -\frac{\beta_1\delta}{N} \\ 0 & \mu+\alpha & 0 \\ \frac{\beta_1\delta}{N} - (1-\chi)\gamma & 0 & \frac{\beta_1\delta}{N} + \mu \end{bmatrix}$$

Evaluating $F$ at the disease-free equilibrium, we obtain

$$F = \begin{bmatrix} \frac{\beta_1 S}{N} & 0 & 0 \\ 0 & \frac{\beta_2 S}{N} & 0 \\ 0 & 0 & 0 \end{bmatrix}$$

and, thus

$$V^{-1} = \frac{1}{|V|}$$
$$\begin{bmatrix} 0 & (\mu+\alpha)(\mu(\mu+\gamma) - \frac{\beta_1\delta}{N}(\mu+\alpha)(1-\chi)) & 0 \\ (\frac{\beta_1\delta}{N} - (1-\chi)\gamma)(\frac{\beta_1\delta}{N}(\mu+\alpha)) & 0 & (\frac{\beta_1\delta}{N}+\mu)(\mu+\alpha)(-\frac{\beta_1\delta}{N}+\mu+\gamma) \end{bmatrix}$$

where

$$|V| = (\mu+\alpha)(\mu(\mu+\gamma) - \tfrac{\beta_1\delta}{N}(\mu+\alpha)(1-\chi)).$$

Now we have

$$FV^{-1} = \begin{bmatrix} \frac{\beta_1 S}{N}a & 0 & \frac{\beta_1 S}{N}b \\ 0 & \frac{\beta_2 S}{N} & 0 \\ 0 & 0 & 0 \end{bmatrix}$$

where

$$a = \frac{(-\frac{\beta_1\delta}{N}+\mu+\gamma)(\frac{\beta_1\delta}{N}+\mu)}{\mu(\mu+\gamma)-\frac{\beta_1\delta}{N}(\mu+\alpha)(1-\chi)}$$

and

$$b = \frac{-\frac{\beta_1\delta}{N}(\frac{-\beta_1\delta}{N}+(1-\chi)\gamma)}{\mu(\mu+\gamma)-\frac{\beta_1\delta}{N}(\mu+\alpha)(1-\chi)}.$$

The eigenvalues for the matrix $FV^{-1}$ are given by

$$\begin{vmatrix} x - \frac{\beta_1\Lambda}{N(\mu+\psi)}a & 0 & -\frac{\beta_1\Lambda}{N(\mu+\psi)}b \\ 0 & x - \frac{\beta_2\Lambda}{N(\mu+\psi)} & 0 \\ 0 & 0 & x \end{vmatrix}$$

So

$$x = 0, \qquad x = \frac{\beta_1\Lambda}{N(\mu+\psi)}a, \qquad x = \frac{\beta_2\Lambda}{N(\mu+\psi)}.$$

The spectral radius is given by

$$x = \frac{\beta_1\Lambda}{N(\mu+\psi)}a, \qquad x = \frac{\beta_2\Lambda}{N(\mu+\psi)}$$

which gives the effective reproduction number.

$R_e$ is referred to as the effective reproduction number rather than the basic reproduction number because vaccination and treatment have been included in the model (3.2). It is defined as the expected number of secondary cases caused by a typical infected individual entering an entirely susceptible population at equilibrium.

**Theorem 4.4.** The disease-free equilibrium $E_0$ of the Covid-19 model under treatment and vaccination interventions is locally asymptotically stable if $R_e < 1$ and unstable if $R_e \geq 1$.

**Proof .** See [5, Theorem 2]. □

As a consequence of Theorem 2.1, a small influx of COVID-infected individuals cannot cause an outbreak within the community if $R_e < 1$. COVID-19 reproduction number $R_0$ measures the average number of new cases generated by an infected individual in contact with a completely susceptible population. The duration of COVID-19 infection is typically defined as the time before a person recovers or dies from the disease. If $R0 = n$, then on average, one infected person will transmit COVID-19 to $n$ others during their infectious status (before they recover or die of the disease). we use the result of this section to compare the two proposed scenarios.

### 4.3 Existence of endemic equilibrium

Consider system (3.2) with right-hand side equal to zero to obtain

$$\Lambda - \frac{\beta_1 S I_1}{N} - \frac{\beta_2 S I_2}{N} - (\mu + \psi)S + \chi\gamma I_1 = 0 \tag{4.2}$$

$$\frac{\beta_1 S I_1}{N} + \frac{\beta_1 \delta V I_1}{N} - (\mu + \gamma) I_1 = 0$$

$$\frac{\beta_2 S I_2}{N} - (\mu + \alpha) I_2 = 0$$

$$\psi S - \frac{\beta_1 \delta V I_1}{N} + (1 - \chi)\gamma I_1 - \mu V = 0$$

together with

$$\Lambda - \mu N - \sigma I = 0$$

Solving system (4.2) gives the endemic equilibrium $E_e = (S, I_1, I_2, V)$.

#### 4.3.1 Local stability of the endemic equilibrium

The Jacobian matrix for system (3.2) is given by

$$J = \begin{bmatrix} -\frac{\beta_1}{N} - \frac{\beta_2}{N} - (\mu + \psi) & -\frac{\beta_1}{N} + \chi\gamma & -\frac{\beta_2}{N} & 0 \\ \frac{\beta_1}{N} & \frac{\beta_1}{N} + \frac{\beta_1 \delta}{N} - (\mu + \gamma) & \frac{\beta_1 \delta}{N} & 0 \\ \frac{\beta_2}{N} & 0 & \frac{\beta_2}{N} - (\mu + \alpha) & 0 \\ \psi & -\frac{\beta_1 \delta}{N} + (1 - \chi)\gamma & 0 & -\frac{\beta_1 \delta}{N} - \mu \end{bmatrix}.$$

For stability of the disease-free equilibrium, it is required that the $trace(J_{E_0}) < 0$ and the $det(J_{E_0}) > 0$. Thus, from the Jacobian matrix, it is clearly seen that

$$trace(J_{E_0}) = -(4\mu + \psi + \alpha) < 0.$$

The determinant of the Jacobian matrix is also given by

$$det(J_{E_0}) = \mu^2(\mu + \psi)(\mu + \alpha) > 0.$$

Therefore, the disease-free equilibrium of the pneumonia model under treatment and vaccination interventions is locally asymptotically stable.

## 5 Numerical simulation

Analytical results of the model are illustrated by numerical simulations using estimated parameter values from the literature. The system is simulated using ODE solvers coded in MATLAB programming language. Simulation of the covid-19 under treatment intervention and vaccination interventions combined is carried out to investigate the impact of the key parameters on the spread of Covid-19 and how their influence can be controlled.

The parameters of the model (3.1) and (3.2) were estimated from the infected individuals data for the entire Iran between 14 April 2021 and 15 June 2021. Figure 5 shows a Comparison of approved infectious cases and vaccinated cases for each dose in Iran. To date, reports of large US studies [9, 4, 23] demonstrate the continued high efficacy of full vaccination (two doses or more ) against severe disease or hospitalization.

We used data on Covid-19 in Iran which reported by Islamic Republic of Iran Ministry of Health and Medical Education [12] to estimate the initial parameters. Further, vaccination is needed in individuals previously infected [6]. We know that the infectious period is about 10 days, so we set the recovery $\gamma$ as $\gamma = \frac{1}{10}$ per day [7, 29]. oOn the other

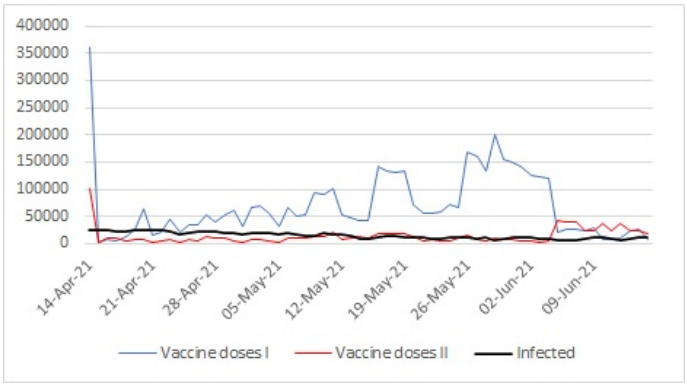


Figure 5: Comparison of approved infectious cases and vaccinated cases for each dose in Iran.

hand, since about 15% of patients are die, Hence, we set $\mu = 0.015$ [7].Other parameters of the model are also estimated by using the data of the reported contaminated cases using MATLAB and the least-squares method that minimize the gap of confirmed cases between the actual data. To implement this method, we used MATLAB-embedded functions, $lsqcurvefit$ and $fminsearch$ and then we found the same results.

The details on MATLAB-embedded functions affecting confirmed cases are shown in Figure 6 show the same results of the estimation of infection cases from the actual data of confirmed cases corresponding to model 3.2 in the date interval between 14/04/2021 and 29/04/2021.

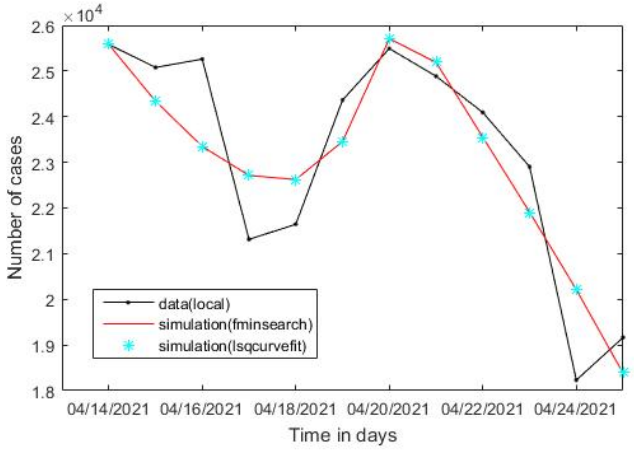


Figure 6: Estimation of the infection cases by different Matlab- functions and the baseline parameter mentioned and compare with actual data of confirmed cases in date's interval between 14/04/2021 and 29/04/2021.

Parameter fitting was performed using MATLAB. We considered both scenarios according to Iran data for 04/14/2021. The parameters for the first scenario are shown at values in Table 2and3.

Table 2: Value of parameters for scenario 1 (3.1)(see text for further details)

| parameter | $\mu$ | $\beta^{Estimated}$ | $\gamma$ | $\chi^{Estimated}$ | $1-\chi$ | $\psi^{Estimated}$ | $\varepsilon^{Estimated}$ |
|---|---|---|---|---|---|---|---|
| value | 0.015 | 0.1092 | $\frac{1}{14}$ | 0.01063 | 0.98937 | 0.6 | $(1-0.7)$ |

Table 3: Initial Value of variables for scenario 1 (3.1)(see text for further details)

| Initial Value | $S_0$ | $I_0$ | $V_0$ |
|---|---|---|---|
| Value | 80000000 | 25582 | 100000 |

We run simulated epidemics model (3.1) using parameters set to the defaults given in Table 2. The results of infected individuals by model (3.1) are shown in Figure 7.

The reproduction number in the presence of vaccination is obtained, $R_0(\psi) = 0.89375$ and the reproduction number of the disease in the absence of vaccination is obtained by letting $\psi = 0$, i.e. $R_0 = 1.26$ which is greater than 1. So these results showed the efficiency of vaccination.

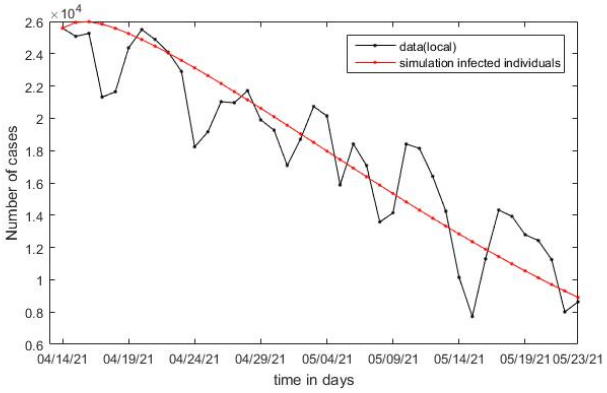


Figure 7: Simulation of the results of infected individuals in first scenario.

As mention in section 3.2, that differential effectiveness of the vaccine leads to strain replacement can be seen from model 3.2. We illustrate this in Figure 8. We note that the overall prevalence before vaccination is greater than the prevalence after vaccination. The parameters are given in Table 4 and we set $I1_0 + I2_0 = 25582$ , $s_0 = 80000000$ and $v_0 = 1000000$. Also, In this case we computed four reproduction numbers, $R1_0(\psi)$, $R1_0(\psi = 0)$, $R2_0(\psi)$ and $R1_0(\psi = 0)$ which is given in Table 5. We have to analyze this table with $R_0$ that will be announced.

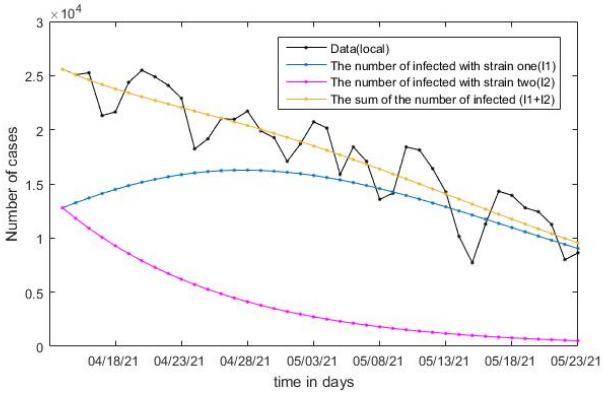


Figure 8: Simulation of the results of infected individuals in second scenario.

Table 4: Value of parameters and variables for scenario 2 section (3.2).(see text for further details)

| parameter | $\alpha$ | $\gamma$ | $\beta_1^{Estimated}$ | $\beta_2^{Estimated}$ | $\mu$ | $\psi^{Estimated}$ | $\chi^{Estimated}$ | $\delta^{Estimated}$ |
|---|---|---|---|---|---|---|---|---|
| value | $\frac{1}{14}$ | $\frac{1}{14}$ | 0.124 | 0.0067 | 0.015 | 0.119 | 1.05 | 0.038 |

Table 5: Reproduction numbers of the model 3.2 with two strain.

| Reproduction number | $R1_0(\psi)$ | $R1_0(\psi = 0)$ | $R2_0(\psi)$ | $R1_0(\psi = 0)$ |
|---|---|---|---|---|
| **value** | 0.8223 | 1.4353 | 0.0431 | 0.0776 |

## 6 Investigate the effect of parameters

We simulated the model 3.1 to, first of all, assess the impact of vaccination rate $\psi$(which, in our study, from 04/14/2021 till 05/23/2021 is about forty days). the results are shown in Figure 9. As shown in this figure by reducing the value of parameter $\psi$, the number of infected people is raised. Also, the reproduction numbers for those $\psi$'s are

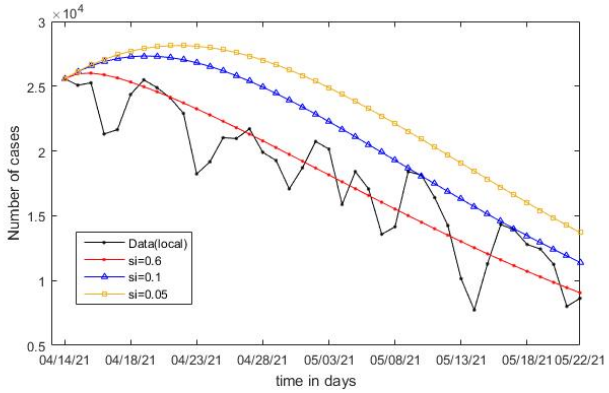


Figure 9: The impacts of vaccination rate $\psi$ on infected individuals. By reducing the value of parameter $\psi = 0.6$ to $\psi = 0.1$ and $\psi = 0.05$, the number of infected people is raised.

presented in Table 6. As expected, by reducing the parameter $\psi = 0.6$ to $\psi = 0.1$ and $\psi = 0.05$, the reproduction number increase.

Table 6: Reproduction numbers of the model 3.1 for different value of $\psi$, By reducing the parameter psi = 0.6 to psi = 0.1 and psi = 0.05, the reproduction number increase.

| $\psi$ | 0.6 | 0.1 | 0.05 |
|---|---|---|---|
| Reproduction number | 0.89 | 0.94 | 0.98 |

Further, in our study, we measured the effect of social-distancing by the overall reduction in the value of the community contact rate parameter $\beta$. As shown in Figure 10 , by reducing the parameter $\beta = 0.11$ to $\beta = 0.05$ and $\beta = 0.01$, the number of infected individuals reduced.

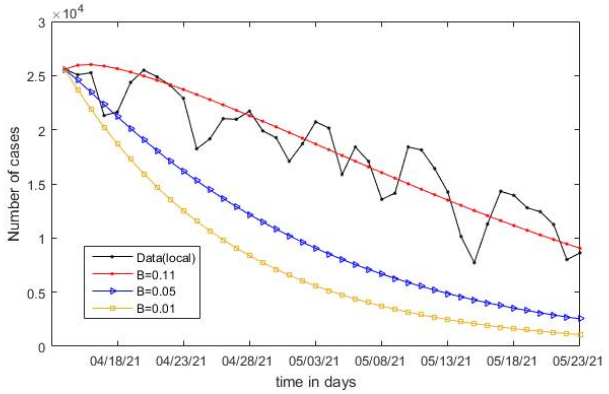


Figure 10: The impacts of the community contact rate parameter $\beta$. By reducing the parameter $\beta = 0.11$ to $\beta = 0.05$ and $\beta = 0.01$, the number of infected individuals reduced.

Also, the variations of reproduction number for different $\beta$'s are listed in Table7.

Table 7: Reproduction numbers of the model 3.1 for different value of $\beta$, By reducing the parameter $\beta = 0.11$ to $\beta = 0.05$ and $\beta = 0.01$, the reproduction number reduced.

| $\beta$ | 0.11 | 0.05 | 0.01 |
|---|---|---|---|
| Reproduction number | 0.89 | 0.4 | 0.081 |

## 7 Conclusion

In this paper, we conducted a study to investigate the impact of vaccination on the number of Covid-19 cases. To model the target population, we utilized the SIS model incorporating vaccination and proposed two scenarios based on the various types of vaccines available in Iran. By employing the proposed model and official data from the Ministry of Health and Medical Education of Iran, we have demonstrated that vaccination and social distancing significantly reduce the number of individuals infected by Covid-19. Additionally, we investigated the vaccination rate per day, $\psi$, revealing that with an increase in this parameter, fewer people became infected, and the transmission rate was correspondingly lower. Furthermore, while maintaining a constant vaccination rate, we investigated the effect of social distancing on decreasing infected cases, showing that a lower parameter $\beta$ leads to a decrease in the reproduction number.

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