Mathematical Modelling of Engineering Problems
Vol. 10, No. 6, December, 2023, pp. 2069-2078
Journal homepage: http://iieta.org/journals/mmep

Simulating the COVID-19 Epidemic: A Numerical Examination of SIR, SIRID, and SIRVI Models

Inasse El Arabi*, Anas Chafi, Salaheddine Kammouri Alami

Industrial Engineering Department, Sidi Mohamed Ben Abdellah University, Fes 30000, Morocco

Corresponding Author Email: Inasse.elarabi@usmba.ac.ma

https://doi.org/10.18280/mmep.100617

Received: 24 April 2023
Revised: 12 July 2023
Accepted: 10 September 2023
Available online: 21 December 2023

Keywords:
numerical simulation, susceptible, infected, recovered, susceptible, infected, recovered, infected, dead, susceptible, infected, recovered, vaccinated, infected, COVID-19

ABSTRACT

A comprehensive understanding of the propagation dynamics of COVID-19 is the paramount goal of this study. Two innovative mathematical models, namely the susceptible, infected, recovered, infected, dead (SIRID) model and the susceptible, infected, recovered, vaccinated, infected (SIRVI) model, are introduced. These models extend the conventional susceptible, infected, recovered (SIR) model by contemplating two pivotal factors: reinfections and the impact of vaccination. The SIRID model encapsulates the potential for a previously infected and recovered population to experience a secondary infection leading to death. The model forecasts crucial phases in this intricate progression: initial infection, recovery, reinfection, and subsequent fatality. Reinfections are underscored as a potentially significant driver of mortality in the SIRID model. The SIRVI model, however, integrates vaccination into the analysis, evaluating how immunization may modulate the virus's spread amid post-vaccination reinfections. In essence, the SIRVI model estimates the key stages: initial infection, recovery, vaccination, and reinfection notwithstanding immunization. This model underscores the potential for vaccination to mitigate the pandemic's severity, while also highlighting the ongoing challenges associated with reinfections. The methodologies employed to construct the SIR, SIRID, and SIRVI models stem from an adaptation of the classic SIR model to incorporate reinfections and vaccination. Each model was built using a comparable approach, albeit with additional compartments to capture the intricate interplay among various pandemic dynamics. The models' compartments (S, I, R, etc.) represent distinct population states based on disease status. The transitions between compartments illustrate the flux of individuals from one state to another. For the SIRID and SIRVI models, an innovative approach was adopted: every compartment accounts for incoming and outgoing fluxes as additions and subtractions, respectively. This allows infections, recoveries, reinfections, and deaths to be represented as dynamic variables, each with specific equations. The interactions between compartments were regulated according to inflows and outflows, capturing the complexity of viral spread, potential reinfections, and vaccination impact. Once the equations were formulated, numerical methods were employed to solve these differential equations. The model parameters were adjusted to align with real-world pandemic data, and iterations were conducted to observe various possible scenarios. This permitted detailed predictions about the pandemic's progression, considering potential reinfections and vaccination, thereby providing valuable insights for public health decision-making.

1. INTRODUCTION

As an interdisciplinary scientific field, epidemiology draws upon mathematical concepts such as statistics to thoroughly study biological phenomena, particularly epidemics [1-5]. Over its evolution, epidemiology has undergone notable advancements, especially in response to major outbreaks like the flu, and the influence of the progression of computer technology, enabling sophisticated numerical simulations [1-5].

Understanding the spread of infectious agents necessitates the application of mathematical models, where ordinary differential equations play a significant role. The SIR model, representing individuals susceptible (S), infected (I), and recovered (R), serves as a fundamental framework to analyze disease transmission dynamics [1-14]. This model considers the distribution of the population across these compartments and introduces parameters such as β, representing infection probability, and γ, the recovery rate or the reciprocal of the average symptom duration [1-14] (Figure 1).

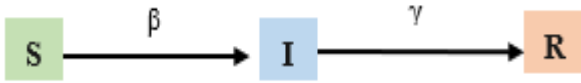

Figure 1. SIR compartment

In the pursuit of monitoring and predicting the behavior of various viruses, numerous studies have been undertaken. These investigations aim to anticipate the disease's trajectory over time, thereby assisting decision-makers in devising public health strategies. Researchers have extended the SIR model to propose novel variations tailored to specific contexts. For instance, Ghostine et al. [15] introduced an enhanced SEIQRDV model comprising susceptible, exposed, infected, quarantined, recovered, deceased, and vaccinated compartments. Poonia et al. [16] presented an improved SEIRV model involving susceptible, infected, recovered, and vaccinated compartments.

Within the scope of this study, we introduced two distinct deterministic nonlinear mathematical models to analyze influenza transmission dynamics, with particular emphasis on the COVID-19 example. These models aim to provide profound insights into scenarios involving reinfection, disease evolution over time, and the impact of vaccinations, which can significantly influence public health decision-making. The significance of this work resides in several key aspects:

Prediction and Epidemic Management: The mathematical models developed in this study enable the prediction of epidemic evolution over time. They provide valuable insights into the potential spread of the disease, infection, recovery, and mortality rates, as well as the effectiveness of intervention measures like vaccination. Such insights are vital for crafting effective epidemic management strategies and guiding decisions of public health officials.

Understanding Re-Infection Phenomena: The models introduce the concept of reinfection, where a population previously infected might face subsequent exposures. This perspective is crucial for evaluating the potential resurgence of epidemics following periods of decline and for anticipating measures necessary to control such resurgences.

Assessment of Vaccination Impact: In an era where vaccines play a significant role in combating infectious diseases, this study proposes specific models to assess the effectiveness of vaccination programs. It helps determine to what extent vaccination can reduce infection, transmission, and mortality rates and anticipates scenarios where infections may occur despite vaccination efforts.

Decision-Making Support: The findings derived from these models provide key insights for decision-makers and public health officials to make informed choices. These insights can guide the implementation of vaccination campaigns, medical resource planning, containment measures, and epidemic management strategies.

Contributions to Research: The SIRID and SIRVI models proposed in this study enrich the body of knowledge in mathematical epidemiology. They provide a robust foundation for future research endeavors aiming to refine models, consider disease-specific variables, and further examine interactions among transmission factors.

In summary, this study addresses critical questions regarding the dynamics of infectious disease transmission and provides analytical tools to anticipate and manage epidemics. The developed models and insights obtained can contribute to understanding and combating diseases affecting global populations.

2. BACKGROUND

As mentioned before, the SIR model describes the evolution of the spread of a disease within a population [1-14]. This spread results from contaminated contact between the infected population and the healthy population, and the number of infected individuals increases as a function of the number of contaminated contacts between infected individuals and healthy individuals. This number is proportional to the size of the infected population and the size of the healthy population, and therefore to the product of these two numbers, *I**S*. Therefore, we can write [1-19]:

$$\frac{dI(t)}{dt} = \beta * I * S \tag{1}$$

The value βSI represents the instantaneous measure of individuals transitioning from the S compartment to the I compartment, and the parameter β is the incidence rate. The proportion of actual contacts between a susceptible individual and an infected individual and the probability of these contacts transmitting the disease from the infected individual to the susceptible individual determine this rate. Symmetrically, the size of the susceptible population decreases. Therefore, it can be written [15-19]:

$$\frac{dS(t)}{dt} = -\beta * I * S \tag{2}$$

If an individual stays on average λ days, I/λ is the instantaneous value of the flow between the "infected" compartment and the "recovered" compartment, i.e., the measure of the flow of individuals who recover, leaving the "infected" compartment, towards the "recovered" compartment. This action governing infected individuals, which we can write as [15-19]:

$$\frac{dI(t)}{dt} = \beta * I * S - \gamma * I \tag{3}$$

The number of recovered individuals I/λ of the healed individuals [15-19], where γ=1/λ.

$$\frac{dR(t)}{dt} = \gamma * I \tag{4}$$

Therefore, we write the SIR model as follows:

$$\frac{dS(t)}{dt} = -\beta * I * S \tag{5}$$

$$\frac{dI(t)}{dt} = \beta * I * S - \gamma * I \tag{6}$$

$$\frac{dR(t)}{dt} = \gamma * I \tag{7}$$

The following improved model is the SIRID model. SIRID is useful for predicting the trends of the re-emergence of a disease during a given period and monitoring the number of deaths during the first and second infection. Thus, it can be important for epidemiologists to model epidemics. Additionally, it helps us visualize the evolution of a disease in a population. Furthermore, it categorizes a population into four categories, namely: susceptible (S), infectious (I), recovered (R), and deceased (D). We call people not yet infected but are at elevated risk of being infected, susceptible, or healthy. We call infected people who are responsible for the spread of the infection infectious (I). We call people who have recovered after being infected recovered (R). We also name people with a second infection infectious (I), and we will add them to the first compartment of infected individuals, and those who will

subsequently die we name them deceased (D).

In this work, we propose a mathematical modeling approach to study the spread of a disease, based on the novel SIRID and SIRVI models. These models are common for the analysis of the spread of infectious diseases within a population. In these models, we divide the population into compartments based on their health status. The typical compartments are as follows:

Susceptible (S): Infected individuals.

Infectious (I): Infected individuals who can spread the disease.

Recovered (R): Individuals who have recovered from the disease and are immune or not likely to catch it again.

Deaths (D): Individuals who have died due to the disease.

Vaccinated (V): Vaccinated individuals against the disease.

In these models, we manage interactions between these compartments based on incoming and outgoing flows, allowing for the consideration of various scenarios, including new infections, recoveries, reinfections, and deaths. We can achieve this by using specific mathematical equations for each compartment that account for transition rates between different states based on model parameters and real pandemic data. We conducted numerical simulations by adjusting the model parameters according to real pandemic data and then running iterations to observe how the disease spreads and evolves in different scenarios. These simulations can help understand the impact of various interventions, such as vaccination, on the disease spread and evaluate strategies to contain it.

The SIRID model uses the coefficients β to represent the term of disease transmission. γ represents the recovery rate, α designates the term of disease transmission for the second time, and μ designates the death rate. The mathematical representation of the SIRCD model is in Figure 2, Eqs. (8)-(11):

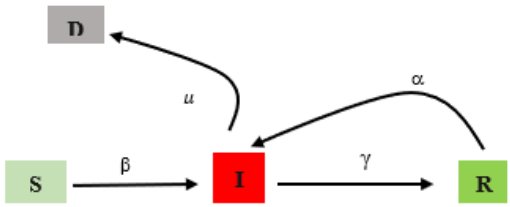

Figure 2. SIRID model

$$\frac{dS(t)}{dt} = -\beta * I * S \tag{8}$$

$$\frac{dI(t)}{dt} = \beta * I * S - \gamma * I + \alpha * R - \mu D \tag{9}$$

$$\frac{dR(t)}{dt} = \gamma * I - \alpha R \tag{10}$$

$$\frac{dD(t)}{dt} = \mu * I \tag{11}$$

The second improved model is the SIRVI model. SIRVI is useful for predicting the trends of disease occurrence for the second time during a given period despite population vaccination. Thus, it can be essential for epidemiologists to model epidemics. Additionally, it helps us visualize disease progression in a vaccinated population. Furthermore, it categorizes a population into four categories, namely: susceptible (S), infectious (I), recovered (R), and vaccinated (V). We call Individuals who are not yet infected but are at elevated risk of infection susceptible or healthy. We call those infected individuals who are responsible for spreading the infection infectious (I). We call those who have recovered after being infected recovered (R). we call those who have received a vaccine vaccinated (V), and those who infected for the second time despite their vaccination infectious (I), and we will add them to the first compartment of the infected.

Table 1. Review of different versions of the SIR model

Acronym	Name of Model	Parameter Added	Definition
SIR	Susceptible-Infectious-Susceptible	Simplest form	Immunity does not build.
SIRD	Susceptible-Infectious-Recovered-Deceased	Deceased	D is the mortality rate.
MSIR	Maternal-Susceptible-Infectious Recovered	Carrier	It applies to those. where infection resides in the body forever, such as TB.
SICR	Susceptible-Infectious-Carrier-Recovered	Carrier	It applies to those. where infection resides in the body forever, such as TB.
SUQC	Susceptible-Unquarantined Quarantine-Confirmed	Unquarantined, quarantine	Number of people who are quarantined and unquarantined.
GSIR	Generalized-Susceptible-Infectious Recovered	Generalized	Assumed that throughout time, many waves of varied peak amplitude and form arise and fade away.
SEIHR	Generalized-Susceptible-Infectious-Hospitalized-Recovered	Hospitalized	Number of persons Hospitalized.
SCEIR	Susceptible-Exposed-Infectious-Recovered-Removed	Confined	When an individual is experiencing lockdown.
ISSEIR	Interacting Subpopulation - Susceptible-Exposed-Infectious Recovered	Interacting subpopulation	Separate SEIR model between each subgroup of the population.
SIRV	Susceptible-Infectious-Recovered-Vaccination	Vaccination	When the population is vaccinated.
SIRVC	Susceptible-Infectious-Recovered-Vaccination-contaminated	Contamination and vaccination	When the population is vaccinated and after that, it has become infected.
SIRCD	Susceptible-Infectious-Recovered-contaminated-Deceased	Contamination and deceased	The population dies, once infected for the second time.

The SIRVI model uses coefficients β to represent the disease transmission term, γ for the recovery rate, ψ to designate the rate of vaccination among individuals, and α to designate the term for disease transmission for the second time despite vaccination. The mathematical representation of the SIRVC model is in Figure 3, Eqs. (12)-(15):

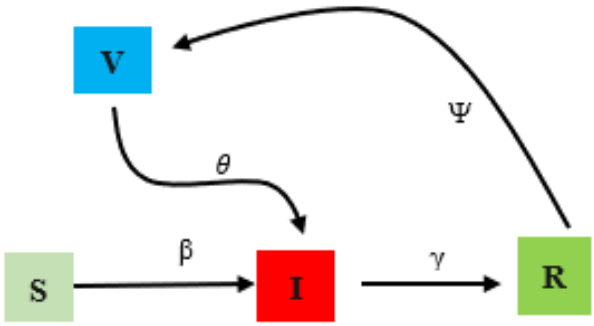

Figure 3. SIRVC model

$$\frac{dS(t)}{dt} = -\beta * I * S \quad (12)$$

$$\frac{dI(t)}{dt} = \beta * I * S - \gamma * I + \alpha V \quad (13)$$

$$\frac{dR(t)}{dt} = \gamma * I - \Psi * R \quad (14)$$

$$\frac{dV(t)}{dt} = \Psi * R - \theta * V \quad (15)$$

We reviewed the different versions of the SIR model. One of the simplest compartmental models is the SIS model, in which individuals cannot develop lasting immunity and can be infected multiple times. The common flu is the best example of the SIS model. Another important model is the maternal sensitive infectious recovered (MSIR) model [15, 16, 20-30]. We present other improved models in Table 1 above, including the addition of two new models proposed in our article.

3. PROPOSED METHOD

3.1 The SIRID model

In this work, we describe an extension of the classic epidemiological SIR (susceptible-infected-reestablished) model. This extended model, called the "SIRID model", incorporates additional compartments to provide a more detailed representation of disease progression as follows:

- Susceptible (S): This compartment represents individuals who are vulnerable to disease and infection once exposed to an infectious person. As the disease spreads, the number of susceptible individuals decreases.
- Mildly infected (I1): These are individuals infected with the disease but who have mild symptoms that do not require hospitalization. This compartment represents the less severe cases of the disease.
- Severely infected (I2): Individuals in this compartment have a more severe form of the disease that requires hospitalization. This could include cases where they require medical intervention and care to manage the disease.
- Critically infected (I3): This compartment includes individuals with critical cases of the disease, requiring admission to intensive care units (ICUs) for specialist medical treatment and monitoring.
- Recovered (R): Individuals who have recovered from the disease and developed immunity are in this compartment. They are no longer susceptible to re-infection. Recovery may be from mild, severe, or critical cases.
- Deceased: Unfortunately, this compartment represents individuals who have succumbed to the disease.

A set of differential equations that governs the flow of individuals between these compartments describes how the disease spreads through the population over time. These equations consider factors such as infection, recovery, and mortality rates, which are influenced by a variety of factors, including disease characteristics, health system capacity and public health interventions.

This extended model provides a more nuanced understanding of the dynamics of the disease, allowing researchers and policymakers to consider different scenarios and interventions to better manage and control the epidemic.

The "SIRID" model appears to be an advanced variation of the classic SIR model, incorporating additional parameters to capture a wider range of disease outcomes.

We illustrate the proposed model design in Figure 4. The proposed model consists of four main compartments, namely Susceptible, Infected, Recovered, and Dead.

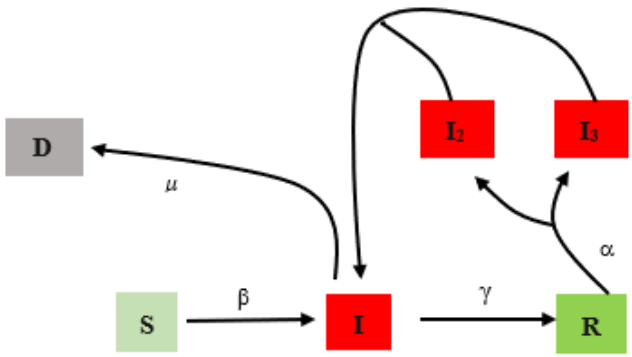

Figure 4. Proposed model SIRID

The mathematical representation of the infection compartment (in Figure 4) is as follows:

$$\frac{dI(t)}{dt} = \beta * I * S - \gamma * (I - I_2 - I_3) + \alpha * R - \mu * D \quad (16)$$

We will add the two secondary compartments (I2) and (I3) to the main compartment (I). This compartment includes people infected for the first time, and people infected for the second time after recovery (I2) and (I3). Hence, the proposed model is in Figure 4.

Then, we defined different coefficients for simulating the SIRID model. We describe these coefficients in Table 2. And we present the proposed model in Eqs. (17)-(20):

$$\frac{dS(t)}{dt} = -\beta * I * S \quad (17)$$

$$\frac{dI(t)}{dt} = \beta * I * S - \gamma * I_t + \alpha * R - \mu * D \quad (18)$$

$$\frac{dR(t)}{dt} = \gamma * I - \alpha * R \quad (19)$$

$$\frac{dD(t)}{dt} = \mu * D \quad (20)$$

3.2 The SIRVI model

In epidemiology, modelling plays a crucial role in understanding and anticipating the spread of infectious diseases within a population. The classic SIR (Susceptible-Infected-Recovered) model has been widely used to describe these dynamics but faced with increasingly complex situations and with the introduction of vaccination, we need an innovative approach. This is where the proposed new SIRVI model comes in.

This model is an extension of the SIR model, designed to capture the finer details of modern epidemiology. It considers eight distinct compartments, each reflecting a particular facet of the dynamics of an infectious disease in each population.

- S (Susceptible): The compartment of individuals who are vulnerable to the disease and not yet exposed to infection nor vaccinated. These individuals are at risk of contracting the disease if exposed.
- I (Slightly infected): This compartment groups together unvaccinated individuals who have contracted the infection but have mild symptoms that do not require hospitalization. This may include symptoms such as mild fever, headache, and fatigue.
- I1 (Vaccinated and infected): A key aspect of the SIRVI model is the consideration of vaccinated individuals who still contract the disease despite their vaccination. This may be due to partial immunity conferred by the vaccine or to a variant of the disease for which the vaccine offers less protection.
- I2 (Severely infected): Here we have unvaccinated individuals who are severely infected and require hospitalization. Symptoms in this category may be more intense, requiring close medical supervision.
- I3 (Critically infected): Unvaccinated individuals with a critical infection requiring admission to an intensive care unit reside in this compartment. These cases are the most serious and require specialized intensive care.
- R (Recovered/immunized): Individuals who have recovered from infection enter this compartment. They have developed immunity to the disease and cannot be reinfected in the short term.
- V (Vaccinated): We place vaccinated Individuals against the disease in this compartment. However, the level and durability of their immunity may vary depending on the vaccine used.

This extension of the SIR model, with its eight distinct compartments, offers a more complete view of the spread of an infectious disease in a mixed population of unvaccinated and vaccinated people. It allows more complex scenarios to explore, such as the impact of different vaccination strategies on reducing infections, and the capacity of the healthcare system to manage serious cases.

We illustrate the proposed model in Figure 5. It comprises four main compartments: susceptible, infected, recovered and vaccinated.

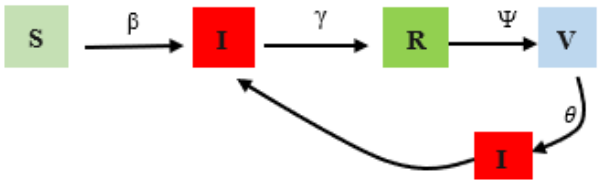

Figure 5. The proposed SIRVI model

The mathematical representation of the infection compartment (Figure 5) is as follows:

$$\frac{dI(t)}{dt} = \beta * I * S - \gamma * (I - I_4) + \theta * V \quad (21)$$

We will add the secondary compartment (I4) to the main compartment (I). This compartment includes individuals infected for the first time, and individuals infected for the second time despite vaccination (I4). Hence, the proposed model is in Figure 5.

Table 2. Coefficient of the proposed methods

Name of Coefficient	Definition
N	Total population (comprising 100 000 individuals in this research)
S	Susceptible individuals
β	The term of transmission of the disease
I	Infected people + people in critical care + people in hospital
I_1	People infected and they are in critical care
I_2	People are infected and they are in hospital
γ	The term of transmission of the disease
R	Set of individuals who have recovered from the disease and are now immune
α	The term of transmission of the disease for the second period
D	Set of removed populations
μ	The death rate of individuals in the most severe stage of the disease
I_4	Infected people despite vaccination
Ψ	the rate of individuals' vaccination
θ	The term of transmission of the disease for the second period despite the vaccine

Next, we defined different coefficients for simulating the SIRVI model. We describe these coefficients in Table 2. And we present the proposed model in Eqs. (22)-(25):

$$\frac{dS(t)}{dt} = -\beta * I * S \quad (22)$$

$$\frac{dI(t)}{dt} = \beta * I * S - \gamma * I_t + \theta * V \quad (23)$$

$$\frac{dR(t)}{dt} = \gamma * I - \psi * \mathrm{R} \quad (24)$$

$$\frac{dV(t)}{dt} = \psi * \mathrm{R} - \theta * \mathrm{V} \quad (25)$$

3.3 The reproductive rate R0

The basic reproductive number, often denoted as R_0 (pronounced "R naught"), is a fundamental concept in epidemiology that measures the potential for a disease to spread within a population. In the context of the SIR model, which is a simplified mathematical framework used to describe the spread of infectious diseases, R_0 we define it as the average number of secondary infections generated by a single infected individual in a completely susceptible population. In the expression $R_0=\beta/\gamma$:

β (beta) represents the transmission rate or the rate at which an infected individual meets susceptible individuals and successfully transmits the disease. It encompasses factors such as the frequency of contact between infected and susceptible individuals, the probability of transmission per contact, and

other relevant parameters. γ (gamma) represents the recovery or removal rate, which is the inverse of the average duration an individual remains infectious. In other words, 1/γ gives you the average time an individual spends in the infectious state before recovering or dying. When R_0 is greater than one, it indicates that each infected individual, on average, infects more than one other individual, leading to the potential for an epidemic outbreak. Conversely, when R_0 is less than 1, the disease will eventually die out because infected individuals are not able to infect enough new individuals to sustain the outbreak. The SIR model assumes a few simplifications, such as constant population size, homogeneous mixing, and lack of birth and death rates. More complex models like SEIR (which includes an exposed compartment) or spatial models consider these factors for a more realistic representation of disease spread. Nonetheless, the basic reproductive number remains a key concept in understanding the initial dynamics of disease outbreaks [31-35].

In this study, the reproductive rates of the two proposed models, SIRID and SIRVI, are as follows:

a) R0 for the SIRID model

The only infected compartment in this model is (I), where, $\frac{dI(t)}{dt} = \beta * I * S - \gamma * I_t + \alpha * R - \mu * D$ -struck can be calculated as $\mathcal{F} = \beta * I * S$, $\mathcal{V} = -\gamma * I + \alpha * R - \mu * D\mathbb{F} = \beta$, $\mathbb{V} = -\gamma + \alpha - \mu$, $\mathbb{V}^{-1} = \frac{1}{-\gamma+\alpha-\mu} R_0 = -\mathbb{F}.\mathbb{V}^{-1} = \frac{\beta}{\gamma+\mu-\alpha}$

b) R0 for the SIRVI model

The only infected compartment in this model is (I), where, $\frac{dI(t)}{dt} = \beta * I * S - \gamma * I_t + \theta * V$, R0 can be calculated as $\mathcal{F} = \beta * I * S$, $\mathcal{V} = -\gamma * I_t + \theta * V\mathbb{F} = \beta$, $\mathbb{V} = -\gamma + \theta$, $\mathbb{V}^{-1} = \frac{1}{-\gamma+\theta} R_0 = -\mathbb{F}.\mathbb{V}^{-1} = \frac{\beta}{\gamma-\theta}$

4. RESULT AND DISCUSSION

The main objective of this article was to develop a mathematical model that could predict cases of COVID-19. We added a new compartment to the SIR base to achieve this goal. And we implemented these COVID-19 epidemic process models using the MATLAB programming language. We conducted an experimental study of the two proposed models using data related to COVID-19 cases in France, presented in the "COVID-19 government information" database. We made the forecasts for 7 days.

The calculated values of the β and γ coefficients were determined using the R0 (reproduction rate) value of 0.74 provided by the "COVID-19 government information" database.

We conducted the validation of our two proposed models on 100,000 inhabitants of France over a period of 7 days. The following figures present the results obtained, with S_{SIR} (0)=92590, I_{SIR} (0)=7410, R_{SIR} (0)=0. S_{SIRID}(0)=92250, I_{SIRID}(0)= 7704, which includes ISIRID (0)=7410 as the initial number of people infected for the first time, and $I2_{SIRID}$(0) + $I3_{SIRID}$(0)=294 as the initial number of people infected for the second time, R_{SIRID}(0)= 0, D_{SIRID}(0)=46. S_{SIRVI} (0)=171724.03, I_{SIRVI} (0)=7434.45, which includes I_{SIRID} (0) =7410 as the initial number of people infected for the first time, and $I4_{SIRVI}$ (0)=24.45 as the initial number of people infected for the second time despite vaccination. V_{SIRVI} (0)=79581.25 is the initial number of vaccinated people.

In this study, we collected samples starting from November 1, 2021, we simulated three models numerically, namely the SIR model, as well as two proposed models, the SIRID and SIRVI models. The three figures presented in the study show the results of these simulations.

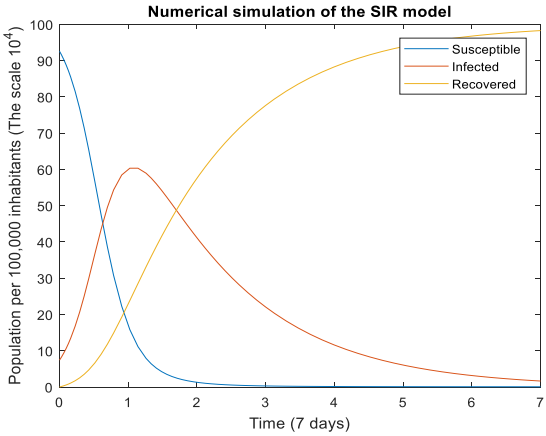

Figure 6. Numerical simulation of SIR of 100 000 inhabitants from France for 7 days

In Figure 6, we meticulously executed a simulation of the SIR model, utilizing data specific to the chosen timeframe. The outcomes derived from this simulation provide a nuanced perspective on the epidemic's progression and furnish a means to quantify the disease propagation rate. The graphical representation in the figure vividly illustrates the dynamic changes over time in three key components: the susceptible population (S), infected individuals (I), and those who have either recovered or succumbed to the disease (R).

It's crucial to emphasize the SIR model's inherent simplicity, as it doesn't encompass the entirety of factors that influence epidemic evolution. Notable exclusions include the effectiveness of preventive and control measures, the potential impact of virus mutations, and considerations related to the geographic and demographic distribution of the population. Despite these omissions, the SIR model retains its utility as a valuable analytical tool. While it may not capture the full complexity of real-world scenarios, its ability to reveal general trends in epidemic dynamics makes it an indispensable resource for informing public health decisions. By acknowledging its limitations, the insights gleaned from the SIR model can be appropriately contextualized within the broader landscape of epidemiological considerations, contributing to more informed and nuanced public health policy decisions.

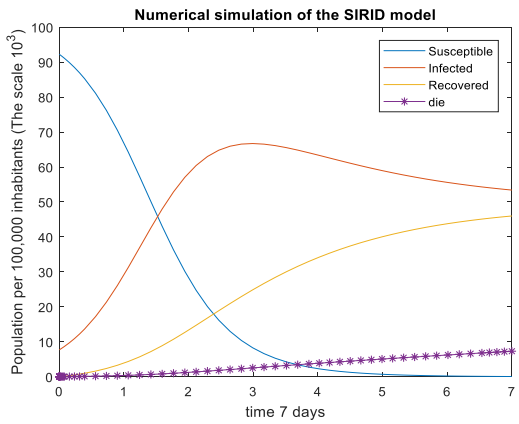

Figure 7. Simulation of SIRID of 100 000 inhabitants from France for 7 days

Figure 7 presents the SIRID model, in which we placed second -time-infected individuals in the I compartment. The curve of infected individuals shows a clear progression compared to Figure 6, while the death curve does not seem to have experienced significant progression. We may explain that by the fact that the number of deaths recorded during the considered period is exceptionally low compared to the number of healthy people, sick people, and recovered people.

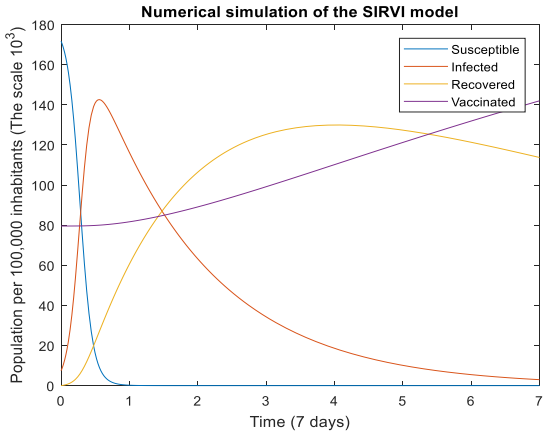

Figure 8. Simulation of SIRVI Of 100 000 inhabitants from France for 7 days

Figure 8 presents the SIRVI model. In this model, we placed the infected individuals for a second time despite vaccination in the I compartment. Therefore, the curve of infected individuals shows a clear progression compared to Figure 6. This emphasizes the importance of continuing to monitor the disease's propagation and developing effective vaccines against emerging disease variants. In addition, the vaccination curve also shows a strong progression. We can attribute this increase to the importance of vaccination in the fight against the spread of the disease. Massive vaccination campaigns conducted in many countries have enabled a large part of the population to be vaccinated, thereby reducing the spread of the disease and the severity of cases. However, it is important to emphasize that the efficacy of vaccines can vary depending on disease variants, underscoring the need to closely monitor disease propagation and develop effective vaccines against emerging variants.

Using the parameters indicated in Table 3, we found that the proposed models reported an R0 value of 0.74 to 1.3 for the SIRID model and 1.07 for the SIRVI model. The R0 (basic reproduction rate) is a measure of the spread of a disease in each population. It represents the average number of people that an infected person can infect in turn. Thus, an R0 value greater than one indicates active disease propagation, while a value less than 1 indicates a decrease in disease propagation.

Table 3. Obtained values of coefficients

Coefficient	**Values** «SIRID»	**Values** «SIRVI»
β	0.01924	0.01924
γ	0.026	0.026
θ	_	0
ψ	_	0.08571429
μ	0.2	_
α	0.057	_

Our results show that, according to the proposed models, a person infected with the coronavirus can infect an average of 1.3 additional people in France using the SIRID model, and 1.07 additional people using the SIRVI model, during the study period. These R0 values indicate that disease propagation is low in France but remains a significant source of concern.

These results are important for understanding disease propagation and can help plan the response and prevention to the COVID-19 pandemic. Using these models, it is possible to predict disease propagation in different situations and implement effective preventive measures to limit disease propagation. These measures can include confinement measures, vaccination campaigns, screening tests, hygiene, and social distancing measures, as well as contact tracing measures.

Several observations and trends emerge from an analysis of the results presented in this study. Firstly, a comparison between the SIR, SIRID, and SIRVI models reveals distinct dynamics in the spread of the disease. Figure 5 highlights the progression of the epidemic according to the SIR model, showing the evolution of the susceptible, infected, and recovered populations. However, it is important to bear in mind that the SIR model does not consider various real factors, such as the effectiveness of prevention and control measures, mutations in the virus, and the geographical and demographic diversity of the population. Despite these limitations, this model provides a general view of epidemic trends, which can help to guide public health policies.

Nevertheless, it is crucial to note the inherent limitations of these models. The SIRID and SIRVI versions take reinfection and vaccination into account, respectively, making them more realistic. However, even these improved models have certain limitations. They do not consider variations in vaccine efficacy as a function of virus variants. In addition, they do not fully consider other complex elements such as behavioral changes in the population, government interventions, and interactions between different regions. Consequently, although these models are powerful tools for predicting epidemics, we must interpret them with caution and with due regard for their simplifications.

The proposed models provide valuable information for public health decision-making. For example, they enable decision-makers to predict the possible evolution of the disease according to different vaccination, containment, or screening strategies. However, it is important to recognize that the results are only estimates based on simplifying assumptions. Variations may be considerable. Consequently, we should consider the implications derived from these models as guides rather than precise predictions. These models are valuable tools for guiding public health policy, but other real data and a thorough understanding of the specific epidemiological context must complement them.

In summary, analysis of the results of this study provides an interesting insight into the spread of COVID-19 using different epidemiological models. The observations, trends, limitations, and implications of these models highlight the importance of considering both their advantages and limitations when formulating public health policies and prevention strategies.

5. DISCUSSION AND CONCLUSION

Many people are now affected by COVID-19, as it is a

global pandemic. Contemporary models are reliable for predicting the spread of a pandemic disease. The classic SIR (Susceptible-Infected-Recovered) model laid the foundations of epidemiological modeling by dividing the population into compartments to predict disease trends. However, this initial model did not consider the effects of vaccination and did not consider cases of reinfection.

To address cases of reinfection, we developed the SIRID model, incorporating new compartments to represent re-infected individuals and associated deaths. This model brought a more realistic perspective to the prediction of the pandemic, although it remains limited by simplifying assumptions about the complex nature of immunity and reinfection.

The SIRVI model also looked at the impact of vaccination on the spread of the virus. By considering both vaccination rates and new infections despite vaccination, this model provides crucial information for assessing the effectiveness of vaccination campaigns. However, it is important to note that vaccination rates and variant effects can significantly influence the model's predictions.

Following the calculations conducted on the basic reproduction rate (R0), based on the system of equations that we have developed, the proposed models demonstrated significant values in terms of predictability of the spread of the virus. For the SIRVI model, we evaluated the basic reproduction rate at 1.07, reflecting the virus's capacity to infect new individuals despite the vaccination efforts in place. On the other hand, the SIRID model showed a base reproduction rate of 1.3, indicating a more pronounced tendency towards reinfection and case severity. These R0 values highlight the crucial importance of factors such as vaccination, reinfection, and control measures in influencing the dynamics of virus spread within the population.

We subjected the proposed models to a rigorous series of mathematical simulations and tests to better understand their behavior under various conditions. We conducted these simulations to assess the relevance and effectiveness of the SIRVI and SIRID models in the actual context of the COVID-19 pandemic.

As part of these simulations, we considered several scenarios to reflect different epidemiological and public health parameters. We evaluated the model in situations such as without vaccination (SIRID) and with vaccination (SIRVI), using a population of 100,000 individuals in France as the basis for the calculations. These contrasting scenarios highlighted how the two models react to different conditions and how they can help inform decision-making in a variety of contexts.

The scenario without vaccination (SIRID) highlighted the effects of the natural spread of the virus without vaccine intervention. This made it possible to determine the extent of reinfection and the associated consequences, as well as the impact on mortality and disease dynamics in an unvaccinated context.

In contrast, the scenario with vaccination (SIRVI) showed how the introduction of vaccination campaigns can influence the spread of the virus. This includes not only the positive effect of reducing new infections among those vaccinated but also considering cases of infection despite vaccination. This situation made it possible to assess how the models manage the nuances of the interactions between vaccination and viral transmission.

By using a real population as the basis for simulation, these tests have provided concrete insights into the performance of the models under realistic conditions. This provides essential information for public health decision-makers, enabling them to anticipate challenges and take informed action to mitigate the spread of the disease.

However, it is important to note that these simulations are based on assumptions and data available at a given time. The results may therefore evolve with the emergence of new data or changing circumstances. Despite this, these tests remain a valuable tool for exploring the implications of the SIRVI and SIRID models for managing the COVID-19 pandemic.

Despite their usefulness, these models have intrinsic limitations. They simplify the complexity of epidemiological reality by assuming constant transmission rates and homogeneous interactions between individuals. In addition, the rapid evolution of science and the variability of data can call into question the accuracy of their predictions.

Although the SIR, SIRID, and SIRVI models have shed valuable light on the prediction of COVID-19, they are fallible oracles. Their value lies in their ability to guide public health decision-makers, providing them with essential information for taking informed action. However, to further refine these models in the future, it is crucial to consider scientific advances and adapt to the constantly changing realities of the pandemic.

Looking to the future, we do not limit the model we have proposed to its current state. We aim to refine and extend this approach so that it is even more representative of the complexity of the propagation of COVID-19 and its interactions within the population. To this end, we plan to incorporate new compartments into the model, which could provide a more complete and nuanced perspective.

One of the avenues we plan to explore is the vaccination of infants and children. These demographic groups play a crucial role in the dynamics of disease spread, and by incorporating this dimension, our model could better reflect epidemiological reality. Understanding how vaccination spreads within these groups and how it impacts overall transmission would be a major step toward more informed decision-making.

In addition, asymptomatic carriers of the virus, although healthy, may play a key role in the silent spread of the disease. Incorporating their influence into our model would enable us to consider more accurately community transmission. This could have significant implications for prevention and control strategies, by identifying at-risk groups even among asymptomatic individuals.

In short, our model is only an initial step in understanding the spread of COVID-19. We are determined to continually improve it in line with new data and scientific discoveries. This evolutionary approach will ensure that our model remains relevant and useful for guiding public health decision-makers while adapting to the changing challenges presented by this global pandemic.

REFERENCES

[1] Allen, L.J.S. (2008). An introduction to stochastic epidemic models. In: Brauer, F., van den Driessche, P., Wu, J. (eds) Mathematical Epidemiology. Lecture Notes in Mathematics, vol. 1945. Springer, Berlin, Heidelberg. https://doi.org/10.1007/978-3-540-78911-6_3

[2] Hethcote, H.W. (2008). The basic epidemiology models: models, expressions for R0, parameter estimation, and applications. In Mathematical Understanding of

Infectious Disease Dynamics, pp. 1-61. https://doi.org/10.1142/9789812834836_0001
[3] Jhung, M.A., Swerdlow, D., Olsen, S.J., Jernigan, D., Biggerstaff, M., Kamimoto, L., Kniss, K., Reed, C., Fry, A., Brammer, L., Gindler, J., Gregg, W.J., Bresee, J., Finelli, L. (2011). Epidemiology of 2009 pandemic influenza A (H1N1) in the United States. Clinical Infectious Diseases, 52(suppl_1): S13-S26. https://doi.org/10.1093/cid/ciq008
[4] Mummert, A., Weiss, H., Long, L.P., Amigó, J.M., Wan, X.F. (2013). A perspective on multiple waves of influenza pandemics. PloS One, 8(4): e60343. https://doi.org/10.1371/journal.pone.0060343
[5] Weiss, H.H. (2013). The SIR model and the foundations of public health. Materials Matematics, pp. 1-17.
[6] Kissler, S.M., Tedijanto, C., Goldstein, E., Grad, Y.H., Lipsitch, M. (2020). Projecting the transmission dynamics of SARS-CoV-2 through the postpandemic period. Science, 368(6493): 860-868. https://doi.org/10.1126/science.abb5793
[7] Kermack, W.O., McKendrick, A.G. (1927). A contribution to the mathematical theory of epidemics. Proceedings of the royal society of London. Series A, Containing Papers of a Mathematical and Physical character, 115(772): 700-721. https://doi.org/10.1098/rspa.1927.0118
[8] Li, R., Rivers, C., Tan, Q., Murray, M.B., Toner, E., Lipsitch, M. (2020). The demand for inpatient and ICU beds for COVID-19 in the US: Lessons from Chinese cities. MedRxiv. https://doi.org/10.1101/2020.03.09.20033241
[9] Pellis, L., Ferguson, N.M., Fraser, C. (2009). Threshold parameters for a model of epidemic spread among households and workplaces. Journal of the Royal Society Interface, 6(40): 979-987. https://doi.org/10.1098/rsif.2008.0493
[10] Allen, L.J., Brauer, F., Van den Driessche, P., Wu, J. (2008). Mathematical Epidemiology. Berlin: Springer. https://doi.org/10.1007/978-3-540-78911-6
[11] Korobeinikov, A., Wake, G.C. (2002). Lyapunov functions and global stability for SIR, SIRS, and SIS epidemiological models. Applied Mathematics Letters, 15(8): 955-960. https://doi.org/10.1016/S0893-9659(02)00069-1
[12] Pellis, L., Ball, F., Trapman, P. (2012). Reproduction numbers for epidemic models with households and other social structures. I. Definition and calculation of R0. Mathematical Biosciences, 235(1): 85-97. https://doi.org/10.1016/j.mbs.2011.10.009
[13] Pellis, L., Ferguson, N.M., Fraser, C. (2011). Epidemic growth rate and household reproduction number in communities of households, schools and workplaces. Journal of Mathematical Biology, 63: 691-734. https://doi.org/10.1007/s00285-010-0386-0
[14] Kendall, W.S., Saunders, I.W. (1983). Epidemics in competition Ii: The general epidemic. Journal of the Royal Statistical Society: Series B (Methodological), 45(2): 238-244. https://doi.org/10.1111/j.2517-6161.1983.tb01246.x
[15] Ghostine, R., Gharamti, M., Hassrouny, S., Hoteit, I. (2021). An extended SEIR model with vaccination for forecasting the COVID-19 pandemic in Saudi Arabia using an ensemble Kalman filter. Mathematics, 9(6): 636. https://doi.org/10.3390/math9060636
[16] Poonia, R.C., Saudagar, A.K.J., Altameem, A., Alkhathami, M., Khan, M.B., Hasanat, M.H.A. (2022). An enhanced SEIR model for prediction of COVID-19 with vaccination effect. Life, 12(5): 647. https://doi.org/10.3390/life12050647
[17] El Arabi, I., Chafi, A., Alami, S.K. (2022). Numerical simulation of the advection-diffusion-reaction equation using finite difference and operator splitting methods: Application on the 1D transport problem of contaminant in saturated porous media. E3S Web of Conferences, 351: 01003. https://doi.org/10.1109/ISACS48493.2019.9068876
[18] Hossain, M.T., Miah, M.M., Hossain, M.B. (2017). Numerical study of kermack-mckendrik SIR model to predict the outbreak of ebola virus diseases using euler and fourth order runge-kutta methods. American Scientific Research Journal for Engineering, Technology, and Sciences (ASRJETS), 37(1): 1-21.
[19] Pirdawood, M.A., Rasool, H.M., Sabawi, Y.A., Azeez, B.F. (2022). Mathematical modeling and analysis for COVID-19 model by using implicit-explicit Rung-Kutta methods. Academic Journal of Nawroz University, 11(3): 65-73. https://doi.org/10.25007/ajnu.v11n3a1244
[20] Gray, A., Greenhalgh, D., Mao, X., Pan, J. (2012). The SIS epidemic model with Markovian switching. Journal of Mathematical Analysis and Applications, 394(2): 496-516. https://doi.org/10.1016/j.jmaa.2012.05.029
[21] Luo, W., Tay, W.P. (2013). Finding an infection source under the SIS model. In 2013 IEEE International Conference on Acoustics, Speech and Signal Processing, Vancouver, BC, Canada, pp. 2930-2934. https://doi.org/10.1109/ICASSP.2013.6638194
[22] Fernández-Villaverde, J., Jones, C.I. (2022). Estimating and simulating a SIRD model of COVID-19 for many countries, states, and cities. Journal of Economic Dynamics and Control, 140: 104318. https://doi.org/10.1016/j.jedc.2022.104318
[23] Bichara, D., Iggidr, A., Sallet, G. (2014). Global analysis of multi-strains SIS, SIR and MSIR epidemic models. Journal of Applied Mathematics and Computing, 44: 273-292. https://doi.org/10.1007/s12190-013-0693-x
[24] Qiao, M., Liu, A., Foryś, U. (2013). Qualitative analysis of the SICR epidemic model with impulsive vaccinations. Mathematical Methods in the Applied Sciences, 36(6): 695-706. https://doi.org/10.1002/mma.2620
[25] Zhao, S., Chen, H. (2020). Modeling the epidemic dynamics and control of COVID-19 outbreak in China. Quantitative Biology, 8: 11-19. https://doi.org/10.1007/s40484-020-0199-0
[26] Singh, P., Gupta, A. (2022). Generalized SIR (GSIR) epidemic model: An improved framework for the predictive monitoring of COVID-19 pandemic. ISA Transactions, 124: 31-40. https://doi.org/10.1016/j.isatra.2021.02.016
[27] Niu, R., Wong, E.W., Chan, Y.C., Van Wyk, M.A., Chen, G. (2020). Modeling the COVID-19 pandemic using an SEIHR model with human migration. IEEE Access, 8: 195503-195514. https://doi.org/10.1109/ACCESS.2020.3032584
[28] Li, B., Saad, D. (2021). Impact of presymptomatic transmission on epidemic spreading in contact networks: A dynamic message-passing analysis. Physical Review E, 103(5): 052303. https://doi.org/10.1103/PhysRevE.103.052303

[29] Marpaung, F., Rangkuti, Y.M., Sinaga, M.S. (2014). The analysis of optimal singular controls for SEIR model of tuberculosis. AIP Conference Proceedings, 1635(1): 153-159. https://doi.org/10.1063/1.4903577
[30] Safarishahrbijari, A., Lawrence, T., Lomotey, R., Liu, J., Waldner, C., Osgood, N. (2015). Particle filtering in a SEIRV simulation model of H1N1 influenza. In 2015 Winter Simulation Conference (WSC), Huntington Beach, CA, USA, pp. 1240-1251. https://doi.org/10.1109/WSC.2015.7408249
[31] Viceconte, G., Petrosillo, N. (2020). COVID-19 R0: Magic number or conundrum? Infectious Disease Reports, 12(1): 8516. https://doi.org/10.4081/idr.2020.8516
[32] Adam, D. (2020). Special report: The simulations driving the world's response to COVID-19. Nature, 580(7802): 316-319. https://doi.org/10.1038/d41586-020-01003-6
[33] Neal, P. (2006). Stochastic and deterministic analysis of SIS household epidemics. Advances in Applied Probability, 38(4): 943-968. https://doi.org/10.1017/S0001867800001403
[34] Flaxman, S., Mishra, S., Gandy, A., Unwin, H.J., Coupland, H., Mellan, T.A., Bhatt, S. (2004). Estimating the number of infections and the impact of non-pharmaceutical interventions on COVID-19 in European countries: Technical description update. arXiv preprint arXiv:2004.11342.
[35] Jacquez, J.A., O'Neill, P. (1991). Reproduction numbers and thresholds in stochastic epidemic models I. Homogeneous populations. Mathematical Biosciences, 107(2): 161-186. https://doi.org/10.1016/0025-5564(91)90003-2