Towards a Stochastic SEIR Model for the COVID-19 Post-Pandemic Scenario

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Abstract — **With the current recession of the global COVID-19 pandemic, the corresponding epidemic models need to be adapted to reflect this new reality and continue assisting public health authorities in the definition of policies and decision making. With that aim, this paper presents a SEIR epidemic model for the representation of the COVID-19 pos-pandemic scenario. The model considers the effect of countermeasures such as vaccination and quarantine, and the consequences of the progressive loss of immunity. A deterministic formulation and a first stochastic version of the model are presented, and their implementation in MATLAB is evaluated and compared. To cope with the computational demands of the application of the Monte Carlo method, the implementation of the stochastic version follows a parallel approach that proved to be highly scalable and efficient in a multi-core computational system. The preliminary evaluation results, with fixed parameters, point to a cyclic evolution of the pandemic and a tendency for stabilization in the future.**

Keywords - COVID-19; post-pandemic scenario; stochastic SEIR model; MATLAB; parallel simulations.

I. INTRODUCTION

The human population has been faced with a significant challenge during the years 2021 and 2022 in the form of the COVID-19 pandemic. And, while the pandemic has largely been brought under control in many countries, sporadic outbreaks continue to be reported, underscoring the ongoing need for vigilance and caution. In such demanding context, it is widely recognized that mathematical modeling and computational tools have proven to be essential in helping public health authorities to define appropriate policies and take impactful decisions aimed at controlling the spread of the coronavirus SARS-CoV-2 [1]. In this regard, numerous academic and scientific studies have been conducted and published over the course of the past two years, with a special focus on the Susceptible-Exposed-Infectious-Recovered (SEIR) mathematical epidemic model [1,2,4,5].

The SEIR model is a widely accepted framework for describing the spread of an infectious disease with a latency period, such as COVID-19 [2]. This model is based on the concept of *compartmentalization*, which separates a population into four distinct compartments: Susceptible (S), Exposed (E), Infectious (I), and Recovered (R). Each compartment corresponds to a state in relation to the disease: the Susceptible individuals are those who have not yet been infected with the disease and thus are at risk of contracting it; the Exposed have been infected but are not yet infectious: the Infectious have developed symptoms and are capable of transmitting the disease to others; finally. the Removed individuals are those who have recovered from the disease.

The SEIR model incorporates into its framework the concept of *latency period*, which is the time elapsed between infection and the onset of symptoms. This characteristic is particularly relevant for COVID-19, which has a latency period of several days. Furthermore, the model takes into consideration the dynamics of disease transmission, including the rate of infection and recovery. The same model can also be used to predict the number of cases, the peak of the epidemic, and the proportion of the population that will be affected.

In addition, the SEIR model can be easily adapted to include other compartments, such as Vaccinated (V) and Quarantined (Q) individuals, corresponding to public health measures which have a significant impact on controlling the spread of the disease. Such flexibility is one of the main reasons why this model has been widely used to simulate the spread of COVID-19, and to analyze and predict the dynamics of the pandemic in different countries and regions.

In previous studies [4][5], the COVID-19 pandemic scenario was modeled, coinciding with the availability of the first vaccines in small quantities. In particular, it was shown that an epidemiological outbreak could be prevented by combining vaccination with the isolation of the infected individuals. The present work focuses on the dynamics of COVID-19 spreading in a post-pandemic scenario, in which a large part of the population is regularly vaccinated. Thus, a new epidemic mathematical model is proposed, adapted to a post-pandemic situation, considering not only the control measures represented

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by vaccination and isolation, but also the effects of the loss of immunity of infected and vaccinated individuals.

The new model, denoted as SE2IQRVD (for Susceptible, Exposed, asymptomatic Infected, symptomatic Infected, Quarantined, Recovered, Vaccinated, and Deceased), was developed, by extending two previous models, namely the SE2IRV [3] and SEIRQD models [4][5]. A deterministic formulation of the SE2IQRVD model is first introduced, followed by a purely stochastic version that incorporates the element of randomness into the spreading of COVID-19.

Simulating the propagation of a disease using stochastic methods is computationally intensive and may be very time-consuming. To overcome this challenge, this paper also focuses on a computationally efficient implementation of the algorithms corresponding to the new SE2IQRVD model. To that end, the parallel computing capabilities of the MATLAB platform are exploited, leading to a highly scalable and efficient implementation of the stochastic variant of that model.

The remaining of the paper is organizes as follows: first, the proposed mathematical model is introduced in section II, in its deterministic (section II.A) and stochastic (section II.B) versions; then, in section III, the parallelization strategy of the stochastic method is presented, along with some parallel execution metrics measured in the testbed system; section IV is devoted to the presentation and discussion of the numerical results of the simulations conducted; finally, section V concludes the paper and lays out directions for future work.

II. Mathematical Models

A. Deterministic Model

The model developed includes eight distinct compartments. Each of them describes a state of a fraction of a population, with N individuals, in the context of the spread of COVID-19. The interactions between the model compartments, along with the corresponding rates of transition, are represented in Fig. 1.

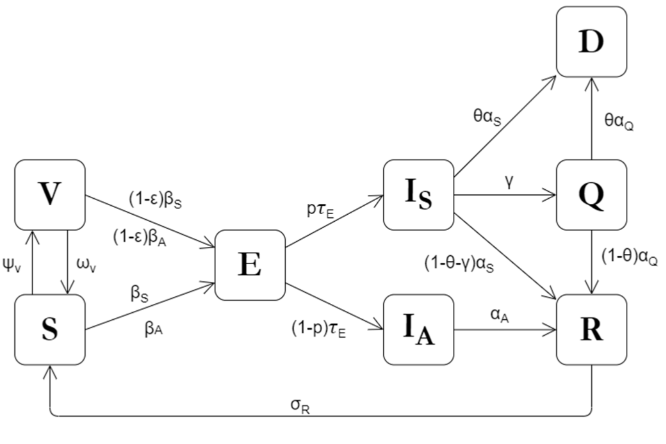

Figure 1. Compartmental Diagram of the SE2IRVQD model.

The variables corresponding to each compartment are:

- **S:** number of individuals susceptible to contracting the disease.
- **E:** number of individuals who have been exposed to the disease but are not yet infectious.
- **IA:** number of individuals who are infectious but are asymptomatic.
- **IS:** number of individuals who are infectious and have symptoms.
- **R:** number of individuals who have recovered from the disease and are now immune.
- **D:** number of individuals who have died from the disease.
- **V:** number of individuals who have received a vaccine.
- **Q:** number of individuals who are in quarantine.

From a deterministic perspective, the dynamics of the model represented in Fig. 1 are represented by the System of (differential) Equations (1):

$$\begin{cases} \frac{\partial S}{\partial t} = \omega_V V + \sigma_R R - \psi_V S - \frac{\beta_S I_S + \beta_A I_A}{N} S \\ \frac{\partial E}{\partial t} = \frac{(\beta_S I_S + \beta_A I_A)}{N}(S + (1-\varepsilon)V) - \tau_E E \\ \frac{\partial I_A}{\partial t} = (1-\rho)\tau_E E - \alpha_A I_A \\ \frac{\partial I_S}{\partial t} = \rho\tau_E E - \alpha_S(1-\gamma)I_S - \gamma I_S \\ \frac{\partial R}{\partial t} = (1-\theta-\gamma)\alpha_S I_S + (1-\theta)\alpha_Q Q + \alpha_A I_A - \sigma_R R \\ \frac{\partial D}{\partial t} = \theta\alpha_S I_S + \theta\alpha_Q Q \\ \frac{\partial V}{\partial t} = \psi_V S - \frac{(\beta_S I_S + \beta_A I_A)}{N}(1-\varepsilon)V - \omega_V V \\ \frac{\partial Q}{\partial t} = \gamma I_S - \alpha_Q Q \end{cases} \quad (1)$$

with initial conditions $S(0) = S_0$, $E(0) = E_0$, $I_A(0) = I_{A_0}$, $I_S(0) = I_{S_0}$, $R(0) = R_0$, $D(0) = D_0$, $V(0) = V_0$, $Q(0) = Q_0$. The system models the dynamic of a population with N individuals, in function of the time t (in days). Each equation describes the evolution of the quantity of individuals that are in each state (compartment) of the infectious disease.

The constants $\beta_A, \beta_S, \alpha_A, \alpha_S, \gamma, \theta, \rho, \varepsilon, \psi_V, \omega_V, \tau_E, \sigma_R$ are the parameters of the model, and have the following meaning:

- ψ_V: vaccination rate, represented as the fraction of the population that receives the vaccine daily.
- ω_V: rate at which the protection given by the vaccine decreases over time. It is expressed as the inverse of the number of days the vaccine remains effective.
- β_A : rate of transmission of the disease from an asymptomatic individual to a susceptible individual.

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- β_S : rate of transmission of the disease from a symptomatic individual to a susceptible individual.
- ε: efficacy of the vaccine, representing the fraction of vaccinated individuals protected from the disease.
- ρ: fraction of exposed individuals who become symptomatic.
- τ_E: average latency period, representing the time between exposure to the disease and the onset of symptoms.
- α_A: rate of recovery for asymptomatic individuals.
- α_S: rate of transition from symptomatic to recovered or deceased.
- α_Q: rate of transition from quarantined to recovered or deceased.
- γ: fraction of individuals placed in quarantine.
- θ: fraction of symptomatic or quarantined individuals who die due to the disease.
- σ_R: rate of loss of natural immunity, representing the fraction of recovered individuals who lose immunity over time.

The values used in this work for these constants were collected from the literature [3][4][7] and are shown in Table 1. These values are crucial in determining the outcome of the simulations, as they define the way in which the events occur [6]. The same values were also used in the stochastic model.

TABLE I. VALUES OF THE SE2IRVQD MODEL PARAMETERS

Symbol	Value	Reference
ψ_V	0.00057	Vaccination rate.
ω_V	1/180	Vaccine decline rate.
β_A	0.251521	Asymptomatic transmission contact rate.
β_S	0.36382	Symptomatic transmission contact rate.
ε	0.95	Vaccine efficiency.
ρ	0.1913	Exposed individuals who become symptomatic.
τ_E	0.20408	Average latency period.
α_A	0.167504	Recovery rate of asymptomatic individuals.
α_S	0.0925069	Rate of transition from symptomatic to recovery or death.
α_Q	1/14	Rate of quarantined who recover or die.
γ	0.025	Quarantine rate.
θ	0.037	Symptomatic individuals who die from the disease.
σ_R	1/240	Natural immunity loss rate.

B. Stochastic Model

A stochastic version of the deterministic SE2IRVQD model, previously introduced, was developed in order to incorporate the randomness inherent to the spread of the COVID-19 disease. The stochastic model is described by the Algorithm 1 pseudo-code that outline the steps involved in simulating the dissemination of the disease and the various factors that influence the transmission dynamics.

These factors can include the rate of contact between individuals, the rate of recovery, and the effectiveness of vaccines and other interventions. By incorporating these factors into the model, it is possible to generate simulations that capture the complex and dynamic nature of infectious disease outbreaks.

Algorithm 1: Stochastic SE2IRDVQ model

Inputs: N, i_0, v_0, max_{days}, ω_V , ψ_V , $\mathcal{E}$, β_S , ρ, τ_E , α_A, α_S , α_Q, θ, γ, σR
Output: res matrix, containing the number of individuals in a state by time in days

for j ← 1 ... N_{sim} **do**
  choose v_0 random individuals and the relative vaccinated period
  choose i_0 random individuals and the corresponding infectious period
  for t ← 1...max_{days} **do**
    for all N **do**
      $latency_N \leftarrow latency_N - 1$
      if $state_N$ = susceptible or vaccinated **then**
        randomly choose 1/β_S , in N, individuals to contact ▷ excluding quarantined and dead
          if any contacted people = symptomatic or asymptomatic **then**
            if $state_N$ = susceptible or randval > ε **then**
              $state_N$ ← exposed ▷ with Poisson random 1/τ_E days
            end if
          else
            if $state_N$ = susceptible and randval < ω_V **then**
              $state_N$ ← vaccinated
            else if $latency_N$ = 0 **then** $state_N$ ← susceptible
            end if
          end if
      else if $state_N$ = exposed **then**
        if $latency_N$ = 0 **then**
          if random value < ρ **then**
            $state_N$ ← asymptomatic ▷ with Exp. random 1/α_A days
          else $state_N$ ← symptomatic ▷ with Exp. random 1/α_S days
          end if
        end if
      else if $state_N$ = symptomatic **then**
        if $latency_N$ = 0 **then**
          $state_N$ ← recovered ▷ with Exp. random 1/σ_R days
        end if
        if random value < γ **then**
          $state_N$ ← quarantine ▷ with Exp. random 1/α_Q days
        end if
        if random value < θ **then** $state_N$ ← died
        end if
        else if $state_N$ = asymptomatic **then**
        if $latency_N$ = 0 **then**
          $state_N$ ← recovered ▷ with Exp. random 1/σ_R days
        end if
        else if $state_N$ = recovered **then**
        if rand < σ_R **then** $state_N$ ← susceptible
        end if
        else $state_N$ = quarantine **then**
          if $latency_N$ = 0 **then**
            $state_N$ ← recovered ▷ with Exp. random 1/σ_R days
          end if
        if random number < θ then $state_N$ ← died
      end if
    end if
    end for
  end for
end for

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In the algorithm, the individuals are represented by a 2D array with two rows and N columns (one per individual). One of the rows represents the individual state (denoted in the algorithm by $state_N$). The other row represents the latency of that state (denoted by $latency_N$).

Noteworthy, the model represents a pos-pandemic context in which almost all the target population is vaccinated. However, even in a pos-pandemic context there are infected individuals in the population. In the algorithm, those two states are initially randomly distributed inside the array (see steps 2 and 3).

Overall, by the application of the algorithm, any individual can assume any of the eight model states during a run, though not all, due to the way in which the transitions between compartments are defined. Also, the model dynamics restricts interactions only to individuals in certain states: susceptible, vaccinated, exposed and susceptible. The number of the interactions between the states are determined by a Poisson distribution with a parameter β_S. When an infection occurs between an infected and a susceptible, the later becomes exposed. In the case of an interaction between the infected and the vaccinated, the later has a small probability (ε) of becoming exposed, due to the expected immunization effect of the vaccine.

The model has two methods to change states: it can be as a result of the interaction that is determined by the Poisson distribution, and by the end of the latency of a state. The latency is determined by the Exponential distribution. The Poisson distribution is a discrete distribution used to model the number of close contacts between susceptible and other individuals that occur in a fixed period. In the stochastic model it determines the number of new infectious cases in the population. In turn, the Exponential distribution is a continuous probability used to model the gap between the events (here, infection and latency periods) [5].

III. Stochastic Model Parallel Implementation

Parallelization is the process of breaking down a computational task into smaller independent tasks, that can be run simultaneously on multiple processors. This is done with the goal of reducing the execution time of a compute-bound application, splitting datasets too big to be stored and processed by a single node, or a combination of both [8].

As it happens, the algorithm of the stochastic SE2IRDVQ model (Algorithm 1) is naturally parallelizable. This algorithm repeats (line 1) a large number of times (N_{sim}) the stochastic simulation of the spread of COVID-19. As all simulations are independent of each other, many of them can be performed simultaneously (the precise amount depends on the effective number of processors of the computational system used).

In this work, Algorithm 1 was implemented in MATLAB, and the Parallel Computing Toolbox [9] was taken advantage of in order to easily achieve the parallel execution of the algorithm. This tool enables the distribution of computations across multiple MATLAB workers, with each worker attached to one CPU-core of a multicore system, therefore offering parallel computing on multiple processors or cores. This tool was thus used in this work to run several simulations simultaneously.

To evaluate the quality of the parallel implementation of the algorithm, a set of N_{sim}=1000 simulations was performed, with a population of N=20000 individuals, along max_{days} = 1500 days. The computational system used was a Linux virtual machine (Ubuntu 20.04 64bits) in the CeDRI cluster, with 32 CPU-cores of an Intel(R) Xeon(R) W-3365 CPU @ 2.70GHz. This allowed to perform the evaluation with a varying number of MATLAB workers (1, 8, 16, 24, 32), using as much CPU-cores.

The parallel execution times (in hours), parallel speedups and parallel efficiencies measured are shown in Table II. Figure 2 offers a graphical representation of the parallel speedups and efficiencies. The speedup with p CPU-cores (S_p) used is given by T_1/T_p, where T_1 is the execution time with 1CPU-core and T_p is the execution time with p CPU-cores. In turn, the parallel efficiency with p CPU-cores (E_p) used is given by S_p/p, measuring how effectively are the p CPU-cores being used.

TABLE II. Stochastic Model Parallel Execution Metrics

Cores (p)	**Execution Time (T_p) (hours)**	**Speedup (S_p)**	**Parallel Efficiency (E_p) (%)**
1	45,84	1,00	100,00
8	5,78	7,94	99,18
16	2,98	15,40	96,27
24	2,09	21,91	91,29
32	1,76	26,02	81,33

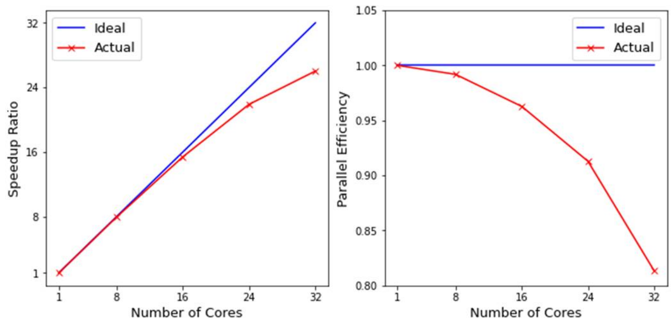

Figure 2. a) Parallel Speedup; b) Parallel Efficiency

From the results, it is possible to conclude that the current parallel implementation of the stochastic SE2IRDVQ model is highly scalable and efficient, which is an incentive to run the simulations in more dense multicore systems. That incentive is also reinforced by the execution times observed with a small number of workers, dictating that performing a higher number of simulations (for more accurate stochastic distributions), for larger periods (more days), and bigger populations, is only feasible by incrementing the scale of the parallel system used.

IV. Numerical Results

Having evaluated the stochastic model implementation from the computational performance standpoint, this section is devoted to the analysis and discussion of the numerical results of both the deterministic and stochastic model variants.

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Starting with the deterministic model, the dimension of the population (considered constant along the time) is given by

$$N = S(t) + E(t) + I_S(t) + I_A(t) + R(t) + V(t) + Q(t) + D(t)$$

with $N = 20000$. Also, the initial conditions were defined as $S(0) = N - V(0) - I_S(0)$, $E(0) = 0$, $I_S(0) = 1$, $I_A(0) = 0$, $R(0) = 0$, $V(0) = 19600$, $Q(0) = 0$ and $D(0) = 0$.

The evolution of the number of individuals in each compartment of the population, generated by the deterministic model of the System of Equations (1), along 1500 days, is shown in Fig. 3. The results presented in the figure were obtained through the numerical resolution of the initial value problem with the system of equations (1) through the built-in MATLAB function ode45, which combines the 4th and 5th-order Runge-Kutta methods.

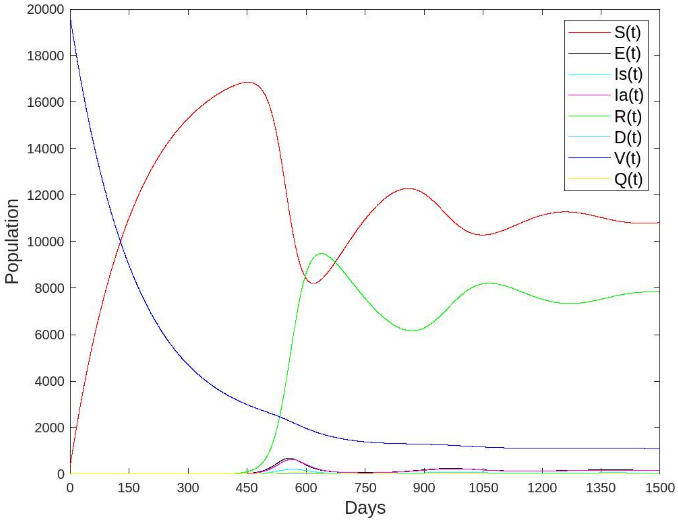

Figure 3. Simulation Results of the SE2IQRVD Deterministic Model.

In Fig. 3, it is possible to observe waves in the evolution of the number of susceptible and recovered individuals, as well as a decrease of the vaccinated population. This is due to the particular values of the parameters of the model (as defined in Table 1), such as the rate of transmission of the infection, the efficacy of the vaccination, the rate of recovery from the disease and the rate of loss of immunity.

Moving on to the stochastic model, Fig. 4 shows the results of the evolution of the number of susceptible individuals along $N_{sim} = 1000$ simulations, when considering $I_{S_0} = 200, V_0 = 19600$, and $S_0 = 200$.

In Fig. 4, the general trend, given by the averaged variation (in dark red), with successive fluctuations, agrees with the results obtained with the deterministic model. The curves produced by each of the individual 1000 simulations (in light red) exhibit variably pronounced fluctuations but, in general, they all maintain the same evolutionary trend. Also, it seems that the evolutions of the number of susceptible individuals tends to stabilize around a value near 5000.

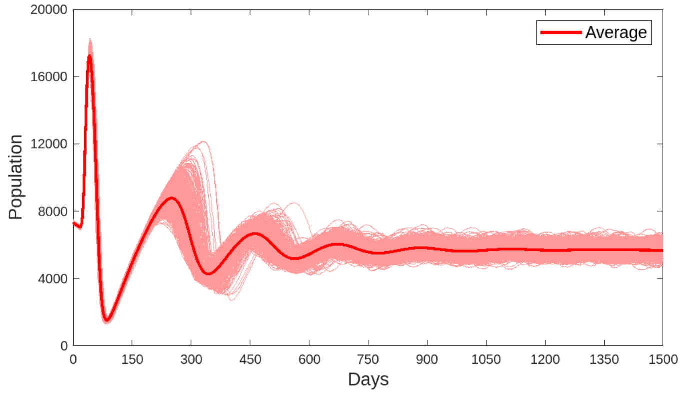

Figure 4. Evolution of Susceptible under the SE2IQRVD Stochastic Model.

The trend of evolution towards a stationary state is reinforced by observing Fig. 5, where the possible evolutions of the total number of infected people (symptomatic and asymptomatic) are represented. The average (in dark blue) of the various simulations (in light blue) points to a stabilization of the number of susceptible in a value close to 200 individuals.

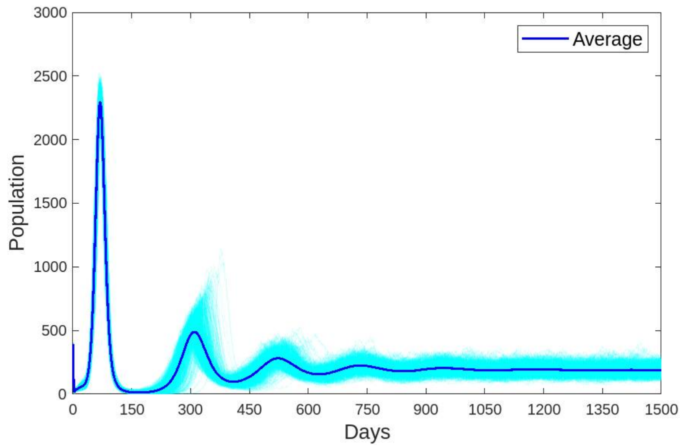

Figure 5. Evolution of Infected under the SE2IQRVD Stochastic Model.

From the point of view of the evolution of the epidemic, the previous observations may indicate that, under these conditions, there is convergence towards an endemic equilibrium. However, further numerical tests, with other parameters, are needed, to confirm this apparent trend.

Fig. 6 shows the results of a single stochastic simulation. It stands out that the wave-form fluctuations are present in most compartments, though with different amplitudes and stability trends. By analyzing the waves, it can be determined that the average number of days between the two first outbreaks is almost 200 days, which represents a growth infection by almost seven months, depending on the simulation. Afterward, the temporal distances between peaks becomes smaller and smaller. There was also a decrease in the amplitude of the outbreaks.

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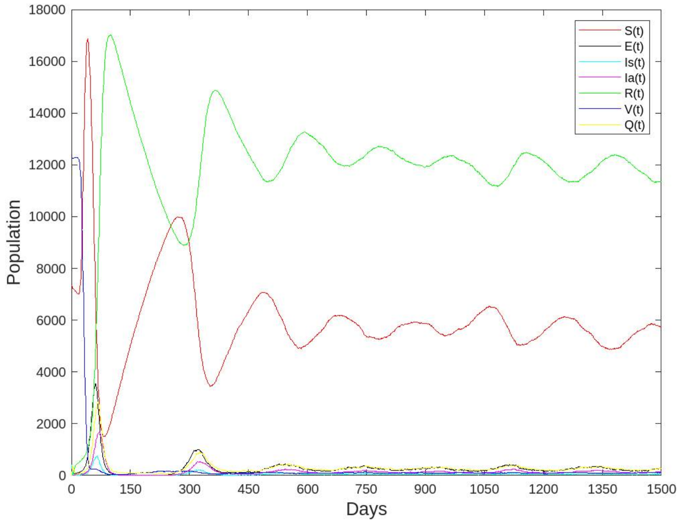

Figure 6. A simulation of the SE2IQRVD Schocastic Model.

V. Discussion and Conclusion

This work presents epidemiological models for the spread of COVID-19 in a given population. Starting from a deterministic formulation, a stochastic equivalent method was also developed.

The models are adapted to the specificities of a pos-pandemic scenario, by accounting for the effect of vaccination and loss of immunity. Furthermore, even though the models were created having in mind the COVID-19 pandemic, they can be easily adapted to the spread of other infectious disease.

In the deterministic version, the epidemic process is described by a system of differential equations that, together with the initial conditions, determines the evolution of the dissemination of the disease. The community is considered homogeneous and it is assumed that individuals mix uniformly with each other. Thus, this version does not incorporate any arbitrariness.

In the stochastic version, the spread of an infectious disease is considered a random process that takes place locally, in the community, through close contact with infectious individuals. For this reason, the stochastic model is considered more realistic than the deterministic model. However, this realism is far from reproducing the complexity of human-to-human contact patterns. Despite its limitations, this model can provide very useful insights into the evolution of the COVID-19 epidemic.

The realism of the stochastic model originates from the application of the Monte Carlo method, whereby multiple simulations are performed, in which random contacts between individuals are considered, each with a certain probability of transmitting the disease. The higher the number of simulations, the more representative of the reality will be the final epidemical distributions.

Because such procedure, if performed by a classical sequential computing approach, may require a considerable amount of time, a parallel implementation of the stochastic method was developed. This allowed for significant performance gains in the computational system used for the simulations. Moreover, it opens the possibility of performing simulations with much more demanding parameters, and it is also a motivation to exploit denser parallel computing systems.

So far, only simulations with fixed parameters and values available in the literature, have been carried out. The results show a cyclic evolution and a tendency towards the stabilization of the epidemic metrics. However, these observations cannot be generalized, due to the specifics of the evaluation conducted.

Thus, it is necessary to carry out a parametric study, in order to analyze the epidemic evolution of the population in function of the effect of prevention and combat measures (such as vaccination and quarantine), as well as the virulence and, transmissibility of the infection, and the loss of immunity of infected and vaccinated individuals. The adequacy of these parameters to the reality of the target population will allow the execution of realistic simulations that may be useful, in the future, to prevent COVID-19 and adjust public health policies.

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