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# Modeling the COVID-19 post-pandemic spread

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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 deterministic SEIR epidemic model for the representation of the COVID-19 post-pandemic scenario. The model considers the effect of countermeasures such as vaccination and quarantine, and the consequences of the progressive loss of immunity. 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 · SEIR model.

## 1 Introduction

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 by vaccination and isolation but also the effects of the loss of immunity of infected and vaccinated individuals. A new compartmental model, SEIRVQD (for Susceptible, Exposed, Infected, Recovered, Vaccinated, Quarantined, and Deceased), was developed. Based on that, a deterministic formulation was created, these dynamics are represented by the System of (differential) Equations (1):

$$\begin{cases} \frac{\partial S}{\partial t} = \omega_V V + \sigma_R R - \psi_V S - \frac{\beta I}{N} S \\ \frac{\partial E}{\partial t} = \frac{\beta I}{N}(S + (1-\varepsilon) V) - \tau_E E \\ \frac{\partial I}{\partial t} = \tau_E E - \alpha_S (1-\gamma) I - \gamma I \\ \frac{\partial R}{\partial t} = \alpha_S (1-\theta-\gamma) I + \alpha_Q (1-\theta) Q - \sigma_R R \\ \frac{\partial D}{\partial t} = \theta \alpha_S I + \theta \alpha_Q Q \\ \frac{\partial V}{\partial t} = \psi_V S - \frac{\beta I}{N} (1-\varepsilon) V - \omega_V V \\ \frac{\partial Q}{\partial t} = \gamma I \alpha_Q Q \end{cases} \tag{1}$$

Each equation describes the evolution of the number of individuals in each state (compartment) on day $t$, with $S(t)$=susceptibles, $E(t)$= exposed to the disease but not infectious, $I(t)$=infected, $R(t)$=recovered from the disease and now immune, $D(t)$=died from the disease, $V(t)$=vaccinated and $Q(t)$=quarantined.

The constants $\psi_V$, $\omega_V$, $\beta$, $\epsilon$, $\tau_E$, $\alpha_S$, $\gamma$, $\theta$, $\alpha_Q$ and $\sigma_R$ are the parameters of the model. Its values are crucial in determining the outcome of the simulations, as they define how the pandemic events occur [1].

The method used to define the vaccination rate ($\psi_V$) and the mortality rate ($\theta$), was a simple linear regression, from the cumulative values available in the dataset [2]. The analysis interval is from January 1 to March 24, 2023. The data refer to Portugal and are the most up-to-date at the time of this study.

The quarantine rates, $\gamma$ and $\alpha_Q$, were arbitrarily defined, once they have currently no meaningful impact due to the low number of infected people.For the transmission rate ($\beta$), a reliable value was calculated based on the reproduction number R(t) reports [3]. The vaccine protection rate ($\omega_V$), the efficacy of the vaccine ($\epsilon$), the average latency period ($\tau_E$), the recovered or deceased rate ($\alpha_S$) and the rate of loss of natural immunity ($\sigma_R$) were collected by a literature research. All constants and corresponding references can be found in Table 1.

Table 1: Values of the SEIRVQD Model Parameters.

| **Symbol** | **Value** | **Description** | **Reference** |
|---|---|---|---|
| $\psi_V$ | 0.00018559 | Vaccination rate | [2] |
| $\omega_V$ | 1/180 | Vaccine decline rate | [4] |
| $\beta$ | [0.1854-0.1945] | Transmission contact rate | [3] |
| $\varepsilon$ | [0.903-0.976] | Vaccine efficiency | [4] |
| $\tau_E$ | [0.1695-0.1961] | Average latency period | [5] |
| $\alpha_S$ | 0.0925069 | Transition rate for recovered or deceased | [4] |
| $\gamma$ | 0.025 | Quarantine rate | Arbitrary |
| $\theta$ | 0.0000006555 | Fraction of individuals who die from the disease | [2] |
| $\alpha_Q$ | [0 - 1/5] | Rate of quarantined who recovered or died | Arbitrary |
| $\sigma_R$ | 1/240 | Natural immunity loss rate | [6] |

## 2 Results

The evolution of the number of individuals in each compartment of a population with $N$=100000 individuals, generated by the deterministic System of Equations (1), over 1500 days, is shown in Fig. 1. The results were obtained through the numerical resolution of the initial value problem given by that system of equations with initial conditions $S(0)$=1999, $E(0)$=0, $I(0)$=1, $V(0)$=98000, $Q(0)$=0, $D(0)$=0 and $R(0)$=0. The system was solved using the built-in MATLAB function `ode45`, which combines the 4th and 5th-order Runge-Kutta methods.

It is possible to observe waves in the evolution of the number of susceptible individuals and recovered ones, as well as a decrease in the vaccinated population. The model also describes the possibility of small infectious outbreaks with decreasing magnitude. This provides motivation to pursue the study of the evolution of the spread of the COVID-19 disease in a post-pandemic scenario.

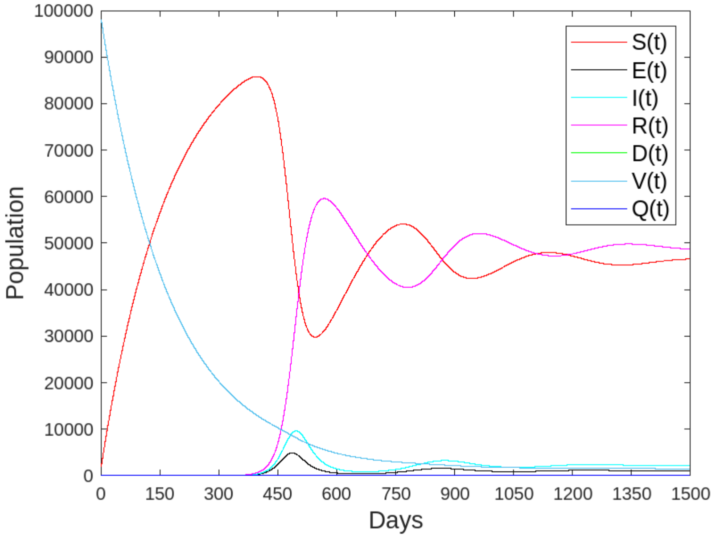

Fig. 1: Simulation Results of the SEIRVQD Deterministic Model.

To conclude, the model proposed is adapted to the specifics of a post-pandemic regime, by accounting for the effect of vaccination and loss of immunity. Furthermore, even though the model was created keeping in mind the COVID-19 pandemic, it can be easily adapted to the spread of other infectious diseases.

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