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MODELING THE COVID-19 POST-PANDEMIC SPREAD

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BACKGROUND

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.

OBJECTIVES

The objectives of this article are:

- **Develop a new epidemic mathematical model**: Create a mathematical model based on previous compartmental models proposed in [1–3] that were adapted to describe the COVID-19 dynamics in a post-pandemic scenario, considering vaccination, isolation, and the effects of immunity loss.
- **Incorporate vaccination and isolation as control measures**: Integrate the impact of vaccination and isolation into the mathematical model to understand how these measures affect virus transmission in a population with a large portion of vaccinated individuals.
- **Consider the loss of immunity in recovered and vaccinated individuals**: Study the duration and effectiveness of immunity acquired through infection or vaccination and how it influences the transmission dynamics of COVID-19 in the post-pandemic scenario.
- **Provide insights for public health interventions**: Utilize the model's findings to inform public health strategies, such as vaccination campaigns and isolation measures, aiming to mitigate virus spread and minimize the risk of future outbreaks.

METHODOLOGY

A new compartmental model, SEIRVQD (for Susceptible, Exposed, Infected, Recovered, Vaccinated, Quarantined, and Deceased), was developed. It's described by the diagram in Fig. 1 and its dynamics are represented by the System of differential Equations (1):

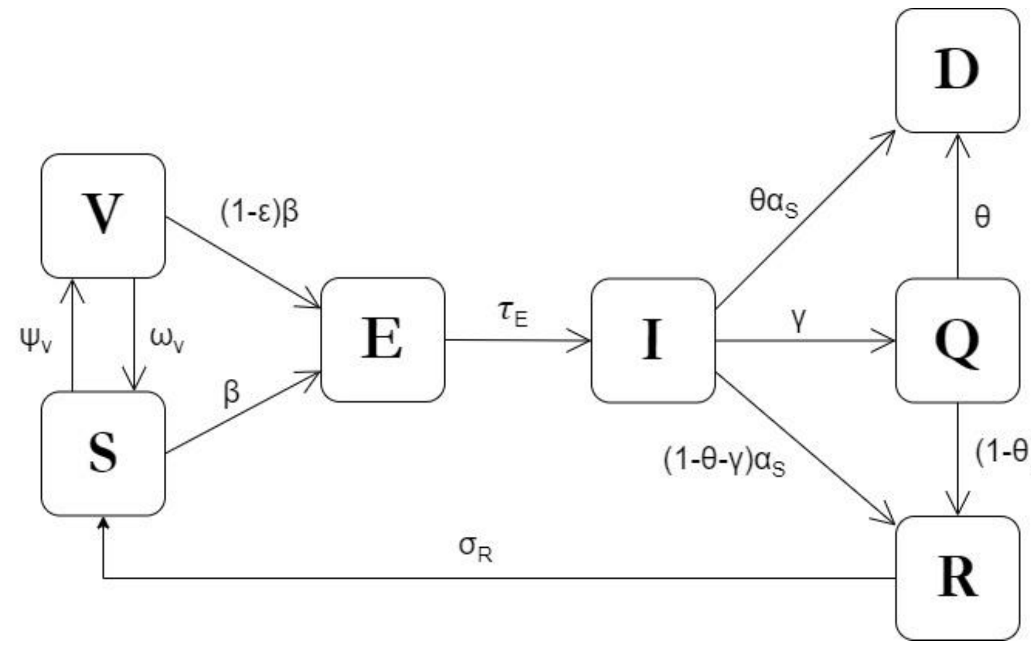

Fig. 1. SEIRDQV Diagram Model.

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

Each equation describes the evolution of the number of individuals that are in each state (compartment). Its values are crucial in determining the outcome of the simulations, as they define how the pandemic events occur [2].

The method used to define the vaccination rate (ψ_V) and the mortality rate (θ), was a simple linear regression, from the cumulative values available in the dataset[4]. The analysis interval is from January 1 to March 24, 2023.

The quarantine rates, γ and α_Q, were arbitrarily defined, once they have currently no meaningful impact due to the low number of infected people.

For the transmission rate (β), a reliable value was calculated based on the R(t) reports[5]. The vaccine protection rate (ω_V), the efficacy of the vaccine (ε), the average latency period (τ_E), the recovered or deceased rate (α_S) and the rate of loss of natural immunity (σ_R) were collected by a literature research.

All constants and corresponding references can be found in Table 1.

Symbol	Value	Description
ψ_V	0.00018559	Vaccination rate
ω_V	1/180	Vaccine decline rate
β	[0.1854-0.1945]	Transmission contact rate
ε	[0.903-0.976]	Vaccine efficiency
τ_E	[0.1695-0.1961]	Average latency period
α_S	0.0925069	Transition rate for recovered or deceased
γ	0.025	Quarantine rate
θ	0.0000006555	Fraction of individuals who die from the disease
α_Q	[0 - 1/5]	Rate of quarantined who recovered or died
σ_R	1/240	Natural immunity loss rate

Table 1. Values of the SEIRVQD Model Parameters.

RESULTS AND CONCLUSIONS

The evolution of the number of individuals in each compartment of the population, generated by the deterministic System of Equations (1), over 1500 days, is shown in Fig. 2.

The results were obtained through the numerical resolution of the initial value problem with System (1) using the built–in MATLAB function ode45, which combines the 4th and 5th–order Runge–Kutta methods.

In Fig. 2, it is possible to observe waves in the evolution of the number of susceptible and recovered individuals, as well as a decrease in the vaccinated population. Assuming the loss of immunity, the model describes the possibility of an infection outcome even in the future. That provides motivation for a deep study and analysis about the possibility of a new pandemic outbreak.

To conclude, the model proposed is adapted to the specifics of a post–pandemic scenario, 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.

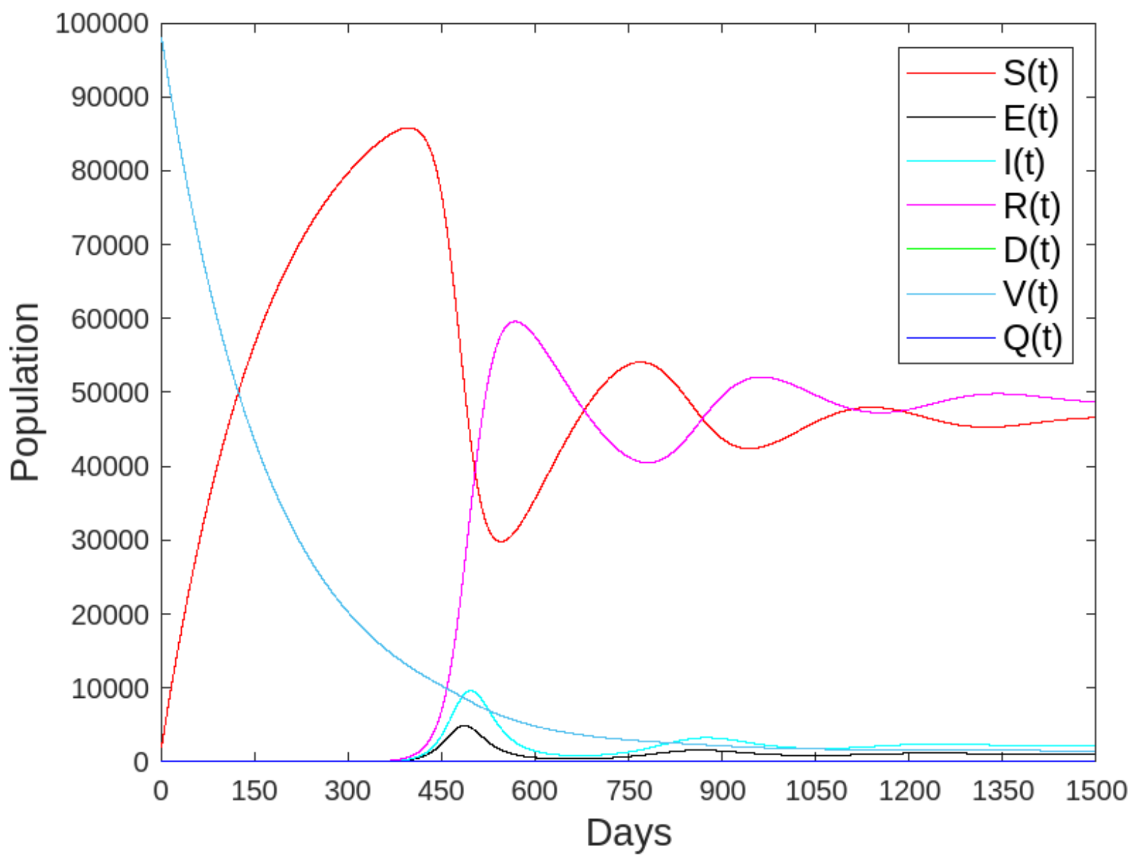

Fig. 2. Simulation Results of the SEIRVQD Deterministic Model.

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Acknowledgements:

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IPCA INSTITUTO POLITÉCNICO DO CÁVADO E DO AVE
ipvc Instituto Politécnico de Viana do Castelo
CeDRI Research Centre in Digitalization and Intelligent Robotics
2Ai APPLIED ARTIFICIAL INTELLIGENCE LABORATORY
ipvc adit-lab Applied Digital Transformation Laboratory
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