Determining the impact of the initial phase of the COVID-19 pandemic with delay differential equations

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Abstract

In this work, a mathematical model is designed to determine the impact of the transmission of the COVID-19 virus, using a system of delayed ordinary differential equations that describes the dynamics of the disease, which is made up of four subpopulations represented by the susceptible $S(t)$, symptomatic infected $I(t)$, asymptomatic infected $A(t)$ and recovered $R(t)$. The dynamics is represented by

$$\begin{aligned}
\frac{dS(t)}{dt} &= \Lambda + \eta R(t) - \beta_I S(t)I(t) - \beta_A S(t)A(t) - \mu S(t)\\
\frac{dI(t)}{dt} &= (1-a)\left[\beta_I S(t-\tau)I(t-\tau) + \beta_A S(t-\tau)A(t-\tau)\right]e^{-\mu\tau} - (\mu+\delta_I+\delta)I(t)\\
\frac{dA(t)}{dt} &= a\left[\beta_I S(t-\tau)I(t-\tau) + \beta_A S(t-\tau)A(t-\tau)\right]e^{-\mu\tau} - (\mu+\delta_A)A(t)\\
\frac{dR(t)}{dt} &= \delta_A A(t) + \delta_I I(t) - (\eta+\mu)R(t).
\end{aligned} \tag{1.1}$$

The equilibrium points of the system are obtained for the qualitative analysis of the solutions and the most important threshold than the basic number of reproduction is obtained. To corroborate the theoretical results, simulations are performed. In addition, a numerical scheme was designed to simulate the solutions of the model through time, it was implemented in Matlab and the stability of the equilibrium points and the designed numerical scheme were studied.

References

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