Global stability and sensitivity of an SQIR model with infectivity during quarantine

✉ Thiago Kfouri De Angelis

Universidade de São Paulo

thiagokda@ime.usp.br

Luiz Eduardo Dos Santos Lopes

Universidade de São Paulo

luislopes@ime.usp.br

Abstract: To measure the impact of isolating individuals infected with direct transmission diseases a compartmental model was obtained and validated mathematically with respect to qualitative behavior.

First, the basal number R_0 was determined through Van den Driessche-Watmough's method, because that parameter sets the stability of the two equilibrium points. Then, using Liapunov's theory, it was proven that when $R_0 < 1$ the disease-free equilibrium is globally asymptotic stable and the endemic equilibrium is globally asymptotic stable when $R_0 > 1$, has a forward bifurcation in $R_0 = 1$ and is unstable otherwise.

Finally, sensitivity analysis was done through numerical simulations, changing the parameters and analyzing the curve of infected. Increasing the number of infected that enter quarantine and reducing the contagion rate both lead to a significant reduction in the number of cases, however the curve was flattened only in the second case, therefore it is expected to be more effective.

Resumen: Para medir el impacto de aislar individuos infectados con enfermedades de transmisión directa se obtuvo un modelo compartimental y se validó matemáticamente con respecto al comportamiento cualitativo.

En primer lugar, se determinó el número basal R_0 mediante el método de Van den Driessch-Watmough, ya que ese parámetro establece la estabilidad de los dos puntos de equilibrio. Luego, utilizando la teoría de Liapunov, se demostró que cuando $R_0 < 1$ el equilibrio libre de enfermedad es globalmente asintótico estable y el equilibrio endémico es globalmente asintótico estable cuando $R_0 > 1$, tiene una bifucación hacia adelante en $R_0 = 1$ y es inestable en caso contrario.

Por último, se ha realizado un análisis de sensibilidad mediante simulaciones numéricas, cambiando los parámetros y analizando la curva de infectados. Tanto el aumento del número de infectados que entran en cuarentena como la reducción de la tasa de contagio conducen a una reducción significativa en el número de casos; sin embargo, la curva se aplanó solo en el segundo caso, por lo que se espera que sea más eficaz.

Keywords: SQIR model, global stability, sensitivity analysis.

MSC2010: 34D23.

1. Introduction

Although compartmental models have been a fundamental tool in epidemiology for decades, the necessity for development in this area has become very evident recently due to the COVID-19 pandemic. One tendency in recent works concerning such models is to incorporate different types of isolation into the classical models. For example, some results where made in [2] to cases where the isolation is given as a function of the distancing between susceptibles. More recently, [1] considered non-lethal diseases in which a portion of the susceptible is isolated and the incubation period is infectious.

In this work, we will be concerned with the isolation of the infected while they are in treatment. The Centers for Disease Control and Prevention of the USA recommend this practice for cases of HIV, Tuberculosis, Rubella, Chickenpox, among others [3] and the World Health Organization and many other agencies adopted this method to handle the COVID-19 [4]. Most of these diseases are lethal and some health professionals and patients can end up infected by those isolated patients due to flexibilization of isolating norms.

2. SQIR model

For the modeling, the main aspects were that individuals might recover or die after being infected, some of them get in quarantine while receiving medical care and that the quarantine is imperfect, changing recovery and deaths rate. The following model was obtained considering all this.

$$
\begin{cases}
\dfrac{\mathrm{d}S}{\mathrm{d}t} = \nu - \beta_1 SQ - \beta_2 SI - \mu S, \\[2mm]
\dfrac{\mathrm{d}Q}{\mathrm{d}t} = \gamma I - (\mu + \alpha_1 + \rho_1)Q, \\[2mm]
\dfrac{\mathrm{d}I}{\mathrm{d}t} = \beta_1 SQ + \beta_2 SI - (\mu + \gamma + \alpha_2 + \rho_2)I, \\[2mm]
\dfrac{\mathrm{d}R}{\mathrm{d}t} = \rho_1 Q + \rho_2 I - \mu R.
\end{cases}
$$

The parameters are values between 0 and 1. Their meaning is shown in Table 1.

Table 1: Summary of all the parameters.

α_1	mortality rate in quarantine
α_2	mortality rate without quarantine
β_1	infection rate in quarantine
β_2	infection rate without quarantine
γ	rate of infected people that go to quarantine
μ	natural deaths (not caused by the disease)
ν	natality and migration rate
ρ_1	recovery rate in quarantine
ρ_2	recovery rate without quarantine

The model dynamic is determined mainly by the domain of the functions S, Q, I, R and the basic reproduction number R_0, which tell us how many people one infected individual will contaminate.

A feasible positively invariant region for the model is

$$
D = \left\{ (S, Q, I, R) \in \mathbb{R}^4 \ : \ 0 < S \le \frac{\nu}{\mu}, 0 \le Q, 0 \le I, 0 \le R \right\}.
$$

To determine a suitable R_0, first the substitutions $\delta = \mu + \alpha_1 + \rho_1$, $\omega = \mu + \gamma + \alpha_2 + \rho_2$ were made, then the compartments with the disease were divided into two matrices F and V such that

$$\frac{\mathrm{d}}{\mathrm{d}t} \left[\begin{array}{c} Q \\ I \end{array} \right] = F - V = \left[\begin{array}{c} \gamma I \\ \beta_1 SQ + \beta_2 SI \end{array} \right] - \left[\begin{array}{c} \delta Q \\ \omega I \end{array} \right].$$

Then, the value of R_0 was established using Van der Driessch-Watmough's method.

$$R_0 = \rho(J(F)J^{-1}(V)) = \frac{\nu(\gamma\beta_1 + \delta\beta_2)}{\mu\omega\delta};$$

here, $\rho(X)$ and $J(X)$ represent the spectral radius and the Jacobian matrix of X, respectively.

3. Results

Through the calculations, it was found that, when $R_0 > 1$, there are two stationary points P_1 and P_2, the first occurs if $I(0) = 0$ in ∂D and the second if $I(0) > 0$ in the interior of D. However, when $R_0 \leq 1$ only P_1 exists. $P_1 = (\frac{\nu}{\mu}, 0, 0, 0)$ reflects the situation where there is no disease to spread and the endemic equilibrium is given by

$$P_2 = \begin{cases} S_2 = \dfrac{\delta\omega}{\beta_1\gamma + \beta_2\delta} = \dfrac{\nu}{\mu R_0}, \\[2mm] Q_2 = \dfrac{\nu\gamma}{\mu\delta^3\omega} - \dfrac{\gamma}{\beta_1\gamma + \beta_2\delta}, \\[2mm] I_2 = \dfrac{\nu}{\mu\delta^2\omega} - \dfrac{\delta}{\beta_1\gamma + \beta_2\delta} = \dfrac{\delta}{\gamma}Q_2, \\[2mm] R_2 = \dfrac{1}{\mu}\left(\rho_1 Q_2 + \rho_2 I_2\right) = \dfrac{Q_2}{\mu}\left(\rho_1 + \dfrac{\rho_2\delta}{\gamma}\right). \end{cases}$$

Defining convenient Lyapunov and anti-Lyapunov functions, it was proven that P_1 is globally asymptotic stable when $R_0 < 1$, it has a forward bifurcation in $R_0 = 1$ and is unstable when $R_0 > 1$. Also P_2 is globally asymptotic stable when $R_0 \geq 1$. Therefore it meets the expected qualitative behavior from the disease, i.e., when $R_0 < 1$ it eventually vanishes, no matter how many infected are in the population, and when $R_0 > 1$ it spreads until almost all the people had contact and are now immunized or dead.

The model was also investigated quantitatively using numerical simulations and sensitivity analysis was done on the parameters γ and β_2. The results for $\beta_1 = 0.01$, $\alpha_1 = 0.01$, $\alpha_2 = 0.02$, $\rho_1 = 0.99$, $\rho_2 = 0.98$, $\nu = 0.03$ and $\mu = 0.00005$ fixed are presented below in Figures 1 and 2.
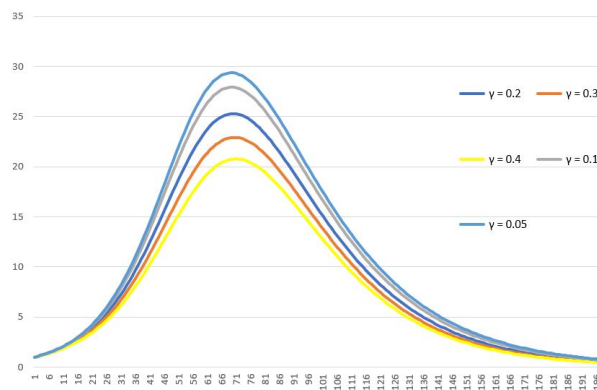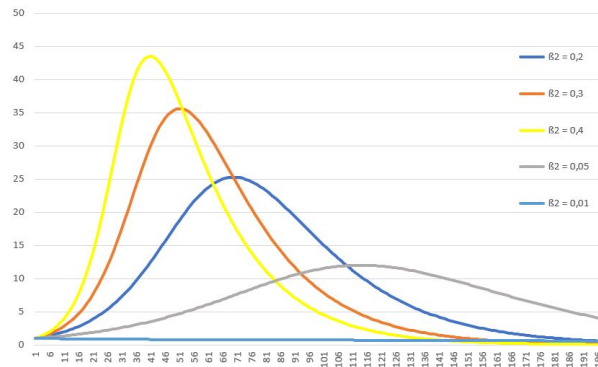
Figure 1: Infected curves for different values of γ.

Figure 2: Infected curves for different values of β_2.

As observed, increasing the number of infected that enter quarantine there was a significant reduction in the number of cases, however the curve maintained its shape, and reducing the contagion rate the number of infected decreased and the curve was flattened, retarding the pinnacle of cases. Therefore, contagion reducing actions, such as washing hand, using masks, etc. are expected to be more effective than this type of isolation.

4. Conclusion

The new coronavirus (SARS-CoV-2) identified in December 2019 in Wuhan in China was a great motivator of recent work in epidemiology, and many of these have isolation as their object of study. Following this trend, a model was obtained with the population divided into susceptible, quarantined, infected and recovered, the isolation is done between infected individuals and is imperfect, that is, some infections come from the encounter between quarantined and susceptible people.

It has been analytically proven that the model follows the expected asymptotic behavior of a disease like COVID-19, which should stabilize and eventually disappear if there are no mutations. Although they have this tendency, it is known that this is a very damaging process for society, causing losses and deaths. It is then necessary to intervene through preventive measures to prevent the rapid increase in the number of infected individuals.

In practice, it is not always possible to implement several measures at the same time, so it is interesting to know which ones are more effective. In order to compare between increasing the isolation proposed by this SQIR model with actions that decrease the contagion rate, it was verified from the numerical simulations with random parameters, a decrease in the number of infected with both, but the flattening of the curve only happened in the second case, and therefore should be prioritized.

References

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