

Vaccination and social distance to prevent COVID-19 ^{*}

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Abstract: In order to analyze the effect of vaccination in a population with the presence of viruses, a variation of the SIR (Susceptible-Infected-Removed) model is proposed taking into account social distancing and the effect of the vaccine. The equilibrium points of the proposed model are calculated and the stability analysis of the system is carried out. For the proposed model, disease-free equilibrium point and endemic equilibrium point are found and the conditions of existence are discussed. For the disease-free equilibrium point the bifurcation conditions are derived and simulations show that reducing the vaccination effort can lead the disease-free equilibrium to the endemic equilibrium. From the theoretical analysis, a minimum value of effort is obtained to guarantee a disease-free equilibrium point. Simulations were carried out from the value obtained from R_v to validate the theoretical results.

Keywords: SIR model, social distancing, stability, vaccination, reproduction number.

1. INTRODUCTION

Nowadays, the risk of a virus becoming a pandemic is huge. This is largely due to technological advances in transportation. What used to take months to travel from one continent to another, today takes only a few hours. That is why the interest on modelling those systems that describe the behaviour of these diseases is increasing over the years.

An example of this is the case of COVID-19, which in a few months became one of the most serious pandemics in history, claiming the lives of millions of people around the world.

Coronavirus disease (COVID-19) is an infectious disease caused by a newly discovered coronavirus. Most people who become ill from COVID-19 will have mild to moderate symptoms and will recover without special treatment.

The virus is mainly transmitted through droplets generated when an infected person coughs, sneezes, or exhales. These droplets are heavy to remain suspended in the air and are quickly deposited on floors or surfaces, facilitating the transmission by touch on contaminated surfaces by

taking the hands to the eyes or upper tracts, in addition to transmission by inhalation of the virus.

In its most severe manifestation, the virus causes an accentuated respiratory condition, leading the patient to hospitalization that can be intensive and prolonged. Another particularity of the new coronavirus is its high transmission rate, which may be caused by the virus's ability to survive longer outside the human body (Kampf et al., 2020).

The interest in understanding the proliferation of infectious diseases is old, as well as the study of epidemiology, although the mathematical study of diseases is recent, Graunt, in 1662, studied statistical methods in public health (Graunt, 1662).

The first attempts to model the spread of a disease date from the second half of the 18th century. In 1760, a swiss mathematician named Daniel Bernoulli, presented a model to study variations in smallpox. In 1927, Kermack and McKendrick proposed the SIR model (Kermack and McKendrick, 1927), (Kermack and McKendrick, 1932), (Kermack and McKendrick, 1933) that considers a disease that develops over time and has only three classes of individuals (Susceptible, Infected and Removed). This compartmental model shows the relationship between the appearance of an epidemic at a critical value, which depends on the number of susceptible individuals, noting that such value depends

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on the infectivity rate, the recovery rate and the mortality rate.

Many compartmental models have contributed to the study of COVID-19, evaluating the importance of social isolation (Pan et al., 2020), quarantine (Volpert et al., 2020), quarantine at different stages of contagion (Mishra et al., 2020), the study of unreported cases (Cotta et al., 2020), (Lee et al., 2020), the impact of vaccination on society (Batistela et al., 2020) and the possibility that the acquired immunity may be temporary (Batistela et al., 2021).

At this moment, the production of vaccines against COVID-19 is very limited. Currently the percentage of the vaccinated population is too low to control the pandemic. Vaccination in the event of a pandemic is one of the most effective interventions for its control. However, the availability of the pandemic vaccine will be very limited during the first wave of the pandemic, especially for countries that are not vaccine producers (Osterholm, 2005).

The mathematical modelling of infectious diseases is the subject of interest in many research papers (Khoshnaw et al., 2020; Zine et al., 2020; Elie et al., 2020). The study that has been developed by various sources consulted, which include publications in prominent media in the area of medicine (Llop, 2020), (Organization et al., 2021), (Organization et al., 2020), (Martí, 2016), (Galindo Santana et al., 2011) as well as in several research institutes (Sanchez-Castro and Pajuelo-Reyes, 2020), (Álvarez and Andrus, 2005), shows the potential of mathematical modelling as a tool.

Mathematical modeling is an important to guide public policy. With a focus on controlling the pandemic, these strategies are needed to reduce the spread of the disease, control the number of infected and prevent the emergence of new variants. In addition, they aim to reduce the number of hospitalizations to avoid a breakdown in the health system and establish qualitative and quantitative information for the vaccination program. Not only to prevent the levels of spread of a virus in general, but also as an instrument in decision-making for resource management and prevention of calamity scenarios, allowing the possibility of projecting simulations with various degrees of precision.

This work aims to achieve a better understanding of the influence caused by the vaccination rate and social distancing on the spread of the epidemic. Study and evaluate what is the minimum effort necessary to achieve a stable disease-free equilibrium point to mitigate the spread of the virus.

The paper also intends to guide, in a macroscopic way, future work regarding the qualitative and quantitative prediction by validating the model using real data for COVID-19.

In addition, it is possible to use the research as a guide for studies of stochastic models, and particularly it is possible to obtain information, taking into account new COVID-19 forms such as Delta variant and the effect of super-spreaders, people who significantly infect more people than normal.

The paper is organized as follows, Section 2 presents the compartmental mathematical model and the equilibrium points. Section 3 presents the stability conditions, showing the possible existence and numerical experiments followed by the conclusions.

2. MODELS DESCRIPTIONS

The proposed model is a modification of the original SIR (Susceptible-Infected-Removed) model (Kermack and McKendrick, 1927), (Kermack and McKendrick, 1932), (Kermack and McKendrick, 1933) as shown in Fig. 1. In this model, the susceptible population S is infected at a rate α when contacted by an infected individuals from I . The effect of social distancing measures in the susceptible individuals is introduced by the parameter θ , and the subject to the constraint $0 < \theta < 1$ and ω is the group to which vaccination is given.

The compartment I represents the infectious population in the incubation stage prior the onset of symptoms and this population can be asymptomatic or symptomatic. The total population is considered constant, the death rate are equal for members of all classes, μ is the death and birth rate which are assumed to be equal and β is the recovery rate.

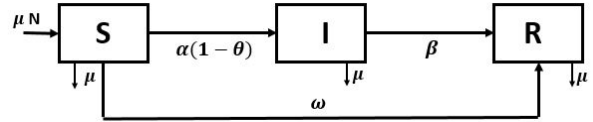


Fig. 1. SIR model with vaccine influence and social isolation.

The model assumes the following hypotheses:

- Fixed population;
- The ways to stop being susceptible is if a person becomes infected, if he is immunized by vaccination or by the mortality rate;
- When the person recovers, they receive permanent immunity;
- The probability of infection is not affected by age, sex or social status;
- The birth and death rate are part of the considerations;
- All births fall into the susceptible class;
- The mortality rate is the same for all compartments and mortality is assumed to be equal to the birth rate.

The model assumes the following notations:

- $S(t)$: Number of susceptible individuals at time (t) ;
- $I(t)$: Number of infected individuals at time (t) ;
- $R(t)$: Number of individuals recovered at time (t) ;
- α : probability of a susceptible individual becoming infected;
- β : probability of an infected recovering;
- θ : social isolation rate;
- ω : vaccination rate of the susceptible;
- μ : mortality rate;
- N : the death is equal for members of all three classes, and it is assumed that the birth and death rates are equal so that the total population is stationary.

2.1 Equations

Considering these elements, the model can be described as:

$$\begin{cases} \dot{S} = \mu N - \frac{\alpha(1-\theta)S(t)I(t)}{N} - \omega S(t) - \mu S(t); \\ \dot{I} = \frac{\alpha(1-\theta)S(t)I(t)}{N} - \beta I(t) - \mu I(t); \\ \dot{R} = \beta I(t) + \omega S(t) - \mu R(t). \end{cases} \quad (1)$$

With constant populations:

$$S(t) + I(t) + R(t) = N. \quad (2)$$

consequently:

$$\dot{S} + \dot{I} + \dot{R} = 0. \quad (3)$$

Taking into account the population density:

$$s = \frac{S}{N}; i = \frac{I}{N}; r = \frac{R}{N}. \quad (4)$$

By substituting (4) in (1):

$$\begin{cases} \dot{s} = \mu - \alpha(1-\theta)si - \omega s - \mu s; \\ \dot{i} = \alpha(1-\theta)si - \beta i - \mu i; \\ \dot{r} = \beta i + \omega s - \mu r; \end{cases} \quad (5)$$

with the initial conditions $s(0) \geq 0$, $i(0) \geq 0$ and $r(0) \geq 0$.

Here μ is the recruitment and natural death rate, α is the effective contact rate between susceptible and infected individuals, ω is the rate of vaccination and θ is the social isolation. All the parameters are positive and for θ the restriction considers $0 < \theta < 1$.

For the proposed model, there are two equilibrium points: one endemic and the other free from infection.

Disease-free equilibrium point:

- $P_1 (s^*, i^*, r^*) = (\frac{\mu}{\omega + \mu}, 0, \frac{\mu\omega}{\omega + \mu})$;

Endemic equilibrium point:

- $P_2 (s^*, i^*, r^*) = (\frac{\beta + \mu}{\alpha(1-\theta)}, \frac{-(\omega + \mu)}{\alpha(1-\theta)} + \frac{\mu}{\beta + \mu}, \frac{\beta}{\mu} \left(\frac{-(\omega + \mu)}{\alpha(1-\theta)} + \frac{\mu}{\beta + \mu} \right) + \frac{\omega}{\mu} \frac{\beta + \mu}{\alpha(1-\theta)})$;

such as:

$$\frac{-(\omega + \mu)}{\alpha(1-\theta)} + \frac{\mu}{\beta + \mu} > 0, \quad (6)$$

then,

$$\omega < \frac{\mu\alpha(1-\theta)}{\beta + \mu} - \mu. \quad (7)$$

From the analysis of the endemic point, it can be seen that to guarantee its existence, it is necessary to respect the condition (6). Analyzing this point, the minimum vaccination effort necessary to reach the point free of infection can be concluded. This result is evidenced in (7).

2.2 Basic Reproduction Number R_0

This parameter describes the behaviour of the system model and represents the number of susceptible individuals that an infected person can infect.

In our model, without considering the impact of vaccination, the basic reproduction number is given by (8). As can be seen in Fig. 1, the effect of vaccination is given by the parameter ω . This parameter influences the reduction of the number of susceptible individuals. This influence causes the R_0 to vary. In the same way that it was carried out in (Chauhan et al., 2014), (Batistela et al., 2020) the new basic reproduction number is defined as in (9).

$$R_0 = \frac{\alpha(1-\theta)}{\beta + \mu}; \quad (8)$$

$$R_v = (1-\omega) \frac{\alpha(1-\theta)}{\beta + \mu}. \quad (9)$$

3. STABILITY ANALYSIS

In order to analyze the local stability of the system, the Jacobian of the model is calculated at the equilibrium points.

$$J = \begin{bmatrix} -\alpha(1-\theta)i^* - \omega - \mu & -\alpha(1-\theta)s^* & 0 \\ \alpha(1-\theta)i^* & \alpha(1-\theta)s^* - \beta - \mu & 0 \\ \omega & \beta & -\mu \end{bmatrix}.$$

Analyzing the Jacobian at point P_1 :

$$J_{P_1} = \begin{bmatrix} -\omega - \mu & -\alpha(1-\theta)s^* & 0 \\ 0 & \alpha(1-\theta)s^* - \beta - \mu & 0 \\ \omega & \beta & -\mu \end{bmatrix}.$$

Using the mathematical tool Matlab 2015, the eigenvalues of the resulting Jacobian matrix are calculated, in order to analyze the stability of the equilibrium point.

Eigenvalues P_1 :

$$\begin{aligned} \lambda_1 &= -\mu; \\ \lambda_2 &= -\omega - \mu; \\ \lambda_3 &= \alpha(1-\theta)s^* - \beta - \mu. \end{aligned}$$

The stability analysis for model (5) presents the disease free equilibrium point and, considering the existence condition, the eigenvalues are given by $\lambda_1 = -\mu$, $\lambda_2 = -\omega - \mu$ and $\lambda_3 = \alpha(1-\theta)s^* - \beta - \mu$. This indicates that if $(s^* < \frac{\beta + \mu}{\alpha(1-\theta)})$ the system is asymptotically stable and if $(s^* > \frac{\beta + \mu}{\alpha(1-\theta)})$ the system becomes unstable indicating a bifurcation in the parameter space.

Analyzing the Jacobian at point P_2 :

$$J_{P_2} = \begin{bmatrix} -\frac{\alpha(1-\theta)\mu}{\beta + \mu} & -\beta & 0 \\ -\omega - \mu + \frac{\alpha(1-\theta)\mu}{\beta + \mu} & 0 & 0 \\ \omega & \beta & -\mu \end{bmatrix}.$$

Solving for the determinant of the resulting Jacobian matrix:

$$\begin{aligned} (-\mu - \lambda)^{3+3} &[-\lambda \left(\frac{-\alpha(1-\theta)\mu}{\beta + \mu} - \lambda \right) + \\ &\beta(-\omega - \mu + \frac{\alpha(1-\theta)\mu}{\beta + \mu})] = 0; \end{aligned} \quad (10)$$

Consequently, one of the eigenvalues $\lambda_1 = -\mu$ and the other eigenvalues are analyzed by:

$$\lambda^2 + \frac{\alpha(1-\theta)\mu}{\beta+\mu}\lambda + \left(\frac{\alpha(1-\theta)\mu}{\beta+\mu} - (\omega + \mu)\right)\beta = 0. \quad (11)$$

The Routh Hurwitz method was used to analyze the stability of the system. To guarantee this stability, the terms of the characteristic polynomial must all be positive since it is a second-order polynomial (Lee, 2008). As can be seen in (11), the independent term is only greater than zero when the condition of existence (6) is satisfied. Therefore it can be stated that the endemic point, if it exists, is asymptotically stable.

3.1 Numerical Experiments

In order to analyze the stability of point P_1 and the existence and stability of point P_2 , numerical experiments were carried out.

The theoretical analysis of point P_1 shows the bifurcation condition $s^* = \frac{\beta+\mu}{\alpha(1-\theta)}$, for which the system can be stable or unstable, depending on the values of the parameters, as shown in Fig. 2 and Fig. 3.

To guarantee the stability condition, the following parameter values were chosen: $\alpha = 0.9, \beta = 0.7, \theta = 0.1, \mu = 0.3$ and $\omega = 0.1$. With the initial conditions $(s, i, r) = (0.1, 0.8, 0.1)$. The parameters values are chosen in order to show explicitly the qualitative behaviour of the system, to the detriment of a more realistic choice of values (Chauhan et al., 2014), as shown in Fig. 2.

On the other hand, when the parameters are $\alpha = 0.9, \beta = 0.3, \theta = 0.1, \mu = 0.3$ and $\omega = 0.1$, the instability of point P_1 can be observed, since starting from a neighborhood of this point, point P_2 is reached. With the initial conditions $(s, i, r) = (0.9, 0.1, 0)$, as shown in Fig. 3.

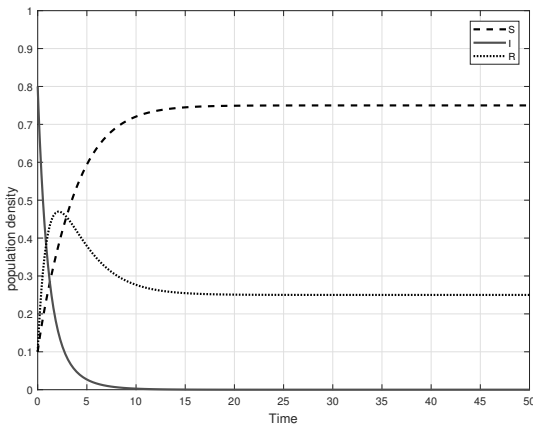


Fig. 2. Point P_1 stable.

The theoretical analysis also shows the existence of an endemic point P_2 . To analyze the behaviour of the system considering the vaccination factor ω , the numerical experiments shown in Fig. 4 and Fig. 5 respectively were carried out. The initial conditions for both cases are: $(s, i, r) = (0.7, 0.3, 0)$.

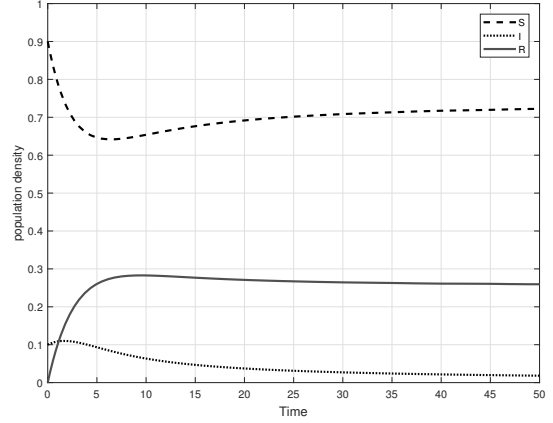


Fig. 3. Point P_1 unstable.

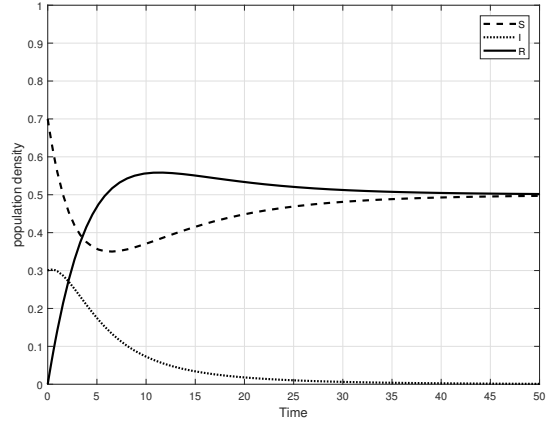


Fig. 4. Stability of P_1 considering $R_v < 1$.

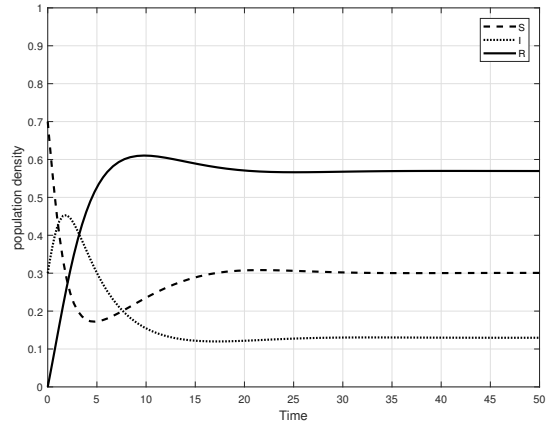


Fig. 5. Stability of P_2 considering $R_v > 1$.

In the Fig. 6 the stability of point P_1 is observed when $R_v < 1$. For any initial condition, the system always reaches the disease-free point. The lines describe the direction of the possible trajectories of the system depending on the initial conditions.

In the Fig. 6 shows the phase diagram of the system with the combination of parameters so that the existence of a

disease-free equilibrium point is guaranteed. Each trajectory represents a possible initial condition of the system variables (Susceptible and Infected) and their evolution over time until reaching the equilibrium point. The arrows indicate the direction of movement of the trajectories.

It can be verified that the disease-free equilibrium point P_1 , if it exists, is asymptotically stable as concluded in the stability analysis in Section 3. This shows that, given this combination of parameters, it does not matter how large the initial population of infected, the system is able to completely eradicate the disease.

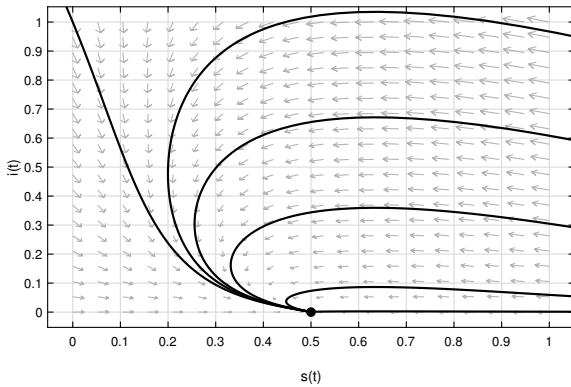


Fig. 6. Phase space for P_1 considering R_v . $\alpha=0.9$, $\beta=0.3$, $\theta=0.3$, $\mu=0.1$ and $\omega=0.1$.

In the Fig. 7 the stability of point P_2 is observed when $R_v > 1$ and shows the phase diagram of the system with the combination of parameters exposed in (7) so that the existence of an endemic point is guaranteed. Each trajectory represents a possible initial condition of the system variables (Susceptible and Infected) and their evolution over time until reaching the endemic equilibrium point. The arrows indicate the direction of movement of the trajectories.

It can be verified that the endemic equilibrium point P_2 , if it exists, is asymptotically stable as concluded in the stability analysis in Section 3. This shows that, given this combination of parameters, it will not be possible to eradicate the disease.

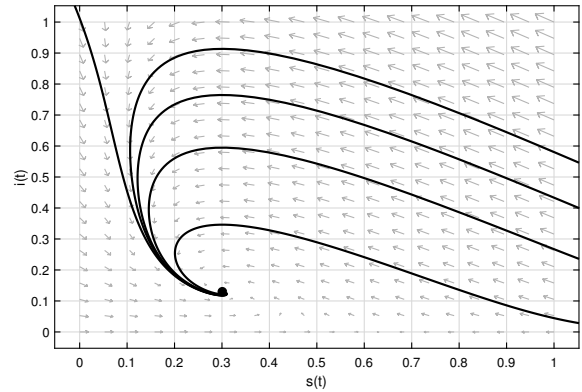


Fig. 7. Phase space for P_2 considering R_v . $\alpha=1.9$, $\beta=0.3$, $\theta=0.3$, $\mu=0.1$ and $\omega=0.06$.

4. CONCLUSION

The model presented shows how a forced vaccination strategy can contribute to the control of a pandemic in general.

Doing a stability analysis of the model, it can be seen that it has two equilibrium points of interest, one endemic (P_2) and the other free of disease (P_1).

The stability study of these points shows how social isolation and the vaccination effort influence the spread of the disease.

For the disease-free equilibrium point P_1 , which there is a bifurcation condition, the stability of these point can be changed by changing R_v . With the decrease in the vaccination effort ω and the consequent increase in R_v , the infection-free asymptotically stable point tends to an endemic equilibrium point P_2 .

The results of the analysis shows:

- $R_v < 1$, the point P_1 free of infection is always reached independently of the number of the infected population.
- $R_v > 1$ the point P_1 is unstable and the system goes to the endemic point P_2 .

For the endemic equilibrium point P_2 , due to the conditions of existence, the study is only possible considering $R_v > 1$, indicating that, regardless of the initial conditions, the point remains stable.

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