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QUALITATIVE ANALYSIS FOR MATHEMATICAL MODELS THAT DESCRIBE THE TRANSMISSION DYNAMICS OF COVID 19.

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ABSTRACT
The main objective of this paper is to show the importance of the qualitative analysis in systems defined by differential ordinary equations, applied to the epidemiology. In particular, mathematical models will be propose that define the dynamics of transmission of COVID 19, considering a single stump of the illness and simulating a vaccination process.
This type of theoretical study, added to the process of modeling, is one of the tools that mathematics can offer to generate effective control strategies, as much for the specialists of applied mathematics, the doctors and epidemiologists as for those who decide politics in the System of Public Health.

KEYWORDS: Mathematical models, qualitative analysis.

MSC: 45M99

RESUMEN
El objetivo principal de este trabajo es explicar la importancia del análisis cualitativo en sistemas definidos por ecuaciones diferenciales ordinarias, aplicados a la epidemiología. En particular, se mostrarán modelos matemáticos que definen la dinámica de transmisión de la CoVid 19 considerando una sola cepa de la enfermedad y simulando un proceso de vacunación. Este tipo de estudio teórico, sumado al proceso de modelado, es una de las herramientas que la matemática puede brindar para generar estrategias de control efectivas, tanto para los estudiosos de las matemáticas aplicadas, los médicos y epidemiólogos como para los decisores del Sistema de Salud Pública.

PALABRAS CLAVE: Modelos matemáticos, análisis cualitativo.

1. INTRODUCTION.

When modeling a practical problem through a system of ordinary differential equations, an alternative for the qualitative or geometric study of this system is, in addition to trying to find analytical solutions or their approximations, to analyze its behavior, in particular to study what happens with these solutions when the independent variable (usually time) tends to infinity.

A key element in this study is finding the equilibrium points or points at which the values of the dependent variables do not change when the value of the independent variable is modified. Once the equilibrium points have been found, we are interested in knowing how the solutions behave in a neighborhood of these points: do they approach to, move away from, or oscillate around this point as the independent variable grows? In the first case, we will say that the equilibrium point is asymptotically stable.

The study of the stability of differential equations allows us to make important predictions about the behavior of the mathematical models that use them, as well as provide a reference framework to validate the various numerical methods used to approximate the exact solutions of the model.

The study of the equilibrium points of differential equations and the behavior of their solutions in a neighborhood of such points is known as analysis of the local stability of differential equations.

The fundamental objective of this work is to present a qualitative analysis of epidemiological models that describe the dynamics of transmission of COVID 19 in Cuba with vaccinated populations, as part of the tools that mathematical modeling can provide to design effective control strategies.

The system of differential equations has the following structure:

$$\dot{x} = F(x) = (F_1(x), F_2(x), \dots, F_n(x))^T \tag{1}$$

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with the initial condition $x(t_0) = x_0$, that is, the right member is independent of t. Here we assume that $x \in R^n$ and that $F \subset C^1(\Omega, R^n)$ where $\Omega \subset R^n$ is an open and connected set, which is called phase space.
We define an equilibrium point of system (1) as a point p of the phase space Ω that meets $F(p) = 0$. The point p is said to be regular if $F(p) \neq 0$. (Ricard., 2022)
Using equivalence classification to catalog these balance points allows us to distinguish saddle, node, focus and center points.
To do this, we consider the Jacobian matrix of system (1), which we will denote by A and take into account the signature of the quadratic form generated by said matrix. For this classification it is not important whether A is diagonalizable or not. The characteristic equation has the following form $\lambda^2 - \tau\lambda + \delta = 0$, where λ is considered to be the determinant of the matrix and δ its trace. Its roots are $\lambda = \frac{\tau \pm \sqrt[2]{\tau^2 - 4\delta}}{2}$ so that we can build a scheme in the complement of the axis $\delta = 0$ in the plane $\tau\delta$. In this scheme, only the signs of the eigenvalues are considered and not the structure of the equivalent Jordan matrix.
Let the plane $\tau\delta$ and a partition defined by the curve $\delta = \frac{1}{4}\tau^2$ and the straight line $\tau = 0$, taking into account that the plane has been cut by the straight line $\delta = 0$. The system of equations (1) is asymptotically stable if and only if it is verified that $\tau = Tr(A) < 0$ and $\delta = Det(A) > 0$.
In the lower half-plane the phase diagram turns out to be a saddle point; in the upper half-plane and below the parabola there is a node that is stable if the trace is positive, and unstable if the trace is negative; in the upper half-plane and above the parabola, there is a focus that is stable if the trace is positive, and unstable if the trace is negative; on the axis of the ordinates in the upper half-plane the aspect of phases turns out to be that of a center. This is illustrated in the figure 1.

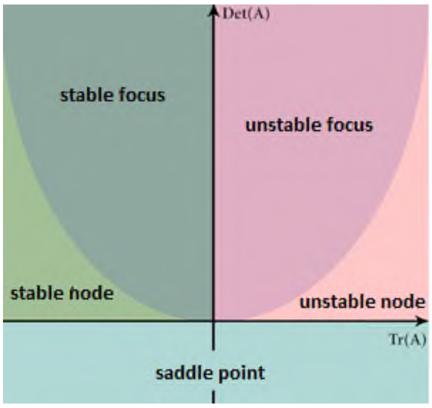


Figure 1: Phase diagram of system (1)

The rest point is Liapunov stable if $\tau = 0$ and $\delta > 0$, while it is unstable if $\tau > 0$ or $\delta < 0$. (Á.G. Estrella-González, 2013)

2. MATHEMATICAL MODELING.

Since time immemorial, mathematical models have played an important role in understanding and predicting the spread of infectious diseases in a population. Different types of models are used to simulate several scenarios and to provide tools in decision making, especially with the development of Mathematical Epidemiology and biomedical applications (Martcheva, 2015), (Murray, 2003). However, ordinary differential equations remain especially useful tools in epidemiological research. Covid 19 has been a challenge for education, see Gaviño Ortiz . et al. (2023) and Moscoso-Paucarchuco et al. (2022). Taking as starting points the invetigations of cuban researchers (I.A. Abelló Ugalde, 2020), (A. Marrero Severo, 2020) as well as in diffente regiosn of the worls during the CoVid 19 pandemic de (Pinzón, 2021), (Orús, 2023); (V. Medina Rodríguez, 2024), we presented two mathematical models, which differ in the linearity of the system of differential equations that governs them, allowing us to compare results and verify the effectiveness of both. But to develop an in-depth study of these models, it is important to carry out a qualitative analysis, since this tool is illuminating in many scenarios, where the solution of such systems does not behave as expected or, as in many other cases, it is necessary to know what happens in a close neighborhood of the stability points.

The variables that govern both model variants are S, I which represent, respectively, the population of susceptible and infected unvaccinated people at time t, and H, which represents the population with immunity, whether natural or due to the vaccine.

In the susceptible population, the increase of people is taken into account, whether due to births or other reasons; this is reflected in the term $(1 - c)Pf$, where c represents the proportion of infected people detected from the floating population P_f. We take into account the vaccination of the susceptible population, therefore with the parameter p_v we reflect the effectiveness rate of the vaccine. Once susceptible individuals are infected, they move to the infected group. This happens with an average infection rate β. When infected individuals beat the disease, they move to the susceptible group in a proportion determined by the parameter γ. We also analyze death from the disease, which is given by the parameter m, and natural immunity, by p_i.

Below are the linear and non-linear variants of the models, as well as their respective transmission diagrams between subpopulations.

2.1. Linear Model

The transition of individuals between different populations is described by the following differential equations:

$$\frac{dS}{dt} = (1-c)P_f + \gamma I - p_v S - \beta S \quad (2)$$

$$\frac{dI}{dt} = cP_f + \beta S - (p_i + \gamma + m)I \quad (3)$$

$$\frac{dH}{dt} = p_v S + p_i I \quad (4)$$

2.2. Nonlinear model

In the nonlinear variant, the variables and parameters remain similar, only the SI term is used to represent the interaction between susceptible and infected populations.

$$\frac{dS}{dt} = (1-c)P_f + \gamma I - p_v S - \beta SI \quad (5)$$

$$\frac{dI}{dt} = cP_f + \beta SI - (p_i + \gamma + m)I \quad (6)$$

$$\frac{dH}{dt} = p_v S + p_i I \quad (7)$$

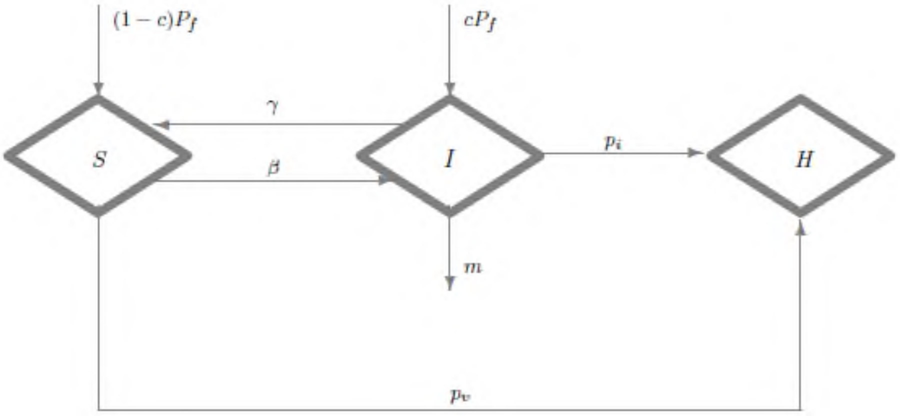


Figure 2: Transmission diagram between the subpopulations of the model

2.3. Qualitative analysis of models for CoVid 19 in Cuba.

To carry out the analytical study of the stability of the linear model (2-4), the critical points of the system of equations were found. The first two equations do not depend on H so it is enough to consider the system with two equations and obtain the values of $S(t)$ and $I(t)$, then the value of $H(t)$ will be obtained using the relationship $S + I + H = N$.

To consider only the equations of S and I, and then to obtaine H, it is certainly necessary that the sum of the subpopulations be a constant value, so that the sums of their derivatives are zero and for that, we must presuppose that $P_f = mI$. This is a frequent hypothesis in this type of research when it is considered, for example, that the recruitment and removal rates are equal (A. D. Baez-Sánchez, 2020), (T. Tulus, 2018).
The equilibrium point is reached when the variable that originally changes with time becomes constant, which means that it is obtained when $\frac{dS}{dt} = \frac{dI}{dt} = 0$.

$$\frac{dS}{dt} = (1-c)P_f + \gamma I - p_v S - \beta S = 0 \tag{8}$$
$$\frac{dI}{dt} = cP_f + \beta S - (p_i + \gamma + m)I = 0 \tag{9}$$

Using the computational tool Wolfram, the critical point $E_0 = (S^*, I^*)$ was obtained, where:

$$S^* = \frac{P_f[(1-c)m + (1-c)p_i + \gamma]}{p_v\gamma + m(p_v + \beta) + p_i(p_v + \beta)}$$
$$I^* = \frac{P_f(cp_v + \beta)}{p_v\gamma + m(p_v + \beta) + p_i(p_v + \beta)}$$

2.4. Local Stability Analysis in E_0.

The nature of the local stability at the equilibrium point E_0 is determined by partially differentiating each function with respect to each variable, thus obtaining the following Jacobian matrix.

$$J(S,I) = \begin{pmatrix} -(\beta + p_v) & \gamma \\ \beta & -(p_i + m + \gamma) \end{pmatrix}$$

The eigenvalues obtained would be:

$$\lambda_1 = \frac{1}{2}(\varphi - \sqrt[2]{\varphi^2 - 4\psi}$$
$$\lambda_2 = \frac{1}{2}(\varphi + \sqrt[2]{\varphi^2 - 4\psi}$$

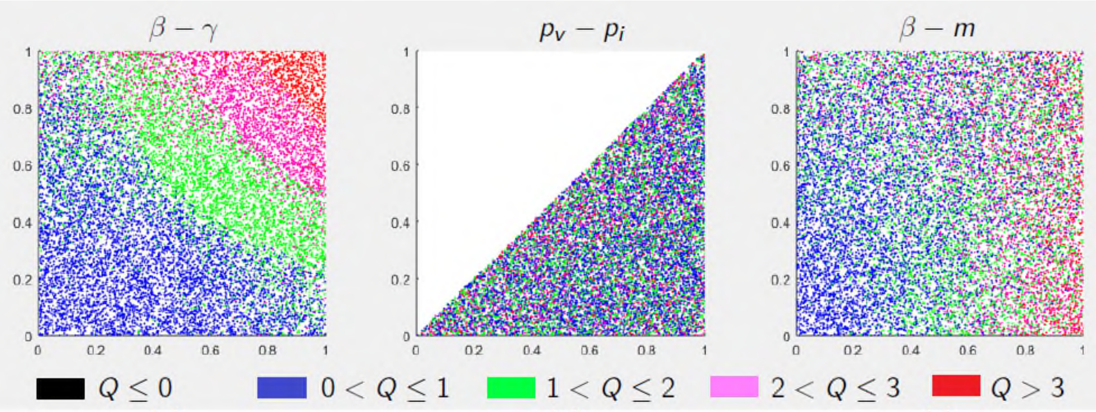
where

$$\varphi = -(\beta + m + p_i + p_v + \gamma) = Tr(J)$$
$$\psi = (\beta m + mp_v + \beta p_i + p_v p_i + \gamma p_v) = Det(J)$$

Obviously, the determinant of $J(S,I)$ is positive and its trace is negative, so, to classify the equilibrium point the sign of the quadratic form $\varphi^2 - 4\psi$ must be found, which depends on 5 variables, defined in the following expression

$$Q(\beta, m, p_v, p_i, \gamma) = \varphi^2 - 4\psi = (\beta + m + p_i + p_v + \gamma)^2 - 4(\beta m + mp_v + \beta p_i + p_v p_i + \gamma p_v)$$

If it holds that the quadratic form $Q \geq 0$, both eigenvalues would be real negative, therefore this critical point is an asymptotically stable node. On the other hand, if $Q < 0$, there are complex conjugate eigenvalues, but not pure imaginary ones, therefore the critical point would be a **focus**. It is important to clarify that Q depends on the model parameters, which indicates that we must focus on analyzing values that oscillate between 0 and 1, since these parameters refer, for the most part, to rates.
Since the quadratic form Q depends on 5 variables, we represent the space R^5 as three simultaneous planes of R^2. A simulation was carried out using the Monte Carlo method, with random points of the parameters that range between 0 and 1, the quadratic form was evaluated at those points that were drawn on a color map, depending on the value of that evaluation. Values between 0 and 1 were characterized with blue points, in green between 1 and 2, in pink between 2 and 3, in red those greater than 3 and in black the values of the quadratic form that are negative.



(a) (b) (c)

Figure 3: Values of the quadratic form Q.

In Figure 3(a), there is a pattern in the distribution of points depending on their value, similar to an inverse function, which shows that the lower the values of the parameters β and γ, the smaller the quadratic form. However, in the Figures 3(b)-3(c) there is a dispersion of points that do not generate any pattern, which is interpreted as a superposition of surfaces, which will be interesting to represent graphically.

Graphing as a function of p_i, p_v and keeping the other variables as constants, for different values of the parameters, the following curves were obtained that show to be positive (apparently), for any value of the parameters between 0 and 1, which are the cases of interest to analyze.

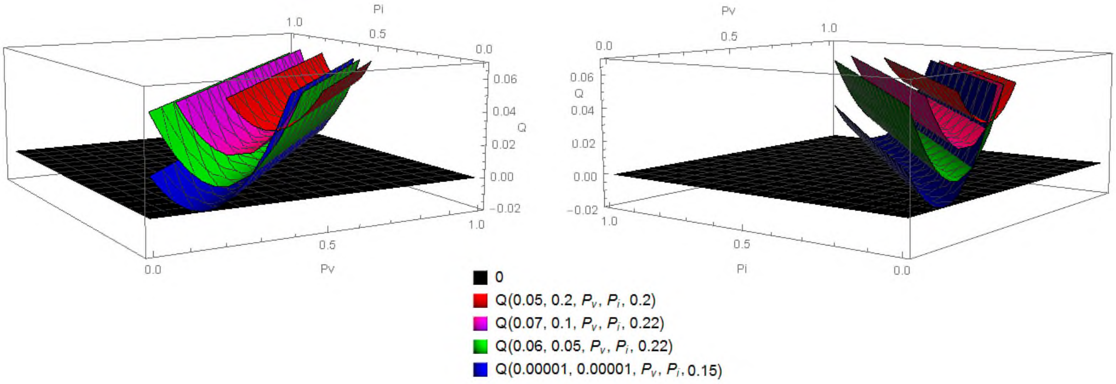


Figure 4: Graph based on $\boldsymbol{p_i}$, $\boldsymbol{p_v}$

To formalize this idea, the minimum of the quadratic form Q was found with respect to the variables p_i, p_v. It was obtained that the minimum has the form of $4\beta\gamma$, which will always be positive since the parameters β and γ are positive.

The previous analysis allows us to reach the conclusion that the quadratic form $Q(\beta, m, p_v, p_i, \gamma) = \varphi^2 - 4\psi$ is always positive, for parameter values between 0 and 1. It can be affirmed, therefore, that the eigenvalues λ_1, λ_2 are always real numbers, different and of the same sign (negative). Consequently, the critical point $E_0 = (S^*, I^*)$, is an asymptotically stable improper node.

If the phase diagram is analyzed, it can be seen that there are four trajectories in the form of semi-straight lines with ends at the origin; all the other trajectories have the appearance of branches of a parabola and, when tending towards the origin, their slopes tend to the slope of one of the semi-straight lines.

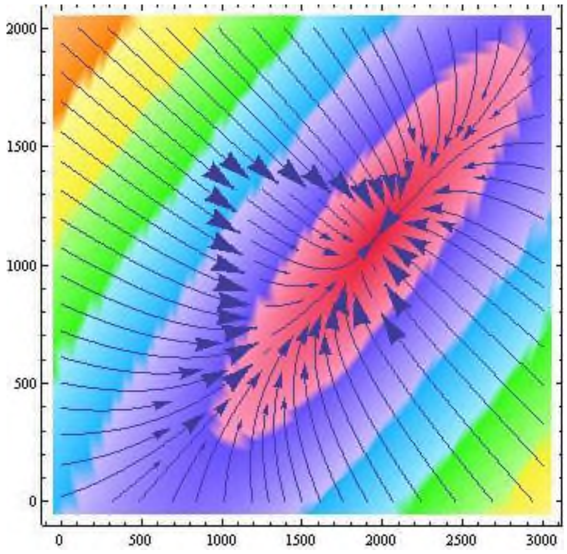


Figure 5: Phase diagram around of E_0

In the case of the non-linear variant of model (5)-(7), in which the variables and parameters are kept similar and the SI term is used, which represents the interaction between susceptible and infected populations, it must be determined at what point a balance between the populations is achieved and then it must be analyzed whether this balance is due to the disappearance of the disease or if the disease is persistent.

The equilibrium points are obtained when the three groups into which the population is divided do not change over time, that is, when the equations that describe the model cancel out. It is enough to set equations (5)-(6) equal to zero since it would imply that the change in the immunized population will also be zero since the total population is constant. (J.J. Hernández Cervantes, 2022)

Two balance points were obtained, one free of disease and another where the disease persists, the endemic balance.

The disease-free equilibrium, denoted by E_1 is $E_1 = (S_1, I_1) = \left(\frac{\delta}{p_v}, 0\right)$, since the variable that describes the infected has 0 value, with $\delta = (1-c)P_f$.

It can be verified that the endemic is:

$$E_2 = (S_2, I_2) = \left(\frac{p_i + m + \gamma}{\beta}, \frac{\beta\delta - p_v(p_i + m + \gamma)}{\beta(m + p_i)}\right)$$

The Jacobian matrix for this model will be:

$$J(S, I) = \begin{pmatrix} -(\beta + p_v) & \gamma - \beta S \\ \beta I & -(p_i + m + \gamma) + \beta S \end{pmatrix}$$

Analyzing the first equilibrium point, the eigenvalues of $J(S_1, I_1)$ are $\lambda_1 = -p_v$ and $\lambda_2 = \frac{\delta\beta}{p_v} - \gamma - m - p_i$
.

For E_1 to be a stable node, the eigenvalues need to be negative. Since it has been assumed that $p_v > 0$, the eigenvalue λ_2 will determine the stability.

2.5. Basic Reproductive Number (R_0)

The parameter R_0, called Basic Reproductive Number, has the physical interpretation of the average number of new infections created by a single infected individual in a completely susceptible population (V. Medina Rodríguez, 2024).

The basic reproductive number of this model has the expression

$$R_0 = \frac{\delta\beta}{p_v(p_i + m + \gamma)}, \text{ being } \lambda_2 < 0 \text{ when } R_0 < 1.$$

The disease-free equilibrium is stable as long as $R_0 < 1$, because each infected person infects, on average, less than one person, so the disease tends to disappear.

On the other hand, when analyzing the second equilibrium point, it is not difficult to verify that the eigenvalues of $J(S_2, I_2)$ are

$$\lambda_{1,2} = -\frac{\eta \pm \sqrt[2]{\eta^2 - 4(m+p_i)^2\eta + 4p_v(m+p_i)^3}}{2(m+p_i)}, \text{ with } \eta = \beta\,\delta - p_v\gamma$$

As in the previous case, this equilibrium point will be a stable node if the eigenvalues are negative; then, the values of $\lambda_{1,2}$ determine the stability of this equilibrium point.

Solving the polynomial of degree two with respect to η, corresponding to the square root argument obtained on the right side of our eigenvalues:

$$p(\eta) = \eta^2 - 4(m+p_i)^2\eta + 4p_v(m+p_i)^3 = 0$$

the solutions are:

$$\eta_{1,2} = 2(m+p_i)^2\left(1 \pm \sqrt[2]{1 - \frac{p_v}{m+p_i}}\right)$$

Therefore, the polynomial $p(\eta)$ can be expressed in the following form $p(\eta) = (\eta - \eta_1)(\eta - \eta_2)$ and the eigenvalues rewritten in the following form:

$$\lambda_{1,2} = -\frac{\eta \pm \sqrt[2]{(\eta - \eta_1)(\eta - \eta_2)}}{2(m+p_i)}$$

It would be necessary to analyze the following two cases:

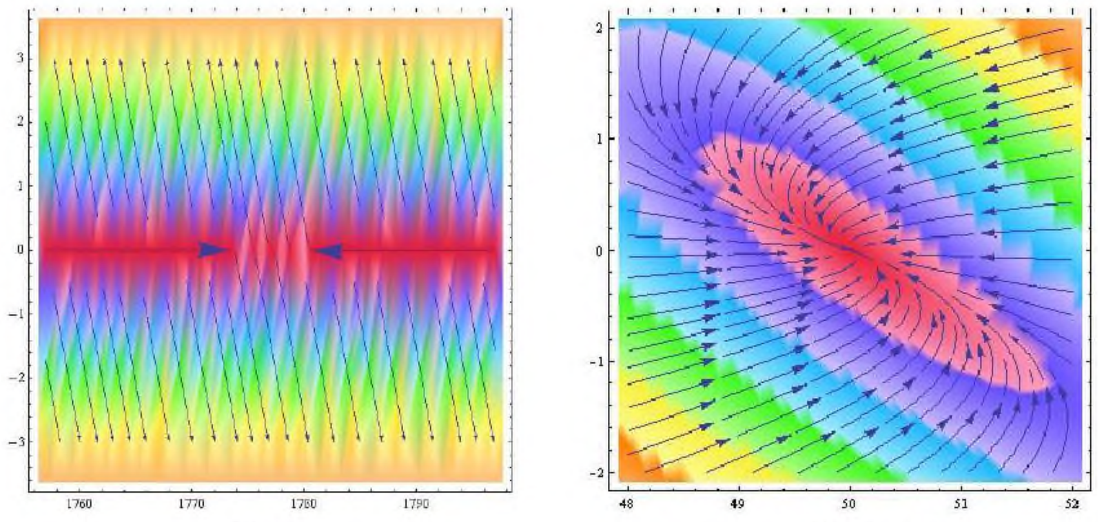
- If $m + p_i + p_v \geq 0$, then the values of $\eta_{1,2}$ will be real positive.
- If $m + p_i + p_v < 0$, then the values of $\eta_{1,2}$ will be imaginary conjugates.

Cases	Subcases	Range of η values	Eigenvalues	Critical point classification
$m + p_i + p_v > 0$	A	$\eta_1 < \eta < \eta_2$	$\lambda_{1,2} \epsilon\, \mathbb{C}, Re(\lambda_{1,2}) < 0$	Stable focus
	B	$\eta > \eta_2$ ó $\eta < \eta_1$	$\lambda_1 < 0, \begin{cases} \lambda_2 > 0\ if\ R_0 < 1 \\ \lambda_2 < 0\ if\ R_0 > 1 \end{cases}$	(i) Unstable saddle point (ii) Stable node
$m + p_i + p_v < 0$	C	para todo valor de η	$\lambda_1 < 0, \begin{cases} \lambda_2 > 0\ if\ R_0 < 1 \\ \lambda_2 < 0\ if\ R_0 > 1 \end{cases}$	(i) Unstable saddle point (ii) Stable node
$m + p_i + p_v = 0$	D	$\eta = \eta_2$ ó $\eta = \eta_1$	$\lambda_1 < 0$ or $\lambda_2 < 0$	Stable focus

Table 1. Classification of critical points.

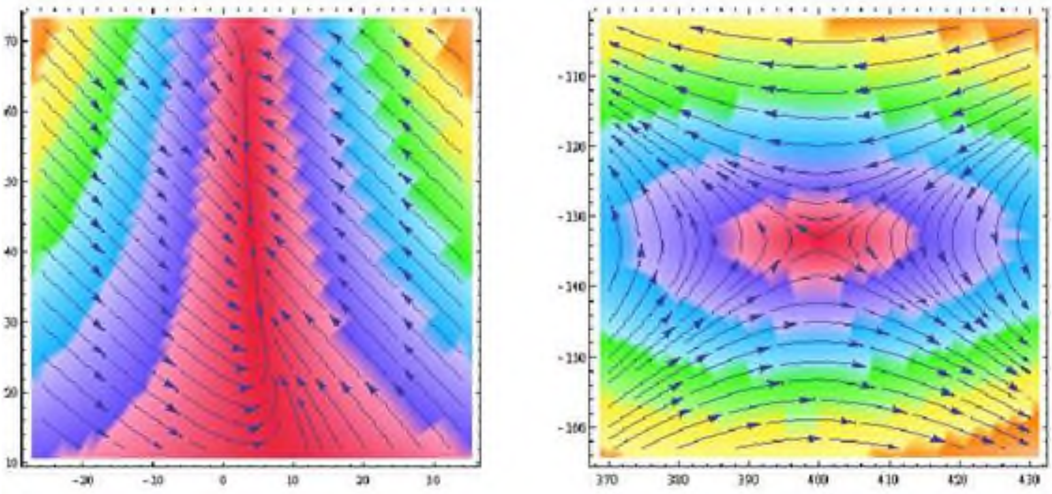
Two examples of the phase plane around the first equilibrium point (S_1, I_1) are shown, where values of R_0respectively greater and less than one were selected.

It can be seen in Figure 6 how, when $R_0 > 1$, the critical point is an unstable saddle point, while for $R_0 < 1$, the critical point is a stable node. It can be noted that there are four trajectories in the form of semi-straight lines with ends at the origin; all the other trajectories have the appearance of branches of a parabola and when tending towards the origin, their slopes tend to the slope of one of the semi-straight lines.



(a) $R_0 > 1$ (b) $R_0 < 1$

Figure 6: Trajectories around the equilibrium point (S_1, I_1).



(a) Stable node point (b) Unstable saddle point

Figure 7**:** Trajectories around the equilibrium point (S_2, I_2).

3. CONCLUSIONS

For this study, the COVID 19 disease was described by means of models defined by a system of ordinary differential equations, presented in (V. Medina Rodríguez, 2024), with initial conditions chosen according to certain measurements and, therefore, inevitably obtained with a certain error. For this reason, the problem arose of analyzing the influence of small variations in the initial conditions on the desired solution.

If arbitrarily small variations of the initial values can change the solution greatly, then the solution determined by the chosen inexact conditions usually has no practical value and cannot even approximately describe the phenomenon studied. Therefore, we pose the problem of finding the conditions under which a sufficiently small change in the initial values causes an arbitrarily small change in the solution.

The qualitative study of these models is of great importance because, to make possible the mathematical description of any real phenomenon, it must inevitably be simplified, idealized, highlighting and taking into account only the most substantial factors that act on it and neglecting the less considerable. Then, the problem inevitably arises as to whether the simplifying assumptions were correctly chosen or not. It is possible that factors not considered strongly influence the phenomenon studied, and change its quantitative and qualitative characteristics. Ultimately this question is resolved in practice, seeing whether or not the conclusions obtained correspond to the experimental data, but in many problems the conditions under which certain simplifications are not possible can be characterized.

The qualitative study of the models is another tool to predict the behavior of the subpopulations under study, since zones of stability can be detected and know exactly where the solutions will converge and whether the transmission dynamics that are simulated will disappear over time or will coexist.

For the linear case, it was obtained that $\varphi^2 - 4\psi$ is always positive for parameter values between 0 and 1 and as $\psi > 0$ and $\varphi < 0$, the solution is an asymptotically stable node, converging to the stationary point.

In the non-linear case, two critical points were obtained, one free of disease and the other endemic. In the first case we conclude that the condition $R_0 < 1$ indicates stability in the system of differential equations, therefore the behavior of the solution is convergent towards the stationary point, which means that the disease will decrease in the population.

On the other hand, around the second critical point there will be stability if $R_0 > 1$.

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