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## RESEARCH ARTICLE

### IDENTIFICATION OF COEFFICIENTS AND PROGNOSIS BY THE SIMPLIFIED MODEL OF DISEASE TRANSMISSION FROM PEOPLE TO PEOPLE

**Annia Ruiz Sánchez<sup>1,\*</sup>, Elvis da Silva Rodrigues<sup>2</sup>, Sandy Sánchez Domínguez<sup>1</sup>, Adolfo A. Fernández García<sup>1</sup> and Antonio I. Ruiz Chaveco<sup>2</sup>**

<sup>1</sup>Faculty of Natural and Exact Sciences, University of Oriente, Santiago de Cuba, Cuba

<sup>2</sup>University of the State of Amazonas, Brazil

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#### ABSTRACT

This article makes use of a model of differential equations that simulates, in a simplified way, the transmission of diseases from people to people; making use of a data table, the coefficients that characterize the model are identified and from this a graph of the system trajectories is made. Here, a period of transmission of COVID 19 in the state of Amazonas is used as data and compared with a period of transmission in the province of Santiago de Cuba. In both cases, it predicts what may happen in a period later than that studied.

#### INTRODUCTION

The problem of prognosing the behavior of a disease is a topical issue, and increasingly important, as this allows health and government authorities to arrive at decision-making to face the health situation presented; the case of the city of Santiago de Cuba can be indicated where, through certain models of the transmission process of COVID 19. Conclusions were reached about the situation of the infection of the population of the province; this allowed the local authorities to know the details of the pandemic situation, thus taking the necessary measures to ensure control of the disease. In (Earn, 2000) this problem was dealt with and day by day the situation was reported and the future behavior was diagnosed by means of graphs and tables that indicated a range of options that were confirmed in the following days, and often this situation was reversed. In health, it is essential to have computational diagnoses of the future behavior of a disease in a person when its symptoms are known; or of a population when certain databases of the behavior of a given epidemic. There are certain software programs that identify the coefficients present in the model and make the corresponding graphs of the possible trajectories. In our case, we used free access software which, as indicated, was last accessed on 07/15/2023. (Python Software Foundation). The PYTHON language is a powerful, syntax-friendly, multi-purpose programming language. Guido Van Rossum, a Dutch programmer, created it in the 80. Its main features are that it

has a wide standard library with different packages and modules to develop different jobs. In addition, there is the Python community that creates many other libraries for various tasks ranging from web development, data science, game creation and much more. Among these libraries, we have SCIPY, used in several areas such as Physics, Engineering and Mathematics itself. It is possible to work, for example, with integrals and optimization, among others; presents an important tool, which is the adjustment of curves, mainly through the CURVE\_FIT function, of the SCIPY.OPTIMIZE submodule. PYTHON is free to access, it can be found on the official PYTHON website, <https://www.python.org/downloads/>, where you can download installers for different operating systems such as Windows and Linux (Python Software Foundation). The processes of contagion by a disease in general are produced from person to person, by some type of contact, through speech, a kiss, among others (Ivorra, 2019; Earn, 2000) there may also be transmission through sexual contact (Soto, 2019). Many of these diseases can become epidemics, (Hamer, 1906; Hethcote, 1994; Hethcote, 1976) as in the case of COVID-19, which became a worldwide epidemic, and even with a percentage of the population vaccinated, several reinfections occurred. There are several examples of works dedicated to the control of epidemics that at the time have prevented major complications. Such as the cases of {2} in Santiago de Cuba where many good results were obtained at these times, (Montero, 2020) and (Zhao, 2020); which were among the first in coping with the COVID-19 pandemic in China; among others where they can be included, (3), (4), (5) and (Halloran, 1994). Although in this work we mainly analyze the transmission of the epidemic produced by SARS-Cov-2, it

\*Corresponding author: **Annia Ruiz Sánchez**

Faculty of Natural and Exact Sciences, University of Oriente, Santiago de Cuba, Cuba

is applicable to other epidemics, such as sexually transmitted diseases, where the fundamental difference lies in the fact that the concentrations between susceptible and exposed individuals are very high (Ruiz, 2020). As consequence of the high transmissibility and lethality of COVID-19, the WHO declared it a public health emergency spread across all continents; affecting a large number of people, which is among the worst cases for human health. Several investigations have been carried out regarding COVID-19; both from the point of view of biochemical characteristics and its treatment, and from the point of view of mathematical modeling to make predictions about its future behavior. Among others that we can cite (Ivorra, 2019); where models by ordinary differential equations are presented, which provide conclusions about the future behavior of the infectious process of the considered population. The model that simulates the appearance of multiple waves that frequently occur in different diseases, especially in COVID-19, is present here, as in the case of Santiago de Cuba more than one wave is perceptible (Yuri, 2022). The essential objective of the present work is to provide health workers with a tool that allows them to guide what can be presented in relation to a patient at a given moment, so that they can make a decision at the right moment that can prevent a crisis. As well as government representatives so that they know the health situation of a region or a country so that measures can be taken to prevent the development of an epidemic with serious consequences for the population (Erick Eduardo Ramirez-Torres, 2020), (Paython Software Fundation, 2023) and (Zhao, 2020).

**MATHEMATICAL MODEL**

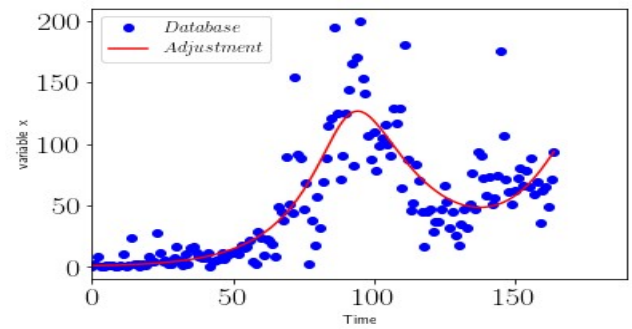
To establish this simplified model for disease transmission we will only consider two states, the population of susceptible individuals and the population of infected individuals, in order to simplify the computational process that we will develop in subsequent works, where  $\tilde{x}_1$  and  $\tilde{x}_2$  are the total number of susceptible individuals at the time  $t$  and the total number of infected individuals at the time  $t$ . Furthermore,  $\bar{x}_1$  and  $\bar{x}_2$  are the values of admissible concentrations of susceptible population and infected respectively, will also the variables  $x_1 = \tilde{x}_1 - \bar{x}_1$  and  $x_2 = \tilde{x}_2 - \bar{x}_2$ . So that, if  $(x_1, x_2) \rightarrow (0,0)$  then  $\tilde{x}_1 \rightarrow \bar{x}_1$  and  $\tilde{x}_2 \rightarrow \bar{x}_2$ , which is our goal, because that way the disease would be controlled and there would be no possibility of an epidemic developing.

The variation of population of the susceptible does not increase or if it increases these values would only reach a maximum value, but they are added in dependence of the concentration of the infected population; on the other hand, the variation of infected population decreases according to the increase of the susceptible, due to the process of recuperation and they are added proportionally to their concentration due to the process of expansion of the disease. Thus, the model will be given by the following system of differential equations.

$$\begin{cases} x_1' = -a_1x_1 + a_2x_2 + X_1(x_1, x_2) \\ x_2' = -b_1x_1 + b_2x_2 + X_2(x_1, x_2) \end{cases}$$

Here the functions  $X_i(x_1, x_2) (i = 1,2)$  represent the action of complementary or control activities carried out by the competent authorities and other physiological activities of the body that may influence the process, as well as any other disturbance that may alter the functioning of our body, favoring

or not the infectious process; these functions are series of potentials that admit the following development



**Fig.1. Santiago de Cuba database and curve fitting**

$$X_i(x_1, x_2) = \sum_{|p| \geq 2} X_i^p x_1^{p_1} x_2^{p_2} \quad (i = 1,2), |p| = p_1 + p_2$$

**The coeficientes indicated in the system have the following meaning:**

$a_1$  represents the decrease in the amount of susceptible as a function of their own concentration.

$a_2$  represents the growth in the amount of susceptible as a function of the concentration of infected people due to recovery.

$b_1$  represents the decrease in the concentration of infected people due to the increase in susceptible.

$b_2$  represents the growth of the concentration of infected people due to their own concentration.

**Remark 1:** It is considered that the initial process is favorable to the development of the disease; otherwise, there would be no infection process. In this case, the signs of the coefficients of the previous development correspond to the characteristics of the problem addressed. The characteristic equation of the linear part of the system has the form,

$$\lambda^2 + (a_1 - b_2)\lambda + (a_2b_1 - a_1b_2) = 0.$$

From here, partial conclusions can be drawn regarding the behavior of the process as a function of the coefficients of variation of the concentrations.

**Theorem 1:** The equilibrium position  $(0,0)$  is asymptotically stable if and only if the conditions  $a_1 > b_2$  and  $a_2b_1 > a_1b_2$  are satisfied.

Making use of the characteristic equation and the conditions of Hurwitz's theorem, in correspondence with the method of first approximation of stability according to Liapunov, one arrives at the result of the theorem.

**Remark2:** When the conditions  $a_1 < b_2$  and  $a_2b_1 > a_1b_2$  are satisfied then, the total concentrations of susceptible and infected people will converge to values of ideal concentrations, therefore, there will be no possibilities for the development of epidemics, otherwise measures must be taken to prevent further complications. Once the coefficients have been identified, this theorem will be used to compare the theoretical result and that

obtained from the geometric point of view depending on the identification made.

## IDENTIFICATION OF COEFFICIENTS AND

### GEOMETRIC REPRESENTATION

Next, the graphical result of the implementation of the model in the PYTHON language is presented, using a curve fitting through the CURVE\_FIT function of the SCIPY.OPTIMIZE submodule of the SCIPY library of the PYTHON language. The database for the period 01/11/2020 to 14/04/2021 of the development of the COVID 19 pandemic in Santiago de Cuba is used here.

**In this case, the following disturbance functions will be used in the system,**

$$X_1 = a_3 x_1^{2m+1} x_2^{2n}$$

$$X_2 = b_3 x_1^{2m} x_2^{2n+1}$$

Dessa forma foram identificados no processo de otimização, tanto os coeficientes  $a_i$  and  $b_i$  ( $i = 1, 2, 3$ ), like the exponents  $m$  and  $n$ .

Because of this process, it was obtained that the coefficients associated with the database indicated above are:

$$a_1 = -0.28$$

$$a_2 = -121591.09$$

$$a_3 = -5.27 \times 10^{-22}$$

$$b_1 = -6.14 \times 10^{-7}$$

$$b_2 = -0.27$$

$$b_3 = 3.73 \times 10^{44}$$

In addition, the best values for  $m$  and  $n$  found were,

$$m = 0.97$$

$$n = 1.09$$

**Remark 3:** If it can be easily verified that the sufficient condition is not satisfied for the total concentrations to converge to the admissible values, this indicates that the pandemic is not under control and therefore the appearance of new cases could increase at any time.

**Remark 4:** It is important to determine the optimal values of the exponents  $m$  and  $n$ , as the series  $X_1$  and  $X_2$  are being replaced by only one term in both cases, and when it comes to critical cases, the behavior of the trajectories is decided by these terms.

Next, the values corresponding to the database are indicated, as well as the optimal adjustment of the curve by the submodule indicated above. Next, using a table of values for the behavior of COVID 19 in the State of Amazonas, the curve is adjusted according to the trajectories of the system (Earn, 2020), where the coefficients are also identified and conclusions about the infection process are given.

$$a_1 = -0.10$$

$$a_2 = 18229.41$$

$$a_3 = -3.36 \times 10^{26}$$

$$b_1 = -9.41 \times 10^{-6}$$

$$b_2 = -14.95$$

$$b_3 = -2.79 \times 10^{-19}$$

$$m = 0.81$$

$$n = 0.58$$

**Observation 6:** Regarding the situation of Santiago de Cuba and the state of Amazonas, it can be inferred that, although the coefficients identified for both cases do not satisfy the conditions of theorem 1, and that, therefore, the cases of infection could multiply at any time, the State of Amazonas indicates a small improvement.

## CONCLUSION

- It is of great importance for health professionals, as well as for government authorities, to carry out a prognosis regarding a given disease, as this allows them to take measures that prevent the appearance of an epidemic.
- When the coefficients of a model that simulates the infection process in relation to a disease are identified, the behavior of the process can be indicated step by step; thus, it is possible the adoption of the necessary measures will put under its control; here lies an extraordinary importance of this process.
- The coefficients identified both in the State of Amazonas and in Santiago de Cuba, do not satisfy the conditions that guarantee the stability of the system (1); this means that there is an absolute lack of control of the disease; alerting health and government authorities to the current situation, as measures are needed to ensure a change in the situation
- The identification of the exponents  $m$  and  $n$  are of extraordinary importance, because when there is a doubtful case, the control or not of the disease is defined by these non-linear terms for which the series was replaced and when this adjustment is optimal, there is more certainty of conclusions regarding the infection process.

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