

## Study of the SIR Model Using Python for the Description of Epidemiological Problems

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### Abstract

*This article aims to investigate the application of the SIR deterministic mathematical model in describing and predicting the spread of infectious diseases in different epidemiological scenarios. To develop this work, we used the Python programming language with the fourth-order Runge-Kutta method, this proved to be valuable tools for studying and predicting the behavior of epidemiological diseases in different sceneries. These techniques can help to better understand the spread and impact of these diseases on the population, contributing to the development of more effective prevention and control strategies.*

**Keywords:** SIR, Python, fourth-order, Runge-Kuttamethod, epidemiological.

### INTRODUCTION

Mathematical modeling has been an important tool in epidemiology to understand the dynamics of the spread of infectious diseases and develop control and prevention strategies. Among the mathematical models used in epidemiology, deterministic models based on differential equations have been widely used to describe the dynamics of infectious diseases in populations.

The SIR model, proposed by Kermack and McKendrick in 1927, is a classic example of a deterministic model used in epidemiology. This model divides the population in to three groups: susceptible, infected and recovered. Differential equations describe the rate of change in the number of individuals in each group over time (Kermack & McKendrick, 1927).

Other deterministic models have been developed to describe the spread of infectious diseases in different contexts. For example, the SEIR (susceptible, exposed, infected, and recovered) model is an extension of the SIR model that includes a class of exposed individuals who have been infected but do not yet have symptoms (Anderson & May, 1991).

Deterministic models are also useful for predicting the evolution of the epidemic in different scenarios and evaluating the impact to control and prevention measures. In a study of the 2009 swine flu pandemic, Ferguson et al.(2005) used a

deterministic model to evaluate the impact of different mitigation strategies, including the use of antiviral drugs and vaccines.

Although deterministic models are useful in describing epidemiological problems, they may not capture all the nuances of disease dynamics in populations. For this reason, simulation-based models are also used in epidemiology. For example, in a study on the spread of SARS-CoV-2 in a Chinese city, Eubank et al.(2004) used a simulation-based model to evaluate the impact of different control measures, such as social isolation and the use of face masks.

The study of deterministic mathematical models in describing epidemiological problems is an area of great relevance and importance for high school students in Brazil. Several academic and scientific works highlight the importance of this topic for the formation of conscious and responsible citizens.

Silva et al.(2020), high light that the study of deterministic mathematical models in the description of epidemiological problems allows students to better understand the dynamics of the spread of infectious diseases in the population and contributes to the formation of more responsible and aware citizens about the importance of following preventive measures.

Oliveira and Santos (2016) highlight the importance of studying mathematical models in solving everyday problems, including epidemiological analysis. The authors emphasize that understanding mathematical concepts is fundamental for interpreting epidemiological data and developing efficient disease control strategies.

Furthermore, the study of deterministic mathematical models in describing epidemiological problems can also be a way to encourage students' interest in mathematics and science. According to Alves et al.(2019), the use of technological resources and the application of mathematical models in the analysis of epidemiological data can make the teaching of mathematics and science more attractive and meaningful for students.

This article aims to investigate the application of the SIR deterministic mathematical model in describing and predicting the spread of infectious diseases in different epidemiological scenarios.

## METHODOLOGY

To develop this work, the following steps were used.

Step 1: Bibliographic review on deterministic models in describing epidemiological problems;

Step 2: Understanding the SIR. The SIR model is one of the most common mathematical models used to study the spread of disease in a population. SIR is an abbreviation for Susceptible, Infected and Recovered. The model divides the population in to three groups: susceptible, who have not yet been infected; infected, who are currently infected; and recovered, who have recovered from the disease and are immune to it. The SIR mathematical model is governed by the differential equations (01) below:

$$\begin{cases} \frac{dS}{dt} = -\frac{\beta IS}{N} \\ \frac{dI}{dt} = \frac{\beta IS}{N} - \gamma I \\ \frac{dR}{dt} = \gamma I \end{cases}$$

Eq. 01

Step 3: Review of the Runge-Kutta Method The Runge-Kutta method is a numerical method used to solve ordinary differential equations (ODEs).The method consists of estimating the value of the solution at a given point, using a weighted combination of increment values at intermediate points.

Step 4: Implementation and Simulation of models in Python Using the Python programming language, implement the SIR model to describe the spread of a disease in a population. Simulating the SIR model involve schooling parameters that describe the disease and the population. Common parameters include transmission rate, recovery rate, and total population. Figure 01 shows the script produced for the SIR model.

```
import matplotlib.pyplot as graph
from numpy import arange

def S0(S): #x
    return -(beta * S * I)
def I0(I): # y
    return (beta * S * I) - gama*I
def RE(I): #a
    return gama * I

for t in tp:
    sus.append(S)
    inf.append(I)
    rec.append(R)
    k1x = h * S0(S)
    k1y = h * I0(I)
    k1a = h * RE(I)

    k2x = h * S0(S + 0.5 * k1y)
    k2y = h * I0(I + 0.5 * k1a)
    k2a = h * RE(I + 0.5 * k1x)

    k3x = h * S0(S + 0.5 * k2y)
    k3y = h * I0(I + 0.5 * k2a)
    k3a = h * RE(I + 0.5 * k2x)

    k4x = h * S0(S + k3y)
    k4y = h * I0(I + k3a)
    k4a = h * RE(I + k3x)

    S += (k1x + 2 * k2x + 2 * k3x + k4x) / 6
    I += (k1y + 2 * k2y + 2 * k3y + k4y) / 6
    R += (k1a + 2 * k2a + 2 * k3a + k4a) / 6

graph.plot(tp,sus, 'g', label="Suscetiveis")
graph.plot(tp,inf, 'r', label="infectado")
graph.plot(tp,rec, 'y', label="recuperados")
graph.xlabel('dias')
graph.ylabel('população')
graph.legend()
graph.show()
```

Figure 01: Script for the SIR model.

Step 5: Viewing the results after the simulation, the results must be visualized in graphs, showing the evolution of the number of susceptible, infected and recovered individuals over time. These plots can be generated using Python library like Matplotlib lib.

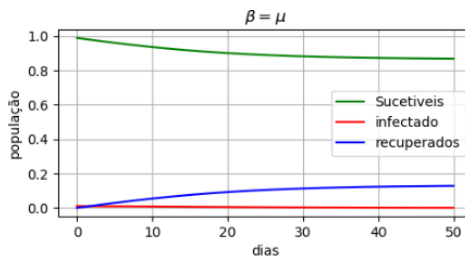
To obtain better results, a script was developed using the fourth-order Runge-Kutt a numerical method, adopting the following data: susceptible, infected, recovered, population, infection rate and recovery rate. We ran the graphs with the percentage of the population in relation to the days on which the disease spread.

## DISCUSSION OF RESULTS:

In summary, the choice to represent the population as a percentage presented in the graphs was made to facilitate understanding, comparison and manipulation of the data, making the results more accessible and intuitive for analysis. This choice assesses the impact of the disease in relation to the total population more conveniently. The choice of days in the SIR model simulation aims to improve computational efficiency, as a simulation with fewer days requires fewer calculations and, therefore, is executed more quickly and to visualize the results clearly.

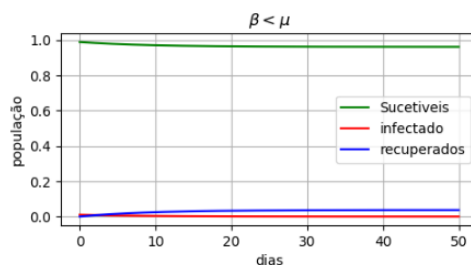
When the infection rate and recovery rate are equal, we present the following result, as shown in Graph 1.

The infection rate is equal to the recovery rate parameter which results in an epidemic that speaks and then gradually declines, without ever completely disappearing. This is because the infection rate equals the recovery rate, meaning that on average, each infected person infects exactly one other person before recovering. As a result, the number of infected individuals remains constant over time.



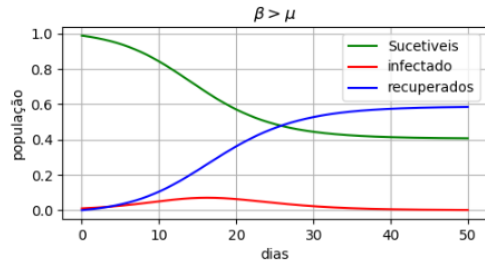
**Graph 1: Evolution of a given disease when the infection rate and recovery rate are equal in the SIS model.**

In graph 2, we show when the infection rate is lower than the recovery rate. When this occurs, the disease does not spread very efficiently in the population, as shown in the graph. In this case, the disease will reach a peak and then gradually sub side, eventually disappearing.



**Graph 2: Evolution of a given disease when the infection rate is lower than the recovery rate in the SIS model.**

Graph 3 shows when the infection rate is higher than the recovery rate. This condition indicates that the disease spreads quickly throughout the population, as shown in the graph. In this case, the disease can become an epidemic, with a large number of people infected.



**Graph 3: Evolution of a given disease infection rate is greater than the recovery rate in the SIS model.**

### FINAL CONSIDERATIONS:

In conclusion, the use of deterministic models, such as the SIR model, and programming in Python with the fourth-order Runge-Kutt a method have proven to be valuable tools for studying and predicting the behavior of epidemiological diseases in different scenarios as presented in results. These techniques can help to better understand the spread and impact of these diseases on the population, contributing to the development of more effective prevention and control strategies.

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