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GENERALIZATION OF THE SIRM EPIDEMIOLOGICAL MODEL WITH NUMERICAL SOLUTION VIA RUNGE-KUTTA FOR MULTIPLE INFECTIOUS DISEASES IN AN INTERACTIVE ENVIRONMENT

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ABSTRACT

This work proposes an extension and generalization of the SIRM epidemiological model, previously applied to COVID-19, to simulate the evolution of various infectious diseases. The system of ordinary differential equations is solved using the fourth-order Runge-Kutta method, known for its accuracy and stability. The developed system is implemented in the Python programming language with an interactive interface, allowing the selection of different diseases, automatic parameterization, and export of results. The goal is to provide an educational and decision-support tool for researchers and public health managers.

I. INTRODUCTION

Mathematical modeling has been a powerful tool in analyzing the dynamics of infectious diseases, especially in the context of outbreaks and pandemics. By constructing systems of differential equations that describe the transition of individuals between different health states (such as susceptible, infected, and recovered), models like SIR (Susceptible-Infected-Recovered) and its extensions enable the understanding and prediction of epidemic evolution over time. The SIRM model, in turn, adds a compartment for deaths (M - Mortality), offering a more realistic view for diseases with significant lethality. Although simplified, these models are useful for estimating the infection peak, the duration of an outbreak, and the impact of intervention measures.

During the COVID-19 pandemic, numerous studies applied variations of the SIR model to simulate the virus's spread in different regions, such as the baseline study used in this work, which applies the SIRM model to COVID-19 in the state of Bahia using the fourth-order Runge-Kutta method implemented in C. Despite the robustness of the numerical method employed, these applications are generally limited to a single disease, require manual code rewriting for new scenarios, and lack flexibility for interactive simulation. Therefore, there is a need for a more general, accessible, and reusable solution that can be used by both researchers and health professionals, even those without technical programming backgrounds.

In this context, this work proposes an expansion of the SIRM model through the implementation of a universal system in the Python programming language, capable of simulating different infectious diseases based on previously known or expert-defined parameters. The tool uses the fourth-order Runge-Kutta method to numerically solve the model’s differential equations, ensuring stability and good accuracy in the simulations. Furthermore, an interactive interface based on widgets was developed, allowing the user to select the disease, adjust the simulation period, and visualize the results graphically, in addition to exporting the data in CSV format. This approach aims to make epidemiological modeling more accessible and useful in educational, academic, and operational settings, promoting a solid foundation for scenario analysis and decision-making in public health [1].

II. THEORETICAL REFERENCE

Compartmental epidemiological models are widely used to mathematically represent the dynamics of infectious diseases in populations. Among the classical models, the SIR (Susceptible-Infected-Recovered) model, proposed by Kermack and McKendrick in 1927, stands out by dividing the population into three groups: susceptible (S), infected (I), and recovered (R). The variation in the number of individuals in each compartment over time is described by a system of ordinary differential equations (ODEs), which considers the transmission and recovery rates of the disease. The SIRM model is an extension of the SIR model, with the addition of a fourth variable: deaths (M), allowing the representation of diseases with a significant mortality rate. This model assumes a closed population, where the sum of all compartments remains constant, disregarding births and migrations. The system of differential equations that defines the SIRM model is given by:

$$\frac{dS}{dt} = -\beta \cdot \frac{S \cdot I}{N} \tag{1}$$

$$\frac{dI}{dt} = \beta \cdot \frac{S \cdot I}{N} - \gamma \cdot I - \mu \cdot I \tag{2}$$

$$\frac{dR}{dt} = \gamma \cdot I \tag{3}$$

$$\frac{dM}{dt} = \mu \cdot I \tag{4}$$

Where:

- β represents the transmission rate;
- γ is the recovery rate;
- μ is the mortality rate;
- $N = S + I + R + M$ is the total population.

To numerically solve this system of ODEs, various methods can be employed. Among them, the Euler method is the simplest, but it presents limitations in terms of stability and precision, especially in long-term simulations. Therefore, this study adopts the fourth-order Runge-Kutta method (RK4), widely used for its balance between computational efficiency and accuracy. RK4 calculates the evolution of the variables in discrete time steps with reduced truncation error compared to lower-order methods. In the RK4 method, each new state estimate is obtained based on four intermediate approximations (k1, k2, k3, k4), which ensures greater fidelity to the exact solution of the ODE. This characteristic is particularly important in epidemiological models, where small variations in parameters can lead to significant differences in simulated outcomes.

III. METHODOLOGY

This work was grounded in a Systematic Literature Review (SLR) on the application of the Runge-Kutta method, with an emphasis on its use in solving ordinary differential equations related to dynamic modeling. The review highlighted that the fourth-order Runge-Kutta method (RK4) offers excellent performance in terms of precision, stability, and applicability, and is widely adopted in epidemiological studies. These findings supported the methodological choice of this project, which aims to build a generalizable and accessible epidemiological model. Based on this theoretical foundation, the SIRM model was implemented in the Python programming language, with an emphasis on flexibility and usability. The system allows users to simulate different infectious diseases using a predefined and easily customizable set of parameters.

Numerical resolution of the model was performed through a manual implementation of the RK4 method, rather than using built-in solutions like *odeint*, to maintain full control over the algorithm and reinforce the educational nature of the tool. The parameters for each disease — such as the transmission rate (β\beta), recovery rate (γ\gamma), and mortality rate (μ\mu) were originally organized in a Python dictionary containing characteristics of diseases such as COVID-19, H1N1, Dengue, Measles, and Malaria. This structure allows for the easy addition of new diseases, making the system scalable and adaptable to various epidemiological contexts.

The simulation takes place in an interactive environment built with *ipywidgets*, where the user can:

- Select the disease to simulate;
- Define the number of prediction days;
- Visualize the evolution of population compartments over time (S, I, R, M);
- Export results in .csv format for further analysis.

The tool was published in Google *Colab* to ensure open and free access, reinforcing its educational and public-oriented character. The notebook is available at:

Figure 1: https://colab.research.google.com/drive/1frnET5lu9mYqsOPviZLU17hi4JzFsfOv?usp=sharing,
Source: Authors, (2025).

This methodological approach combines mathematical rigor, technical foundation, and practical accessibility, making the model suitable for both educational purposes and decision support in public health contexts. To enhance interactivity and pedagogical utility, the interface was expanded to allow manual selection of key epidemiological parameters. Users can adjust the transmission rate, recovery rate, and mortality rate using sliders, which enables the exploration of various hypothetical scenarios without modifying the source code. This feature transforms the tool into a flexible environment for educational use, comparative simulations, and parameter sensitivity analysis.

IV. BIBLIOGRAPHIC REVIEW

IV.1 RUNGE-KUTTA METHOD AND NEURAL NETWORKS FOR NUMERICAL APPROXIMATION OF ORDINARY DIFFERENTIAL EQUATIONS

In this article, a combination of numerical methods and artificial intelligence is employed to obtain solution points for an initial value problem [2], based on the justification that numerical methods are often more efficient than analytical ones when dealing with nonlinear problems in Engineering and Science. The authors train a neural network to approximate the solution using data points generated by the fourth-order Runge-Kutta method (RK-4). Both the numerical method and the neural network are implemented in Python. The results show that the hybrid model outperforms the RK-4 method when both are applied with the same number of points over an extended interval but does not surpass RK-4 when it uses a fixed step size — highlighting the importance of choosing an appropriate numerical step. Moreover, the hybrid model performs better than a previous version based on Euler's method, especially in problems involving more challenging parameters. The study concludes that, although promising, the approach requires further optimization of the neural network architecture to improve its generalization, suggesting future investigations into adaptive loss functions and more complex network structures.

IV.2 SIR MODEL SOLUTION USING 2ND ORDER RUNGE-KUTTA

The SIR model (Susceptible-Infected-Recovered) is an epidemic forecasting model that uses the number of infected individuals within a population to predict the progression of a disease. Menezes and Santos (2021) applied the SIR model, along with its components and a second-order Runge-Kutta algorithm, to simulate the progression of COVID-19 in the state of Paraíba, Brazil. The authors calculated the contagion rate and recovery factor using real data. The method was tested over two different periods: July 2020 and April 2021. The results show that the estimates were accurate during the early stages, but less reliable in later phases, due to the underestimation of the transmission rate once the infection had become widespread. It was concluded that the SIR model with Runge-Kutta is effective in the initial phases of an epidemic but requires adjustments or alternative methods for later stages, when the dynamics of contagion become more complex [3].

IV.3 SIRM POPULATION DYNAMICS MODELING APPLIED TO COVID-19 IN THE STATE OF BAHIA USING THE 4TH ORDER RUNGE-KUTTA METHOD

During the COVID-19 pandemic, the state of Bahia experienced a high number of infections and deaths due to its large population. While the SIR model was used across the country to predict local disease progression, [1] proposed an adaptation of the model to SIRM (Susceptible-Infected-Recovered-Deceased) and developed a computational implementation of the fourth-order Runge-Kutta method in C to solve the SIRM system. The authors analyzed real data from July to August 2021, adjusting parameters such as transmission, recovery, and mortality rates. The results showed high accuracy in estimating cumulative deaths, with a relative error of less than 2%, and satisfactory performance for active and new cases, despite some discrepancies attributed to underreporting and weekend data delays. The study concluded that the model is effective for short-term forecasting and useful for guiding public policies, highlighting the viability of numerical methods in epidemiology even when simplifications — such as excluding reinfections and vaccination — are made. The source code is publicly available for replication and future improvements.

IV.4 4th ORDER EULER AND RUNGE-KUTTA METHODS USING A GEOGEBRA APPLET

This article presents the development of an interactive applet in GeoGebra designed to teach and compare the numerical methods of Euler, Improved Euler, and fourth-order Runge-Kutta in solving Initial Value Problems (IVPs) associated with Ordinary Differential Equations (ODEs). The applet allows users to input an ODE and an initial condition, view approximate solutions, and adjust the step size h, facilitating the understanding of the relationship between accuracy and step size. Bezerra and Ramos (2020) demonstrate, through examples, that the Runge-Kutta method provides greater accuracy compared to the Euler and Improved Euler methods. The applet, available online, serves as an accessible educational tool that does not require advanced programming knowledge and can be adapted for other types of ODEs [4].

IV.5 INTEGRATING ARTIFICIAL INTELLIGENCE WITH MECHANISTIC EPIDEMIOLOGICAL MODELS

Recent research has explored the integration of artificial intelligence with mechanistic epidemiological models to enhance their predictive capabilities. [5] proposed a framework that combines traditional compartmental models, such as SEIR, with deep learning components to adjust parameters dynamically and improve forecasting in real-time. Their results indicate that hybrid approaches can outperform purely data-driven or purely mechanistic models, especially when working with incomplete or noisy epidemiological data. This integration represents a significant advancement in the adaptability and accuracy of simulation tools used in public health monitoring and planning.

IV.6 COMPARISON OF NUMERICAL SIMULATION OF EPIDEMIOLOGICAL MODEL BETWEEN EULER METHOD WITH 4TH ORDER RUNGE KUTTA METHOD

The choice of numerical method can significantly impact the accuracy of simulations in compartmental epidemic models. [6] conducted a comparative analysis between the Euler method and the fourth-order Runge-Kutta method (RK4) applied to the SIR model. Their findings confirmed that RK4 produces more stable and accurate results, especially in long-term simulations or when the system exhibits nonlinear dynamics. The study reinforces the rationale for choosing RK4 in scenarios where computational reliability is critical.

IV.7 NEURAL NETWORKS TO MODEL COVID-19 DYNAMICS AND ALLOCATE HEALTHCARE RESOURCES

The use of neural networks to model disease progression has gained prominence due to their capacity to learn nonlinear relationships from data. [7] applied a neural network-based model to predict the dynamics of COVID-19 and allocate healthcare resources efficiently. By training the model with real-world case data, they achieved high accuracy in forecasting short- and mid-term infection curves. Their approach demonstrates the effectiveness of combining AI methods with epidemiological modeling, especially in rapidly evolving scenarios like pandemics.

IV.8 NEURAL NETWORK-ENHANCED DISEASE SPREAD DYNAMICS OVER TIME AND SPACE

Caga-anan (2024) proposed the use of neural networks to dynamically estimate epidemiological parameters in models that evolve over time and space. The study introduced a hybrid approach where a neural network is trained to adjust parameters such as transmission and recovery rates based on synthetic time-series data. This approach enhances the model's adaptability to changing conditions and opens new possibilities for real-time forecasting in public health applications [8].

V. DISCUSSION

The implementation of the SIRM model using the fourth-order Runge-Kutta method (RK4) was successfully applied to simulate various epidemiological scenarios of infectious diseases, including COVID-19, H1N1, Dengue, Measles, and Malaria. The parameters used in each simulation were obtained from scientific literature or based on realistic estimates of transmission, recovery, and mortality rates. The use of a configurable disease dictionary and an interactive graphical interface allowed for quick adaptation of the model to different contexts, highlighting the flexibility of the proposed approach. The generated plots showed that the model was able to reproduce epidemiological behaviors consistent with expectations for each disease.

In the case of COVID-19, for example, the simulation exhibited a marked peak in infections followed by stabilization as individuals transitioned to the recovered or deceased compartments. For highly contagious diseases like Measles, the growth of the infected population was more explosive, while for vector-borne diseases such as Dengue and Malaria, the model still generated useful dynamics despite the simplification of not explicitly modeling the vector (e.g., mosquitoes). Figures 1 to 4 show simulations generated by the SIRM model for COVID-19, H1N1, Measles, and Malaria, respectively. The results highlight the model's ability to represent different epidemic patterns and validate its application to diverse diseases.

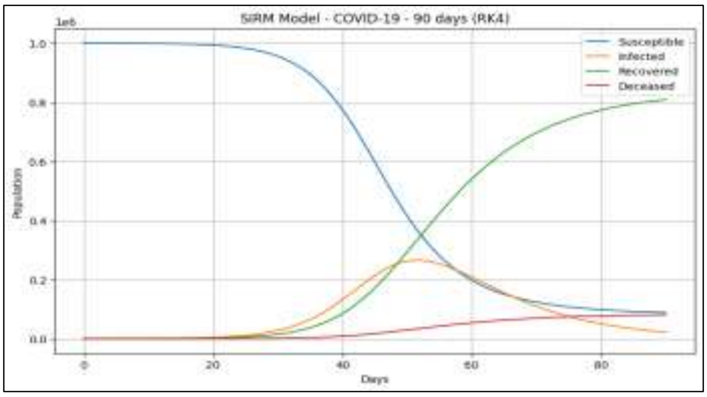

Figure 2: Simulation of the COVID-19 epidemic using the SIRM model over a 90-day period.
Source: Authors, (2025).

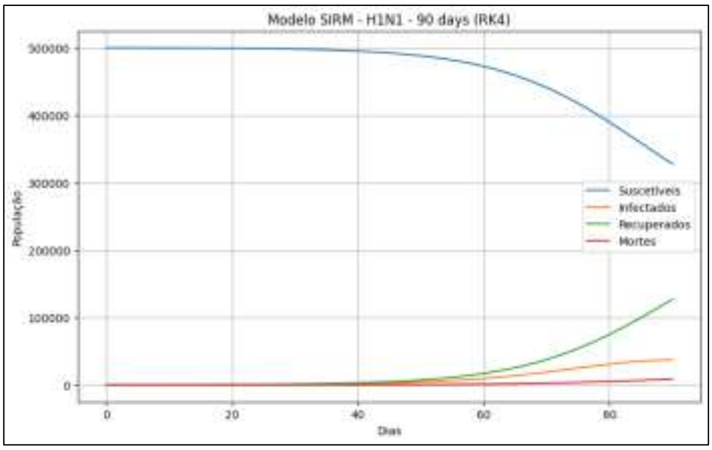

Figure 3: SIRM model simulation for H1N1 over 90 days.
Source: Authors, (2025).

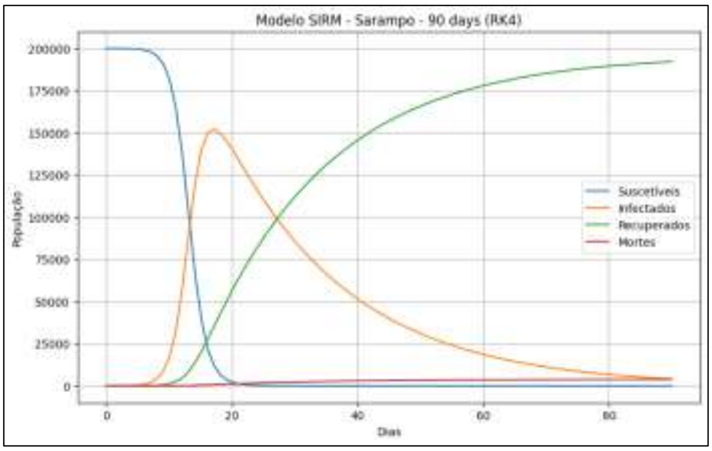

Figure 4: Simulation results for Measles.
Source: Authors, (2025).

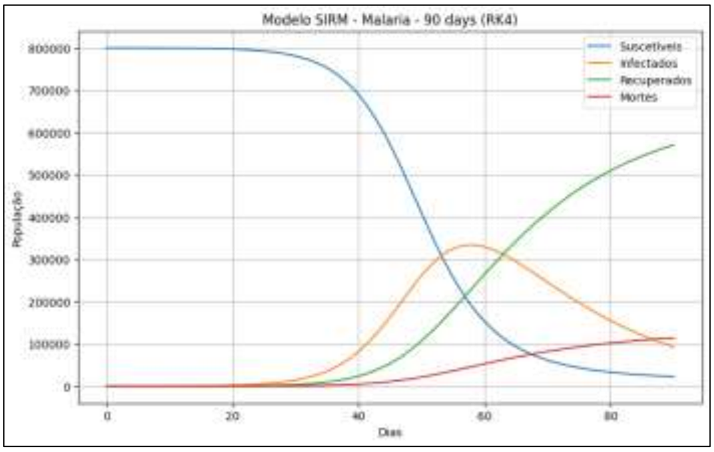

Figure 5: Simulation of Malaria dynamics.
Source: Authors, (2025).

Exporting the results to CSV files enabled quantitative analysis of the S, I, R, and M values over time. These data can be used for comparative studies, calibration with real-world datasets, and as support for decision-making processes — providing insights into potential strategies such as vaccination campaigns, social distancing policies, or hospital resource allocation. Regarding the numerical method employed, the RK4 method proved to be highly effective, delivering stable and accurate results in all simulations. When compared to lower-order methods such as explicit Euler, RK4 was found to be less sensitive to oscillations and numerical errors, especially in long-term simulations or in scenarios involving high parameter sensitivity.

Execution time remained efficient even in simulations ranging from 90 to 180 days. Another important feature of the system is its accessibility. Implemented in Python with an interactive interface built using *ipywidgets*, the model can be used in educational settings, workshops, or training environments, enabling users with little to no programming experience to explore different epidemiological scenarios in a visual and intuitive way. This sets it apart from previous static implementations, such as the C-language version focused solely on COVID-19, which offered little flexibility for generalization or interaction.

Despite the promising results and flexibility of the proposed SIRM-based simulation system, several limitations must be acknowledged. First, the current model does not account for vector-borne transmission dynamics, which are essential for accurately modeling diseases such as Dengue and Malaria. These infections involve mosquito vectors, and their population behavior significantly influences the spread of the disease — a factor not captured in the present formulation. Additionally, the model assumes a closed population with no reinfection, vaccination, migration, or seasonal effects, which limits its realism in long-term or complex epidemiological contexts.

Another constraint is related to the fixed-step fourth-order Runge-Kutta method: while it offers strong accuracy and stability, it may not be optimal for scenarios involving rapid changes or multiple peaks, where adaptive time-stepping methods could perform better. Lastly, the simulations rely on predefined parameters and not real-time epidemiological data, which restricts the model's capacity for real-world forecasting without external calibration. Although the model is a simplification of reality, it provides a solid foundation for preliminary outbreak studies and can be expanded to include new compartments (e.g., vaccinated, hospitalized, exposed) or integrated with real-time data. The modularity of the current implementation makes it a promising starting point for more advanced applications in computational epidemiology.

VI. CONCLUSION

This study presented an expansion of the SIRM epidemiological model, aiming to make it more flexible, accessible, and applicable to various infectious diseases. The implementation in Python, combined with the numerical solution provided by the fourth-order Runge-Kutta method (RK4), enabled the creation of an efficient and interactive system capable of simulating multiple epidemiological scenarios with precision and stability. Unlike static models tailored to specific diseases, such as COVID-19, the proposed solution incorporates a parameterized disease dictionary, allowing for model generalization without code rewrites. The use of an interactive graphical interface makes the tool suitable for use by non-programmers, broadening its potential in educational, research, and public health contexts.

The simulations demonstrated that the model successfully captured the dynamic behavior of various diseases. The automatic generation of plots and export of simulation results in CSV format further enhanced the system's utility for quantitative analysis and health planning.Future work may include the integration of new compartments into the model (e.g., vaccinated or exposed individuals), connection to real-world epidemiological databases via APIs, and the use of machine learning techniques to automatically calibrate parameters based on historical data. The current system's modular design provides a robust foundation for these future developments, with strong potential to support real-time outbreak monitoring and control.

VII. AUTHOR'S CONTRIBUTION

Conceptualization: Matheus Eduardo Amazonas Costa and Manoel do Socorro Santos Azevedo.
Methodology: Manoel do Socorro Santos Azevedo.
Investigation: Matheus Eduardo Amazonas Costa and Manoel do Socorro Santos Azevedo.
Writing – Original Draft: Matheus Eduardo Amazonas Costa and Manoel do Socorro Santos Azevedo.
Writing – Review and Editing: Matheus Eduardo Amazonas Costa and Manoel do Socorro Santos Azevedo.
Resources: Manoel do Socorro Santos Azevedo.
Supervision: Matheus Eduardo Amazonas Costa and Manoel do Socorro Santos Azevedo.
Approval of the final text: Matheus Eduardo Amazonas Costa and Manoel do Socorro Santos Azevedo.

VII. REFERENCES

[1] G. C. Clemente, J. G. C. Cassimiro, J. W. F. Queiroz et al., Modelagem da Dinâmica Populacional SIRM Aplicada à COVID-19 no Estado da Bahia Pelo Método de Runge-Kutta de 4ª Ordem, Recife, Brasil: Anais do Encontro Nacional de Modelagem Computacional e Encontro de Ciência e Tecnologia de Materiais, 2021. DOI: 10.29327/154013.24-72.

[2] G. S. Hida and C. S. Hida, Método de Runge-Kutta e redes neurais para aproximação numérica de equações diferenciais ordinárias, Revista Interface Tecnológica, Taquaritinga, SP, vol. 21, no. 1, pp. 257–267, 2025. DOI: 10.31510/infa.v21i1.1965.

[3] J. L. Menezes Neto and T. J. Santos Neto, Resolução do modelo SIR através de Runge-Kutta de 2ª ordem. ResearchGate, 2022. [Online]. DOI indisponível.

[4] F. Bezerra and M. Ramos, *Métodos de Euler e Runge-Kutta de 4ª ordem por meio de um applet do Geogebra*, Revista Professor de Matemática On-line, vol. 8, no. 1, pp. 1–10, 2020. DOI: 10.21711/2319023x2020/pmo82.

[5] R. Salomon, J. Liu, M. Chughtai, M. Miura-Kochi, and D. He, Integrating artificial intelligence with mechanistic epidemiological models, Nature Communications, vol. 15, no. 1, 2024. DOI: 10.1038/s41467-024-47191-7.

[6] M. Ashgi, M. Rafiqul Islam, and Z. M. Aspar, Comparison of numerical simulation of epidemiological model between Euler method with 4th order Runge Kutta method, International Journal of Global Operations Research, vol. 2, no. 1, pp. 37–44, 2021. DOI: 10.5281/zenodo.4652107.

[7] A. Kumar, S. Gupta, M. Fernandes, and L. T. Wei, Neural networks to model COVID-19 dynamics and allocate healthcare resources, Scientific Reports, vol. 15, no. 1, 2025. DOI: 10.1038/s41598-025-11011-3.

[8] R. L. Caga-anan, Neural Network-Enhanced Disease Spread Dynamics Over Time and Space, arXiv preprint arXiv:2410.20592, 2024.