# SIR MODEL APPLIED TO THE SPREAD OF DENGUE IN SÃO PAULO

## **ABSTRACT**

This article presents the application of the SIR (Susceptible, Infected, and Recovered) epidemiological model to analyze the spread of dengue in the city of São Paulo. Using real incidence data, the model was adjusted to estimate the infection rate ( $\beta$ ) and predict the epidemic's progression. The simulation allows for understanding the disease dynamics and assessing possible mitigation measures.

### INTRODUCTION

Dengue is a mosquito-borne viral infection that poses a significant public health challenge, particularly in tropical and subtropical regions. It is caused by the dengue virus (DENV), which is transmitted to humans primarily by *Aedes aegypti* mosquitoes. Dengue infections can range from mild flu-like symptoms to severe complications such as hemorrhagic fever and dengue shock syndrome, which can be fatal. In densely populated urban areas like São Paulo, the combination of high human density and favorable environmental conditions for mosquito proliferation increases the risk of outbreaks.

To understand and mitigate the spread of infectious diseases such as dengue, mathematical models play a crucial role. One of the most widely used models in epidemiology is the SIR model, which categorizes a population into three compartments: Susceptible (S), Infected (I), and Recovered (R). The SIR model helps analyze the transmission dynamics of diseases and predict epidemic trends based on parameters such as infection and recovery rates. By applying the SIR model to real epidemiological data, it becomes possible to estimate key variables influencing the progression of an outbreak and assess the potential impact of intervention strategies.

This study focuses on implementing the SIR model using real-world dengue data from the city of São Paulo. The aim is to analyze the historical evolution of the disease, estimate the infection rate ( $\beta$ ), and provide insights into how dengue spreads over time within an urban population. Through computational modeling, we seek to contribute to a better understanding of dengue epidemiology and support public health efforts in designing effective control measures.

## **METHODOLOGY**

The SIR model divides the population into three groups:

• Susceptible (S): Individuals who can contract the disease.

- Infected (I): Individuals currently infected and capable of transmitting the disease.
- Recovered (R): Individuals who have recovered and acquired immunity.

The data used were obtained from epidemiological records and processed using the Python programming language. Data normalization and linear regression were performed to estimate the infection rate ( $\beta$ ). The code was developed using Pandas, NumPy, Matplotlib, and scikit-learn libraries.

### RESULTS AND DISCUSSION

The generated graphs demonstrate the evolution of the disease in the population, showing fluctuations in the S, I, and R groups over the weeks. Data normalization allowed for better visualization of trends and epidemic phases. The analysis of the  $\beta$  parameter revealed disease transmission patterns and helped identify critical moments of the epidemic. However, despite its effectiveness, the SIR model is not the most suitable for modeling dengue, as it does not account for crucial factors such as vector dynamics and environmental influences.

## CONCLUSION

The application of the SIR model to dengue data in São Paulo enabled the analysis of epidemic dynamics and its progression. The results highlight the importance of mathematical models in outbreak prediction and supporting disease control policies. However, while the SIR model is a powerful tool, it is not the most appropriate for modeling dengue, as it omits important parameters such as vector population dynamics and climatic factors that significantly influence disease transmission. Future work should incorporate additional variables, such as seasonality and intervention measures.

#### REFERENCES

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