

# Retrospective Analysis - Modeling the 2008 Dengue surge in Rio de Janeiro, Brazil

Lalitha Gadde ; Sri Haneesha Davuluri

Department of Computer Science

## INTRODUCTION

- Dengue fever, a severe mosquito-borne illness, has seen a dramatic global rise over the past fifty years, with Brazil, particularly Rio de Janeiro, being a major hotspot.
- The city has experienced five significant epidemics since 1986, with all four Dengue Virus (DENV) serotypes circulating and causing widespread urban outbreaks.
- Aedes Aegypti mosquitoes are the main transmitters in the Americas.
- In early 2008, Rio faced a drastic increase in dengue cases, with a 2.2-fold rise from the previous year, accounting for 38% of Brazil's total cases.
- On 2 April 2008, the State of Rio de Janeiro reported 57010 cases of dengue fever (DF) including 67 confirmed deaths and 58 deaths.

## DATA

- Data regarding dengue cases was obtained from DATASUS [4], the Ministry of Health's official online resource in Brazil (gov.br).
- The temperature and precipitation information for Rio de Janeiro was compiled from the Weather Underground website.
- Daily average temperatures were used, and due to the unavailability of daily precipitation figures, monthly average values were employed to estimate daily precipitation.

## MODEL DEVELOPMENT

Variable	Description	Value
NH	Total Human Population	6093472
NV	Total Vector Population	3 * NH
E_s0	Initial Susceptible Eggs	1000
L_s0	Initial Susceptible Larvae	1000
P_s0	Initial Susceptible Pupae	1000
E_i0	Initial Infected Eggs	1000
L_i0	Initial Infected Larvae	1000
P_i0	Initial Infected Pupae	1000
A_em_s0	Initial Susceptible Emerging Adults	NV/4
A_h_s0	Initial Susceptible Host-Seeking Adults	NV/4
A_g_s0	Initial Susceptible Gonotrophic Adults	NV/4
A_o_s0	Initial Susceptible Ovipositing Adults	NV/4
A_h_e0	Initial Exposed Host-Seeking Adults	1000
A_g_e0	Initial Exposed Gonotrophic Adults	1000
A_o_e0	Initial Exposed Ovipositing Adults	1000
A_em_i0	Initial Infected Emerging Adults	1000
A_h_i0	Initial Infected Host-Seeking Adults	1000
A_g_i0	Initial Infected Gonotrophic Adults	1000
A_o_i0	Initial Infected Ovipositing Adults	1000
H_s0	Initial Susceptible Humans	NH
H_e0	Initial Exposed Humans	0
H_i0	Initial Infected Humans	1
H_r0	Initial Recovered Humans	0

Table 1: Initial Conditions- Fitted Values and from [1]

Variable	Description	Value
beta	Number of eggs laid by ovipositing females (per females)	300
rho	Probability of vertical transmission	0.078
d_tp	Dengue transmission probability per bite	0.216
d_mi	Dengue incubation rate in mosquitoes per day	0.1
r	Recovery rate from dengue, Humans	1/5
mu_E	Egg mortality rate per day	0.1
mu_L	Minimum larva mortality rate per day	0.08
mu_P	Minimum pupa mortality rate per day	0.1
mu_em	Mortality rate during adult emergence per day	0.17
mu_A	Minimum adult mortality rate per day	1/30
T_E	Minimal temperature needed for egg development in Celsius	16
T_DD_E	Total number of degree-days necessary for egg development in Celsius	42
gamma_Aem	Development rate of emerging adults per day	0.25
gamma_Ao	Transition rate from oviposition site-seeking to host-seeking adults per day	2
gamma_H	Progression rate from exposed to infectious human	1/5.5
T_Ag	Minimal temperature needed for egg maturation in Celsius	9.9
T_DD_Ag	Progression rate from exposed to infectious human	36
sigma	Sex-ratio at the emergence	0.5
t0	Time value after which new infectious people are introduced in days	30
CR	Contact Rate in percentage	50
immunity	Time period during which a person remains immune to reinfection	1/60

Table 2: Model Parameters, referenced from [5]

## METHODOLOGY

Our project employs a compartmental model approach, integrating both the SEIRS (Susceptible, Exposed, Infected, Recovered, Susceptible) model for human populations and the SEI (Susceptible, Exposed, Infected) model for mosquito vectors. The methodology is designed to simulate the transmission dynamics of dengue fever in Rio de Janeiro in the year 2008, capturing the interaction between humans and mosquitoes and the impact of environmental factors on disease spread.

**Model Structure:**

- Human SEIRS Model:** Tracks the human population's transition through the susceptible, exposed, infectious, and recovered stages.
- Mosquito SEI Model:** Simulates the mosquito life cycle, including the susceptible, exposed, and infectious phases.
- Mosquito Life cycle Integration:** Incorporates the developmental stages of mosquitoes—eggs, larvae, pupae, and adults—to account for vector population dynamics.

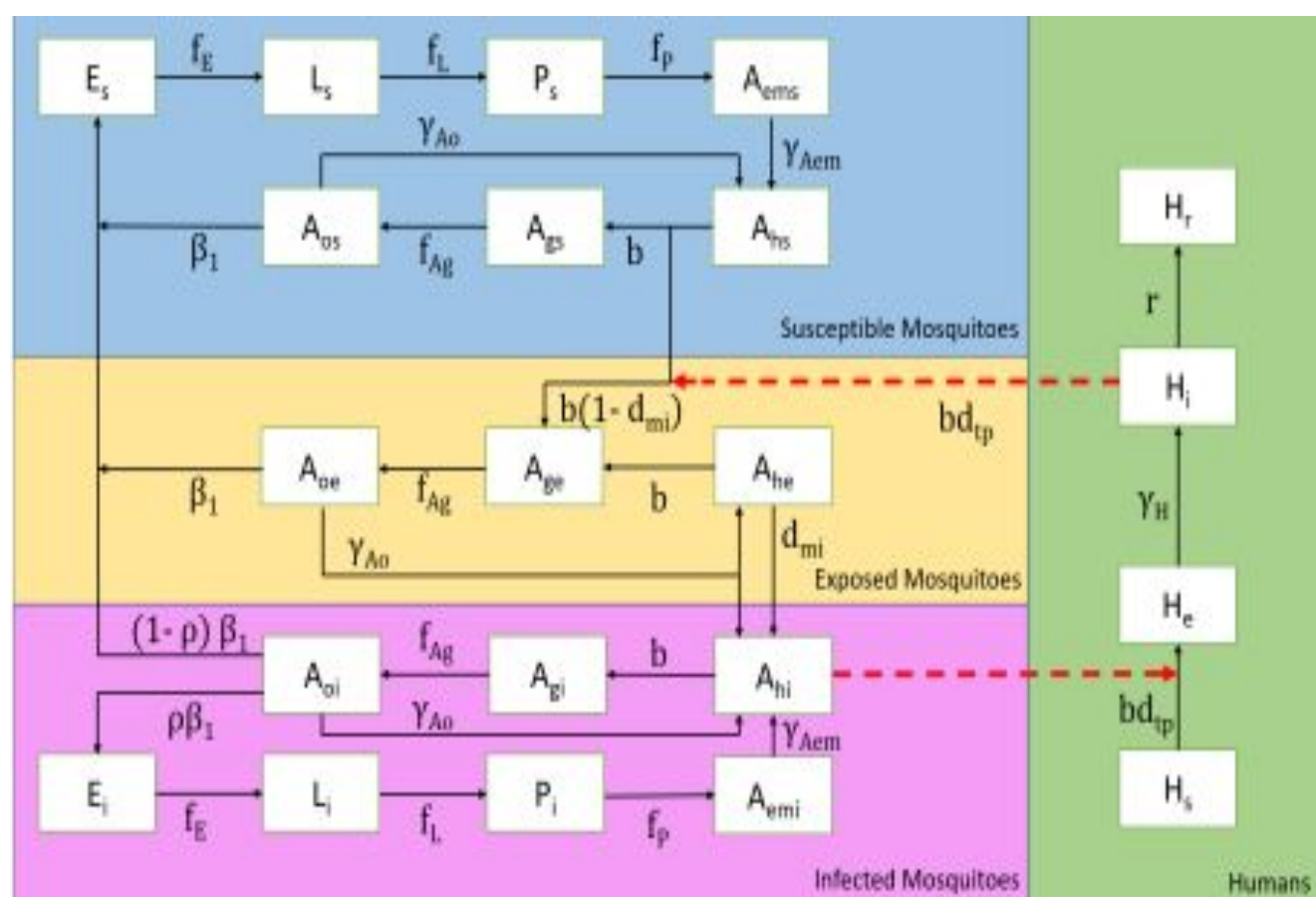


Figure 1: Human SEIR-Mosquito SEI-Mosquito ecology Compartmental models from [5]

**Environmental Data Integration:**

- Temperature and Precipitation:** We integrated daily temperature and precipitation data sourced from local weather services to account for their impact on mosquito breeding, survival rates, and virus incubation periods.
- Data-Driven Parameter Estimation:** Environmental factors influence key model parameters such as mosquito mortality rates, biting rates, and reproductive numbers, which were adjusted according to the weather data.
- Seasonal Variations:** The model accounts for seasonal changes by cycling through the temperature and precipitation data, reflecting the annual weather patterns of Rio de Janeiro.

**Model Calibration and Validation:**

- Initial Conditions:** Set based on historical data of dengue cases and mosquito density estimates for the region.
- Validation:** Due to the lack of access to localized validation data within the scope of this study, we used general case data from similar epidemiological studies for preliminary validation.

**Computational Implementation:**

- Numerical Simulation:** The model's differential equations were solved using numerical integration techniques.
- Software Utilization:** Implemented in Python, leveraging scientific libraries such as NumPy and SciPy for numerical analysis, and Matplotlib for visualization of results.

## RESULTS

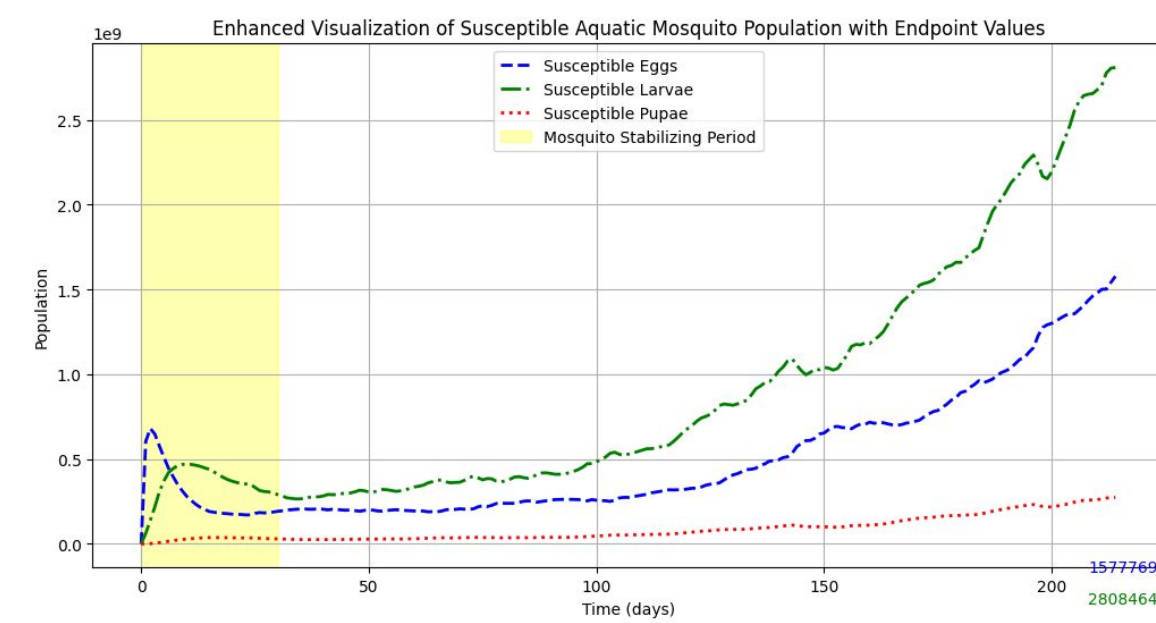


Figure II: Susceptible Aquatic Mosquito Population

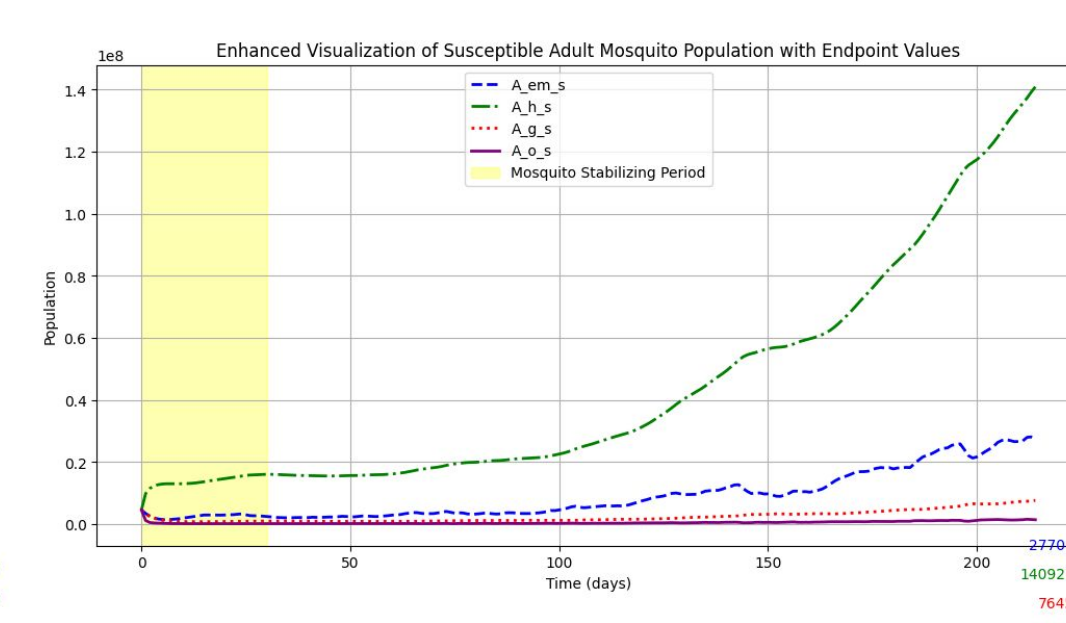


Figure III: Susceptible Adult Mosquito Population

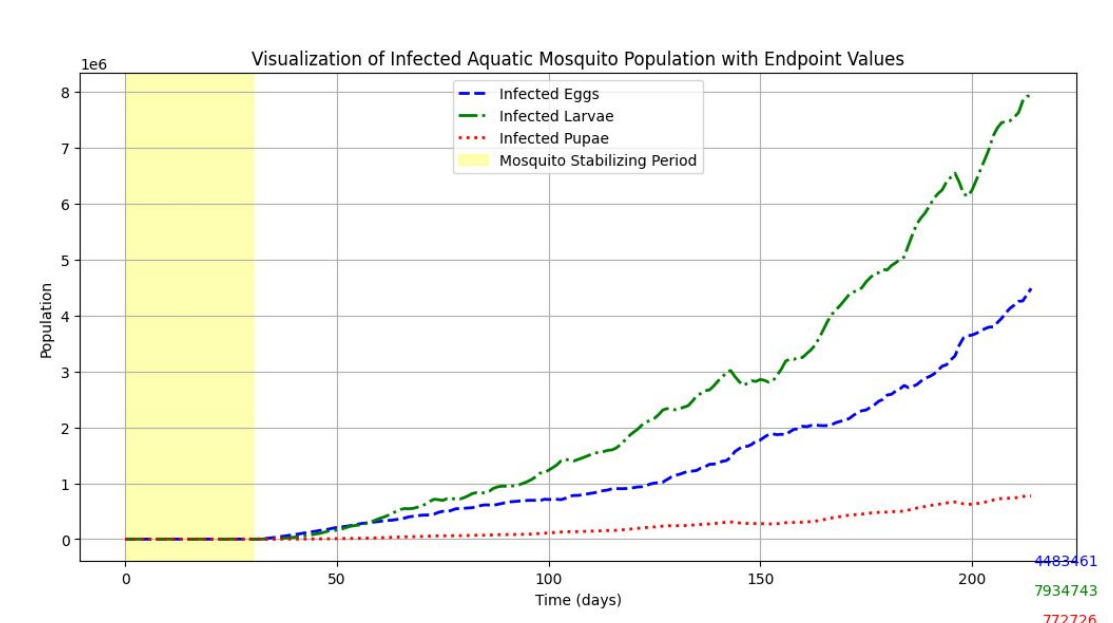


Figure IV: Infected Aquatic Mosquito Population

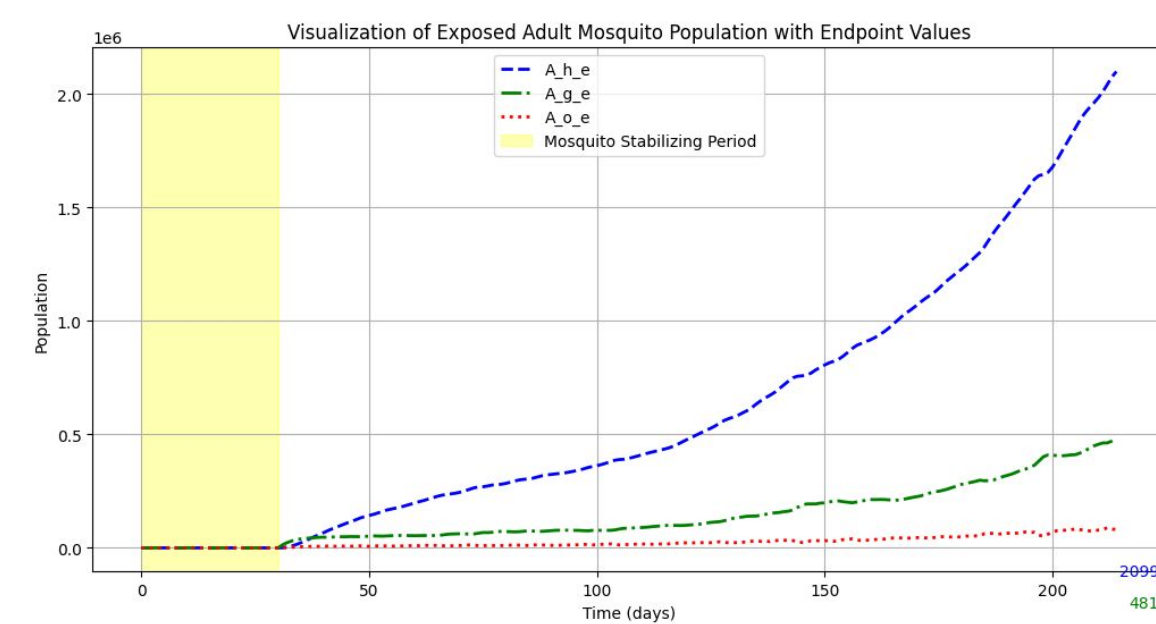


Figure V: Exposed Adult Mosquito Population

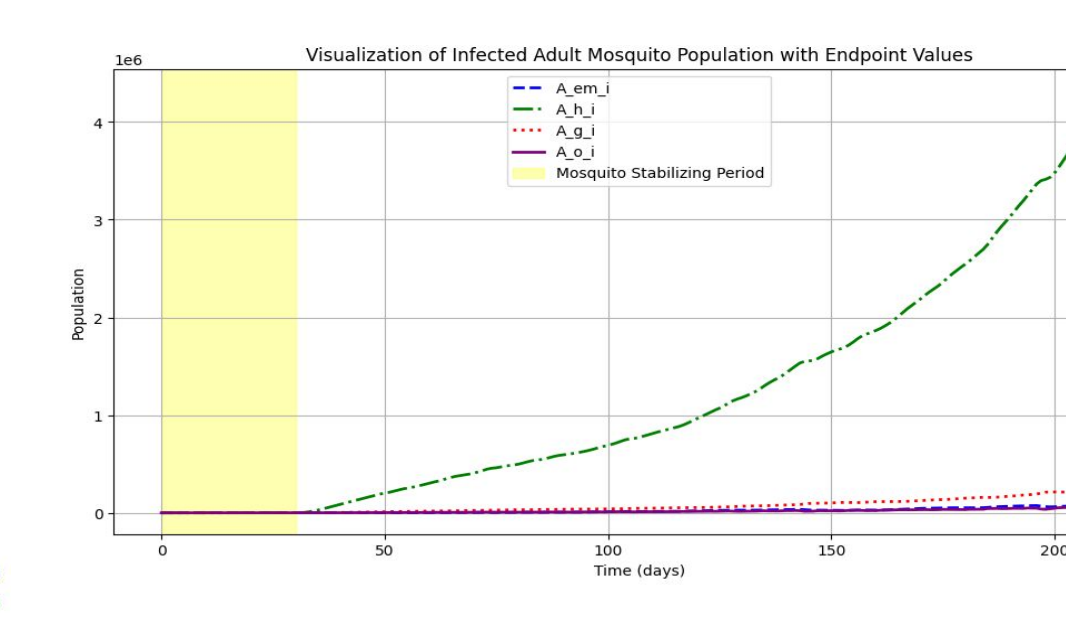


Figure VI: Infected Adult Mosquito Population

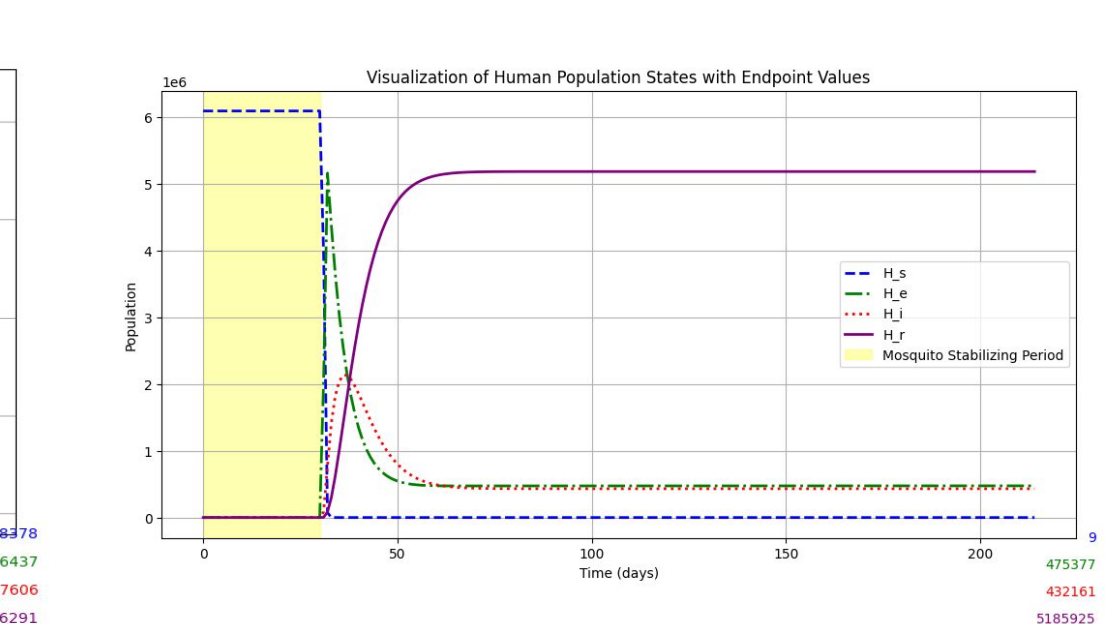


Figure VII: SEIR Values for Human Population

- The methodology employed for compartmental models, including the SEIR model for humans and the SEI model for mosquitoes, has been adapted from a source referenced as [5]. However, it's important to note that the approach described in [5], does not consider the possibility of reinfection and contact rate, which are relevant for vector-borne diseases like dengue.
- To address this limitation, we have modified the SEIR model proposed in [5] to a SEIRS model (Susceptible - Exposed - Infected - Recovered - Susceptible). In this adapted model, individuals who have recovered can transition back to the susceptible state based on a parameter called "immunity." The value of immunity represents the time period during which a person remains immune to reinfection, and for dengue, this period is typically 2-6 months, as indicated by the CDC [6].
- In the original approach described in [5], it was assumed that all mosquitoes come into contact with the entire susceptible human population. However, in reality, not all mosquitoes are likely to come into contact with all humans. To account for this, we introduced a contact rate. The simulation graphs presented above are based on a 50% contact rate.
- Validation** was a critical aspect of our study, and our initial intent was to compare our simulation results with the original data from [3]. However, a significant disparity emerged between the outcomes of our simulations and the real-world case data. We attribute this discrepancy to the absence of certain real-life factors in our model, such as intervention strategies and mosquito eradication programs.

## REFERENCES

- Gwalani, H., Hawamdeh, F., Mikler, A., & Xiong, K. (2018). Modeling the 2013 Zika Outbreak in French Polynesia: Intervention Strategies. *Applied System Innovation*, 1(3), 31. <https://doi.org/10.3390/asi1030031>
- Liu-Helmersson, J., Stenlund, H., Wilder-Smith, A., & Rocklöv, J. (2014). Vectorial Capacity of Aedes aegypti: Effects of Temperature and Implications for Global Dengue Epidemic Potential. *PLoS ONE*, 9(3), e89783. <https://doi.org/10.1371/journal.pone.0089783>
- TabNet Win32 3.2: DENGUE - Notificações registradas no Sistema de Informação de Agravos de Notificação - Rio de Janeiro. (n.d.). Tabnet.datasus.gov.br. Retrieved November 26, 2023, from <http://tabnet.datasus.gov.br/cgi/defohtm.exe?sinanet/cnv/denguerj.def>
- Rio de Janeiro, Brazil Weather History | Weather Underground. (n.d.). Www.wunderground.com. <https://www.wunderground.com/history/monthly/br/rio-de-janeiro/SBRJ>
- Schmidt, G., Whipple, B., Chellamuthu, V., & Xie, X. (2023). A Dynamical System Model of Dengue Transmission for Rio de Janeiro, Brazil. *Spora: A Journal of Biomathematics*, 9(1), 1–11. <https://doi.org/10.30707/SPORA9.1.1675492827.528788>
- Immunity. (n.d.). Www.cdc.gov. Retrieved December 1, 2023, from <https://www.cdc.gov/dengue/training/cme/ccm/page45893.html#:~:text=Lifelong%20type%2Dspecific%20immunity>.
- <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6025315/#FD6-ijerph-15-01128>

## CONCLUSION

Our endeavor to model the spread of dengue through a coupled SEIR model for humans and an SEI model for mosquitoes, augmented by considerations of the mosquito life cycle, has provided valuable insights into the dynamics of disease transmission. While our simulation results did not align with empirical case data, this discrepancy underscores the complexity of accurately modeling infectious diseases. The parameters governing the transmission and progression of dengue are numerous and sensitive to a variety of factors, including environmental conditions and population behavior.

**Challenges and Considerations:**

- We noted discrepancies between modeled outcomes and actual case data, attributed to potential inaccuracies in parameter estimation and the need for more granular local data.
- The complexity of dengue transmission, influenced by serotype variations and human behavior, was also acknowledged as an area for further refinement.

## ACKNOWLEDGEMENTS

We thank **Dr. Mikler** for his invaluable mentorship in simulations and special thanks to **Sara Edwards** and **Emma McDaniel** for their unwavering support throughout this project.