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Modeling Vaccination and Treatment Strategies for Dengue Control

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Abstract. Assessing strategies for managing dengue is crucial. While many studies have examined interventions' impact on transmission dynamics, few focus on combining multiple therapeutic approaches. This study presents an epidemic model incorporating vaccination and treatment for infected individuals. It employs ordinary differential equations with seven-state variables, analyzing disease-free and endemic equilibria. Results show the disease-free equilibrium is globally stable when the basic reproduction number is below one. When vaccine effectiveness is low, treatment proves more effective in reducing dengue cases. However, a highly effective vaccine alone significantly reduces dengue occurrences. Additionally, the study introduces an optimal control problem, combining vaccination and treatment. The analysis suggests implementing both strategies is more effective than a single approach in mitigating disease spread.

Keywords. *Dengue; Vaccination; Treatment; Disease control; Epidemiological modeling*

1 Introduction

Dengue fever, a global health concern, affects millions annually, with significant morbidity and mortality. Various interventions, including vaccine research and vector control, aim to mitigate its impact. While supportive care is crucial, severe cases require specialized medical attention. Although a vaccine is available, recent safety concerns have emerged. Given its economic burden, effective intervention strategies are imperative. Mathematical models have been instrumental in understanding transmission dynamics and evaluating intervention efficacy [3, 6, 18]. However, the combined impact of vaccination and treatment remains underexplored. This study aims to fill this gap by assessing their individual and combined effectiveness [5, 12, 17, 7, 21]. A novel mathematical model is proposed to analyze their interplay and potential synergies. Numerical analyses validate the model and explore the effects of vaccine efficacy and treatment rate on epidemic growth.

2 Model

The mathematical model [19] consists of two parts: human (h) and vector (v) compartments. It employs an $SVITR$ (Susceptible, Vaccination, Infectious, Treatement, Recovered) model to

depict human disease spread. Each compartment is represented by $S_h(t)$, $V_h(t)$, $I_h(t)$, $T_h(t)$ and $R_h(t)$ at time t. The total mosquito population $N_v(t)$ includes susceptible ($S_v(t)$)) and infected ($I_v(t)$) subpopulations. The model assumes a single serotype dengue without secondary infections, granting lifelong immunity to recovered individuals. Transmission occurs through mosquito bites represented by parameter b. Figure 1 illustrates a schematic model flow, with variables detailed in the caption.

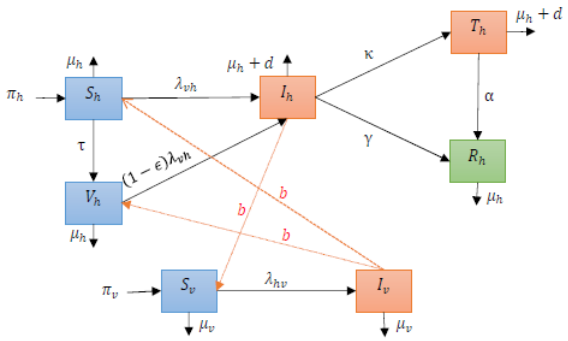


Figure 1: The flow chart represents the model. The host population is either Susceptible (S_h), Vaccinated (V_h), Infectious (I_h), under Treatement (T_h) and Recovered (R_h).The vector population is either Susceptible (S_v) or Infectious (I_v). Dashed arrows show direction of transmission between humans and mosquitoes.π_h is the Recruitment rate of human. b is the Mosquito biting rate. β_{vh} represents the probability of infection of a susceptible human per bite by an infected mosquito. γ is the human rate recovery.τ is the vaccination rate.μ_h is the human natural mortality rate. ϵ is the vaccine efficacy;κ is the Infectious humans treatement rate. α is the Recovery rate of hospitalized individuals. d is the human Disease-induced mortality rate. π_v is the Recruitment rate of vector. μ_v is the natural mortality rate of adult mosquitoes.

The system of ordinary differential equations (ODEs) describing the model is subjected to initial conditions to ensure non-negativity and boundedness over finite time. The analysis focuses on a biologically feasible region defined by a positive invariant set.

$$\begin{aligned}
\frac{dS_h}{dt} &= \pi_h - b\lambda_{vh}S_h - (p+\mu_h)S_h \\
\frac{dV_h}{dt} &= \tau S_h - (1-\varepsilon)\lambda_{vh}V_h - \mu_h V_h \\
\frac{dI_h}{dt} &= \beta_{vh}S_h + (1-\varepsilon)\lambda_{vh}V_h - (\gamma+\kappa+d+\mu_h)I_h \\
\frac{dT_h}{dt} &= \kappa I_h - (\alpha+d+\mu_h)T_h \\
\frac{dR_h}{dt} &= \gamma\ I_h + \alpha T_h - \mu_h R_h \\
\frac{dS_v}{dt} &= \pi_v - \lambda_{hv}S_v - \mu_v S_v \\
\frac{dI_v}{dt} &= \lambda_{hv}S_v I_h - \mu_v I_v
\end{aligned} \tag{1}$$

with the initial conditions

$$S_h(0) \geq 0, V_h(0) \geq 0, I_h(0) \geq 0, T_h(0) \geq 0, R_h(0) \geq 0, S_v(0) \geq 0, I_v(0) \geq 0 \tag{2}$$

3 Experimental Results

The basic reproduction ratio R_0, gives the average number of secondary cases of infection resulting from a single primary infection in a population where everyone is susceptible. It is the indicator of persistence or eradication of diseases. Indeed, an epidemic is said under control when $R_0 < 1$. The effective reproduction number R_0 is given by

$$R_0 = \sqrt{\frac{b^2\beta_{vh}\beta_{hv}\mu_h^2\pi_v}{\pi_h(\mu_v + d_v)^2(p + \mu_h)(\gamma + \kappa + d + \mu_h)}\left[1 + \frac{\tau(1-\varepsilon)}{\mu_h}\right]} \tag{3}$$

We conduct numerical simulations to explore the impact of vaccination and treatment on dengue transmission. Model parameters are estimated and validated using reported dengue infection data from Kaohsiung in 2014–2015.

We observe how the cure rate influences disease transmission dynamics, with intensified treatment reducing the infected population. Similarly, we investigate the effect of vaccination efficacy on disease transmission, noting a decrease in the infected population as vaccination efficiency increases.

We investigate dengue reduction under three scenarios: vaccination, treatment, and combination. Treatment alone significantly reduces dengue cases compared to vaccination alone, highlighting the importance of treatment when vaccine efficacy is low. Despite a high vaccination rate, treatment remains more effective than the vaccine, possibly due to low vaccine efficacy leading to reinfections.

At a vaccination rate of 0.5 and vaccine efficacy of 0.8, vaccination demonstrates superiority over treatment in reducing dengue cases. This emphasizes the importance of considering vaccine efficacy and vaccination rate in vaccination strategies. We analyze the critical vaccination coverage rate necessary for disease eradication, illustrating the threshold vaccination level for population protection. Disease control does not require complete population vaccination, as each vaccinated individual contributes to collective immunity. However, additional efforts are needed to reduce R0 below unity, even with high vaccination coverage.

Treatment outperforms vaccination in reducing dengue transmission when vaccine efficacy is low. However, even with high vaccine efficacy, treatment remains essential for disease control. Sensitivity analysis reveals significant impacts of various parameters on R0, particularly transmission probability, bite rate, vaccine effectiveness, and treatment. The synergy between vaccination and treatment significantly reduces disease spread. Optimal control analysis suggests combining vaccination and treatment is the most effective strategy for reducing infection.

Our model has limitations. For example, it does not include seasonality effects [1, 2]. Future research directions could explore the interplay between dengue and other vector-borne disease such as Zika [20] or person to person disease such as COVID-19 [13, 14], focusing on understanding potential interactions, co-infections, and their impact on disease outcomes. Furthermore, research into developing integrated control strategies that address epidemic transmission could help optimize resource allocation and enhance public health responses [8, 11, 9, 10, 16, 15, 4].

References

[1] Md Arquam, Anurag Singh, and Hocine Cherifi. Impact of seasonal conditions on vector-borne epidemiological dynamics. *IEEE Access*, 8:94510–94525, 2020.

[2] Md Arquam, Anurag Singh, and Hocine Cherifi. Integrating environmental temperature conditions into the sir model for vector-borne diseases. In *Complex Networks and Their Applications VIII: Volume 1*, pages 412–424. Springer, 2020.

[3] Samir Bhatt, Peter W Gething, Oliver J Brady, Jane P Messina, Andrew W Farlow, Catherine L Moyes, John M Drake, John S Brownstein, Anne G Hoen, Osman Sankoh, et al. The global distribution and burden of dengue. *Nature*, 496(7446):504–507, 2013.

[4] Debayan Chakraborty, Anurag Singh, and Hocine Cherifi. Immunization strategies based on the overlapping nodes in networks with community structure. In *CSoNet 2016, Ho Chi Minh City, Vietnam, August 2-4, 2016, Proceedings 5*, pages 62–73. Springer, 2016.

[5] Ananya Dwivedi, Ram Keval, and Subhas Khajanchi. Modeling optimal vaccination strategy for dengue epidemic model: a case study of india. *Physica Scripta*, 97(8), 2022.

[6] Lourdes Esteva and Cristobal Vargas. Analysis of a dengue disease transmission model. *Mathematical biosciences*, 150(2):131–151, 1998.

[7] Neil M Ferguson, Isabel Rodríguez-Barraquer, Ilaria Dorigatti, Luis Mier-y Teran-Romero, Daniel J Laydon, and Derek AT Cummings. Benefits and risks of the sanofi-pasteur dengue vaccine: Modeling optimal deployment. *Science*, 353(6303):1033–1036, 2016.

[8] Zakariya Ghalmane, Chantal Cherifi, Hocine Cherifi, and Mohammed El Hassouni. Extracting backbones in weighted modular complex networks. *Scientific Reports*, 10(1):15539, 2020.

[9] Zakariya Ghalmane, Mohammed El Hassouni, Chantal Cherifi, and Hocine Cherifi. Influential spreaders in networks with community structure. In *International Conference on Complex Systems (ICCS)*, page 1, 2020.

[10] Zakariya Ghalmane, Stephany Rajeh, Chantal Cherifi, Hocine Cherifi, and Mohammed El Hassouni. Finding influential nodes in networks with community structure. In *Network Modeling, Learning and Analysis (NMLA), WorldCIST2020 Workshop*, page 3, 2020.

[11] Prem Kumar, Puneet Verma, Anurag Singh, and Hocine Cherifi. Choosing optimal seed nodes in competitive contagion. *Frontiers in big Data*, 2:16, 2019.

[12] Meksianis Z Ndii, Yudi Ari Adi, and Bertha S Djahi. Deterministic and stochastic dengue epidemic model: Exploring the probability of extinction. *BAREKENG: Jurnal Ilmu Matematika dan Terapan*, 16(2):583–596, 2022.

[13] Benjamin Perrette, Christophe Cruz, and Hocine Cherifi. A local agent-based model of covid-19 spreading and interventions. In *French Regional Conf. on Complex Systems*, 2023.

[14] Khubaib Ahmed Qureshi, Rauf Ahmed Shams Malick, Muhammad Sabih, and Hocine Cherifi. Complex network and source inspired covid-19 fake news classification on twitter. *IEEE Access*, 9:139636–139656, 2021.

[15] Stephany Rajeh and Hocine Cherifi. Ranking influential nodes in complex networks with community structure. *Plos one*, 17(8):e0273610, 2022.

[16] Stephany Rajeh, Marinette Savonnet, Eric Leclercq, and Hocine Cherifi. Comparative evaluation of community-aware centrality measures. *Quality & Quantity*, 57(2), 2023.

[17] Eunha Shim. Optimal dengue vaccination strategies of seropositive individuals. *Mathematical Biosciences and Engineering*, 16(3):1171–1189, 2019.

[18] B Singh, S Jain, R Khandelwal, S Porwal, and G Ujjainkar. Analysis of a dengue disease transmission model with vaccination. *Advances in Applied Science Research*, 5(3), 2014.

[19] Abdoulaye Sow, Cherif Diallo, and Hocine Cherifi. Interplay between vaccines and treatment for dengue control: An epidemic model. *Plos one*, 19(1):e0295025, 2024.

[20] Abdoulaye Sow, Cherif Diallo, Hocine Cherifi, et al. Effects of vertical transmission and human contact on zika dynamics. *Complexity*, 2022, 2022.

[21] J Torresi, G Ebert, and M Pellegrini. Vaccines licensed and in clinical trials for the prevention of dengue. *Human vaccines & immunotherapeutics*, 13(5):1059–1072, 2017.