

**MODELING OF THE DENGUE OUTBREAK USING MODIFIED SEIR MODEL IN
JAFFNA DISTRICT**

V. Selvabavitha^{1*} and T. Thanusika²

¹*Department of Interdisciplinary Studies, Faculty of Engineering, University of Jaffna, Jaffna,
Sri Lanka*

²*Postgraduate Institute of Science, University of Peradeniya, Peradeniya, Sri Lanka*

**bavirathnam@eng.jf.ac.lk.*

Dengue fever is a mosquito-borne viral disease transmitted to humans through the bite of infected *Aedes* mosquitoes, mostly *Aedes aegypti*. In the Jaffna District, about 200 cases of dengue fever per 100,000 people in 2019 was reported. A better understanding of the transmission dynamics of the dengue disease epidemic in Jaffna is vital for public health. Mathematical modeling is a useful technique for analysing transmission dynamics. This research aims to improve the theoretical understanding of dengue transmission through a simulation and the related changes in the dengue epidemic in the Jaffna District. The four-compartment (susceptible (S_h), exposed (E_h), infected (I_h), and removed (R_h)) (SEIR) models for human and two compartment (susceptible (S_v), exposed (E_h), and infected (I_v)) model for vectors with seven nonlinear differential equations were used to formulate a mathematical model. Relevant data from 2019 were collected from Jaffna regional health authorities and analysed with the developed model. Two equilibrium points were found: the first point was locally asymptotically stable, and the other was focus asymptotically stable. Moreover, the reproduction number $R_0 > 1$. The proposed model shows that the focus of dengue fever would be stable in the Jaffna District except in some specific places.

Keywords: Dengue fever, Equilibrium, Reproduction number, SEIR model, Stability