# An Enhanced Early Detection Model of Dengue Fever Outbreaks Using SEIR Infectious Disease Epidemiological Compartments, Generalized Linear Regression, and Statistical Computing

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Dengue Fever is the most rapidly spreading mosquito-borne disease, with more than 25,000 deaths annually. To date, no vaccine has been developed for Dengue Fever due to the existence of four virus serotypes. This project aims to innovate a novel approach to detect outbreaks of this fatal disease. My primary motivation to continue this research was the “2019 Dengue Epidemic,” in which there was an unexpected surge in case count in several Latin American and Southeast Asian countries. I used the SEIR model to track the dynamics and transmission of the disease between humans and vectors (mosquitoes). Using outbreak data collected from Singapore’s Health Database, I then created a linear regressional relationship between variables and the Density of Infectious Mosquitoes. The independent climatic variables were Temperature, Rainfall, and Humidity. Each variable was tested for predictive significance at different amounts of delay or “lag time.” With the ability to predict the Density of Infectious parameter in the SEIR model, I was then able to conduct week by week simulations in R. The model was then tested on five actual Singapore Dengue Outbreaks from years 2013-2019. Statistical testing using cross-correlation showed a significant similarity between the test data and actual Dengue outbreaks. These were a 2013 value of 0.827, a 2014 value of 0.678, 2015 value of 0.813, 2017 value of 0.968, and 2019 value of 0.806. In addition, the model was applied to 2019 outbreaks Honduras and Cambodia with successful results of 0.935 for Cambodia and 0.899 for Honduras. With this reliable early detection framework, health organizations gain lead time to implement intervention strategies to eradicate mosquito populations, and resultingly, large outbreaks of Dengue Fever.

**Awards Won:**