A Novel Mathematical Model for the Early Detection of Dengue Fever using SIR Infectious Disease Epidemiological Compartments, Ordinary Differential Equations, and Statistical Computing

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Dengue Fever is a debilitating viral disease of the tropics, transmitted by female Aedes mosquitoes, causing sudden fever, acute pains in the joints and hemorrhaging. The World Health Organization(WHO) estimated more than 25,000 deaths annually. To date, no vaccine has been developed for Dengue Fever due to the existence of four virus serotypes that are extremely difficult to develop an immunity against. Early detection of Dengue is proving to be the only viable option of mitigating the transmission of this disease and potentially containing it. The purpose of my project is to innovate a novel approach to detect the outbreak of Dengue disease. Using actual 2005 Dengue disease outbreak data from Singapore, as well as 10 years' worth of Singaporean climate data, the average temperature and vector-human population were calculated. Thousands of simulations with varying susceptible human populations and mosquito bite rates were done to produce a quartic function relationship between the climate and bite rate. The resulting simulation data were tested on an actual 2013, 2014 and 2015 Singapore Dengue outbreaks, with 2013 R-value of 0.74, 2014 R-value of 0.53 and 2015 R-value of 0.61. These positive results indicate that we can use this novel model to accurately predict Dengue disease outbreaks and as a tool for early detection with proactive vector control measures in place, which ultimately reduces the number of deaths associated with this disease. This tool will be the only viable measure today until a promising vaccine is developed to control and curb the century-long Dengue diseases that, to date, have killed more than 5 million humans worldwide.

Awards Won:

Air Force Research Laboratory on behalf of the United States Air Force: First Award of \$750 in each Intel ISEF Category