

Sensitivity analysis of a model of Japanese encephalitis transmission

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Ph.D. expected duration: 2015-2018

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Abstract: Japanese Encephalitis (JE) is an endemic disease in Asia and the most important cause of human encephalitis in several Asian regions and the Pacific. The first case of JE was documented in 1870 in Japan and was isolated for the first time in Tokyo in 1934. It is estimated that 3 billion of people are living in countries where the disease is endemic. The annual incidence of JE is estimated between 30000 and 50000 cases with 10,000 to 15,000 deaths annually. Japanese encephalitis virus is a flavivirus of the family of flaviviridae, such as the viruses of the dengue, yellow fever and West Nile. It is an arthropod-borne-virus (arbovirus) transmitted from animal to human by mosquitoes. Wild birds (aigrettes, herons) and domestic birds (ducks, chickens) are the natural hosts, pigs are the amplifier hosts, humans and horses are accidental hosts, i.e. they can contract the disease, but they can not transmit the virus to the mosquitoes. We have developed a generic mathematical model of JE transmission and determined the basic reproduction number, R_0 . R_0 is defined as the number of secondary infections caused by a single infection of the same type (vector or host) during its infectious period in an entirely susceptible population. R_0 is a threshold value in the model. If $R_0 < 1$ the disease can not invade the population. If $R_0 > 1$, then the disease can invade the population. Therefore, to control the spread of JE we must reduce R_0 below 1. In some cases, for an infectious disease transmitted between at least two types of hosts, the R_0 can be misleading when we want to control the disease. So, we have determined the type-reproduction number T for disease such as JE. T is used to determine the control effort required to eliminate an infectious disease when control is applied to a specific sub population of hosts. In this work, we present three sensitivity analysis. The first one on the parameters of the model, the second one on the basic reproduction number R_0 and the third one on the type-reproduction number T . The results of the first sensitivity analysis will be used to identify the parameters we should know with precision and will determine the future field experiments we have to conduct to measure those parameters. The sensitivity analysis on R_0 and T will be used to determine the important parameters to control the disease, and how sensitive the spread of the disease can be regarding the control.

Short biography – I have a Master degree in applied mathematics from the University of Bordeaux. My research concerns the modeling of the epidemiological cycle of the Japanese encephalitis, a major cause of encephalitis in Southeast Asia (SEA). My thesis is funded by CIRAD and l'Institut Pasteur. The thesis activities are supported by two projects : "Southeast Asia encephalitis" (SEAE, <http://ur-agirs.cirad.fr/en/projects/seae>) and "Companion Approach for Cross-sectoral collaboration in health risk management in SEA (ComAcross, <http://www.onehealthsea.org/comacross>).