Statistical and Mathematical Modeling for a Better Understanding of Dengue Dynamics in Southern Asia

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Keywords: Dengue, Wavelet Decomposition, Dengue Stochastic Models, Bayesian Inference, Model Selection, Time-Varying Parameter

Dengue is the most important arboviral disease worldwide and a major public health problem in the tropics and subtropics. The dengue vector and virus are extremely sensitive to environmental conditions such as temperature, humidity and precipitation that influence mosquito biology, abundance, habitat and viral replication rate. Thus, such climatic factors must have significant influence on dengue propagation in the population.

The first analyses presented concern the quantification of the role of climate on dengue epidemics in Thailand and Cambodia provinces using wavelet decomposition[1-2] (wavelet power spectrum, wavelet partial coherency, wavelet mean field and wavelet clustering), to account for the non-stationary relationships[3].

The second analyses presented are related to mathematical modeling at different scales: provinces, districts or rural villages, using classical 1-strain or 2-strain dengue stochastic models[4] with Bayesian inference. Exact inference was conducted using recently developed algorithms such as particle MCMC[5], coupled with an initial exploration of the likelihood surface with the extended Kalman filter[6]. This allows model selection by a quantification of the importance of different models and of their underlying hypothesis through likelihood computation and statistical information criteria[7]. First results show that vector dynamics or strain coexistence appears crucial to provide a coherent epidemic trajectory. This approach also permits reconstruction of the dynamics with time-varying transmission parameters showing that these time-varying parameters can be statistically related to local or global climatic forcing. Therefore, one can expect that forecast climate information has utility in a dengue decision support system using mechanistic models.

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