# Mechanistic models of dengue dynamics : coupling particle filter and MCMC for parameter inference and model selection

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**Abstract:** Detected for the first time in Southeast Asia in the 1950s, dengue fever is an infectious disease which became a major issue in the tropical and sub-tropical regions of the globe over the last decades [4]. In endemic regions such as Cambodia, dengue fever follows a recurrent dynamic, with a seasonal peak in incidence every year. This dynamic is shaped by the complex interplay between several factors, including vector seasonality, interaction between four strains, and asymptomatic infections. Nevertheless, model complexity and data availability often restrain from taking them all into account.

In order to explore separately the importance of those mechanisms in models, we rely on local scale data collected in the rural province of Kampong Cham (Cambodia). As part of the DENFREE study, serological status was documented in village neighborhoods of confirmed hospitalized dengue cases during the 2012 and 2013 peak transmission seasons. Thanks to this rich database, we build several epidemiological SIR-type models, each one relying on a particular set of hypotheses, which focus on one aspect of dengue transmission. Comparing models in the light of data enables the comparison of the underlying hypotheses, in order to identify which hypotheses are decisive to describe the observed disease dynamic [5] [2].

Stochastic models are chosen to account for unobserved heterogeneity, measurement errors and demographic stochasticity inherent to the dynamic of a small population. Relying on the state space model framework, the parameters of the system are estimated using Bayesian inference techniques based on particle filter. In particular, we use the PMCMC algorithm (particle Markov Chain Monte Carlo [1]), implemented in the open source software SSM [3], which is robust to stochastic formulation of the model. This method allows computation of statistical information criteria but also simulations of the model, in order to explore present and future scenarios.

We therefore estimate and compare several stochastic models, taking successively into account asymptomatic infections, two different virus strains, and mosquito-borne transmission. For each model, information criteria and simulations of the system are computed. Likelihood-based information criteria seem to favor the simplest model. However, robustness to simulations and the qualitative coherence of the underlying epidemiologic scenarios appear also decisive in these comparisons. It is indeed important to take into account the evolution of the susceptible population and the capacity of the model to predict a resurgence of the epidemic, similar to the annual pattern observed in Cambodia. In this context, considering two virus strains is useful to maintain a sufficient number of susceptible individuals at the end of the epidemic.

Moreover, in this study on an endemic region, uncertainty remains on the initial conditions of the system. This creates identifiability problems, because of high correlation between the initial susceptible population and the force of infection. Hence, seroprevalence study and virus sequence analysis in Cambodia would be precious to precise the results and to reduce identifiability issues.

**References**

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**Short biography** – Clara Champagne has a diploma in statistics and economics from ENSAE-Paristech and a master in epidemiology from Universit Paris Sud. She is currently a PhD student at IBENS Eco-Evolutionary Mathematics (Paris), with a funding from the CREST-GENES (Paris).