

# HOW MUCH COMPLEXITY IS NEEDED TO DESCRIBE THE FLUCTUATIONS OBSERVED IN DENGUE FEVER INCIDENCE DATA?

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## ABSTRACT

Dengue fever epidemiology dynamics shows large fluctuations of disease incidence and mathematical models describing transmission of disease ultimately aim to be used as predictive tools to evaluate the introduction of intervention strategies, such as vaccination and vector control. Several mathematical models found in the literature have been formulated to describe the transmission of dengue fever. Multi-strain dynamics are generally modeled with extended Susceptible-Infected-Recovered (SIR-type) models, and have demonstrated qualitatively a very good result when comparing empirical data and model simulations

Here, we present a set of models motivated by dengue fever epidemiology and compare different dynamical behaviors originated when increasing complexity into model framework, anticipating that temporary cross-immunity and difference between primary and secondary infections appear to be the key factors determining disease transmission, outcome of infection and epidemics. These models are parametrized on the official notification dengue data from Bureau of Epidemiology, Ministry of Public Health in Thailand [1].

The extended models show complex dynamics and qualitatively a very good result when comparing empirical data and model simulations. The predictability of the system does not change significantly when considering two or four strains, giving approximately the same prediction horizon in time series.

The two-strain model in its simplicity is a good model to be analyzed, giving the expected complex behavior to mimic the fluctuations observed in empirical data, and would be indeed the best

option to be used for parameter estimation, which is notoriously difficult for chaotic time series, based on the available incidence data.

## **References**

- [1] Aguiar, M. et al. (2013). How much complexity is needed to describe the fluctuations observed in dengue hemorrhagic fever incidence data? *Ecological Complexity*; **16**: 31–40.