

The role of seasonality and import in a minimalistic multi-strain dengue model capturing differences between primary and secondary infections

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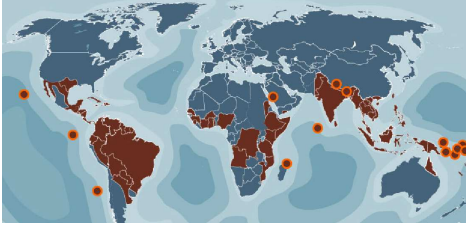


Figure 1: Worldwide dengue distribution 2008 - © Biogenets AG

Introduction

In many countries in Asia and South-America dengue fever (DF) and dengue hemorrhagic fever (DHF) has become a substantial public health concern leading to serious social-economic costs. Mathematical models describing the transmission of dengue viruses have focused on the so called antibody-dependent enhancement (ADE) effect and temporary cross immunity trying to explain the irregular behavior of dengue epidemics by analyzing available data. However, no systematic investigation of the possible dynamical structures has been performed so far. We investigate the extended multi-strain model with temporary cross immunity and possible secondary infection, motivated by dengue fever epidemiology presented first in [3] and [4]. We add seasonal forcing into the previous multi-strain dengue model, mimicking the vectorial dynamics, and a low import of infected individuals, which is realistic in the dynamics of dengue fever epidemics. The complete analysis of the extended models shows complex dynamics and qualitatively a very good result when comparing empirical DHF data and model simulation. The effects of the vector dynamics are only taken into account by the force of infection parameters in the SIR-type model, but not modelling this mechanisms explicitly. Since vector models without multi-strain aspects only shows stationary dynamics [5] and seasonally forced SIR systems can show already deterministic chaos [6], the presented model is minimalistic in the sense that it can capture the essential differences of primary versus secondary infection under periodic forcing but is not too high dimensional so that future parameter estimation can still attempt to estimate all initial conditions as well as the few model parameters.

Our Model:

$$\begin{aligned} \dot{S} &= -\frac{\beta(t)}{N} S(I_1 + \rho \cdot N + \phi I_{21}) \\ &\quad - \frac{\beta(t)}{N} S(I_2 + \rho \cdot N + \phi I_{12}) + \mu(N - S) \\ \dot{I}_1 &= \frac{\beta(t)}{N} S(I_1 + \rho \cdot N + \phi I_{21}) - (\gamma + \mu) I_1 \\ \dot{I}_2 &= \frac{\beta(t)}{N} S(I_2 + \rho \cdot N + \phi I_{12}) - (\gamma + \mu) I_2 \\ \dot{R}_1 &= \gamma I_1 - (\alpha + \mu) R_1 \\ \dot{R}_2 &= \gamma I_2 - (\alpha + \mu) R_2 \\ \dot{S}_1 &= -\frac{\beta(t)}{N} S_1(I_2 + \rho \cdot N + \phi I_{12}) + \alpha R_1 - \mu S_1 \\ \dot{S}_2 &= -\frac{\beta(t)}{N} S_2(I_1 + \rho \cdot N + \phi I_{21}) + \alpha R_2 - \mu S_2 \\ \dot{I}_{12} &= \frac{\beta(t)}{N} S_1(I_2 + \rho \cdot N + \phi I_{12}) - (\gamma + \mu) I_{12} \\ \dot{I}_{21} &= \frac{\beta(t)}{N} S_2(I_1 + \rho \cdot N + \phi I_{21}) - (\gamma + \mu) I_{21} \\ \dot{R} &= \gamma(I_{12} + I_{21}) - \mu R \end{aligned}$$

Par.	Description	Values
N	population size	100
μ	birth and death rate	$1/65y$
γ	recovery rate	$52y^{-1}$
β_0	infection rate	$2 \cdot \gamma$
η	degree of seasonality	0.1 to 0.35
φ	phase	0
ρ	import parameter	0 to 10^{-10}
α	temporary cross-immunity rate	$2y^{-1}$
ϕ	ratio of secondary infections contributing to force of infection	variable (< 1)

Abstract

Our study focuses on a seasonally forced model with temporary cross immunity and possible secondary infection, motivated by dengue fever epidemiology. The notion of at least two different strains is needed in a minimalistic model to describe differences between primary infections, often asymptomatic, and secondary infection, associated with the severe form of the disease. We extend the previously studied non-seasonal model by adding seasonal forcing, mimicking the vectorial dynamics, and a low import of infected individuals, which is realistic in the dynamics of dengue fever epidemics. A comparative study between three different scenarios (non-seasonal, low seasonal and high seasonal with a low import of infected individuals) is performed.

Bifurcation diagram

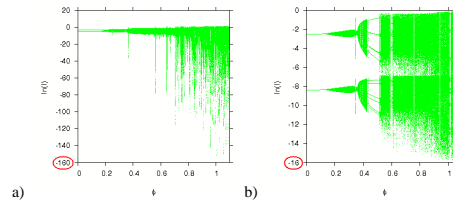


Figure 3: Bifurcation diagram comparison between seasonal models. In a) bifurcation diagram for the low seasonal model without import of infected, where the degree of seasonality $\eta = 0.1$ and in b) bifurcation diagram for the high seasonal model with a low import of infected. Here, the degree of seasonality $\eta = 0.35$ and the import factor $\rho = 10^{-10}$

Time series

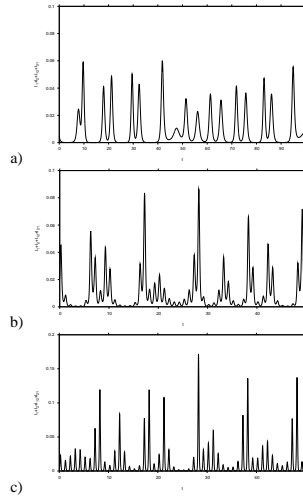


Figure 4: Time series simulations. In a) time series simulation for the non-seasonal model ($\eta = 0$). In b) time series simulation for the low seasonal model, with seasonality $\eta = 0.1$. In c) time series simulation for the seasonal model with a low import of infected. Here, the degree of seasonality $\eta = 0.35$ and the import of infected $\rho = 10^{-10}$.

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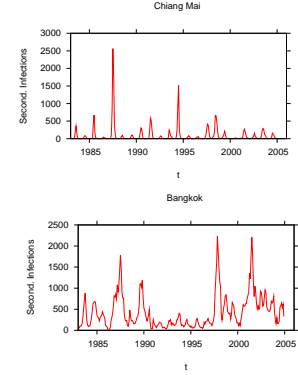


Figure 2: Empirical DHF incidence data [8, 7]

Lyapunov exponents and predictability

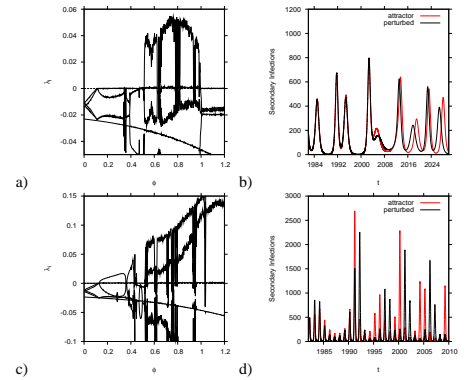


Figure 5: Qualitative insight into the predictability in the monthly time series.

Implications for data analysis

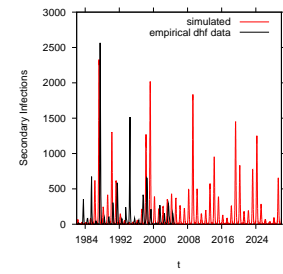


Figure 9: Empirical DHF incidence data matched with the model simulation

Conclusions

The extended models show complex dynamics and qualitatively a good agreement between empirical DHF monitoring data and the obtained model simulation. We discuss the role of seasonal forcing and the import of infected individuals in such systems, the biological relevance and its implications for the analysis of the available dengue data. At the moment only such minimalistic models have a chance to be qualitatively understood well and eventually tested against existing data. The simplicity of the model (low number of parameters and state variables) offer a promising perspective on parameter values inference from the DHF case notifications.

Acknowledgements

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