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Time-scale separation in models for dengue fever

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Dengue fever is a vector-borne disease posing threat to millions of people. Its epidemiology is characterised by co-circulating multiple variants of the pathogen, the dengue virus. Mathematical modelling of dengue faces the challenges of finding a balance between accurate description of the disease dynamics, the different scales of modelling, and the associated levels of complexity which allow for establishing tractable causal relationships. One approach in modelling dengue and other vector-borne diseases has been to use host-only models that include the vector dynamics in an implicit fashion. However, these models are not directly suited for studies of intervention measures such as vector control or personal protection, which may influence the mosquito dynamics in a nonlinear manner.

We present the theoretical rationale that allows us to reduce the model complexity via a time-scale separation argument and rigorously derive the quasi-steady state approximation in models for vector-borne diseases using singular perturbation theory. This approach rests upon the observation that the dynamics of some phase variables can be taken as if in a quasi-steady state, and transforms the original system of ordinary differential equations into a system of algebraic-differential equations.

Then we discuss some issues which emerge repeatedly in the mathematical models of dengue: differences in structure (host-only vs. host-vector models), ecological effects due to seasonal changes in the vector population, immunological effects such as disease severity, and exert an effect on the dynamic behaviour of the model. Numerical bifurcation analysis is used to compare the bifurcation structure of a host-vector model of dengue (with two variants and reinfection) and its variant with reduced complexity resulting from a quasi-steady-state approximation to that of a previous host-only model of dengue. It turns out that in biologically-relevant parameter regimes, models with higher complexity (host-vector models) may exhibit fewer types of bifurcations and tend to have smooth dynamics (convergence to equlibria or limit cycles) compared to host-only models unless there is seasonal variation in the mosquito vector population.

Keywords: dengue, epidemiological dynamics, time-scale separation, bifurcation analysis, multi-variant models