Time-scale separation in a minimal model for a vector-borne disease

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We use a minimal model to study the interaction of the host and vector dynamics in context of a vector-borne epidemic. With dynamics occurring at different time scales for host and vector, we employ several approaches: a) a quasi steady-state assumption (QSSA) to reduce the model dimensionality, and replace the equations for the slow variables by algebraic equations and b) singular perturbation theory and invariant manifolds, which can be approximated by asymptotic expansions in the small parameter that represents the ratio of the two time scales.

We consider two examples: the host follows either a susceptible-infected-susceptible (SIS) or susceptible-infected-recovered (SIR) model and the vector - a susceptible-infected (UV) model. For the SISUV model, the QSSA algebraic equation is just a hyperbolic relationship, resembling that of the Holling type II functional response in ecology. In the SIRUV model a higher-order approximation is necessary because the slow scale is two-dimensional. However, more care is needed because of a condition on the convergence of asymptotic expansion. In addition, we perform a heuristic analysis of the SIRUV model's behaviour which exhibits damped oscillations [1].

Parametrising the model with values relevant for dengue fever [2], we study the effect of seasonality where the force of infection changes in time corresponding to annual sinusoidal fluctuations of the mosquito population. The resulting non-autonomous system is studied analogous to the autonomous system using numerical bifurcation analysis.

References

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