Vector-borne diseases with non-stationary vector populations: the case of growing and decaying populations

Àlex Giménez-Romero[1], Rosa Flaquer-Galmés[1,2], and Manuel A. Matias[1]
[1]Instituto de Fsica Interdisciplinar y Sistemas Complejos, IFISC (CSIC-UIB), Campus UIB, E-07122 Palma de Mallorca
[2]Grup de Fsica Estadstica, Departament de Fsica, Facultat de Cincies, Universitat Autnoma de Barcelona, E-08193 Bellaterra (Barcelona)

Compartmental models have emerged as powerful tools to predict and control epidemic outbreaks, helping to mitigate its impacts. A key quantity for these models is the so-called *Basic Reproduction Number*, R_0, that measures the number of secondary infections produced by an initial infected individual in a fully susceptible population. Standard methods like the Next Generation Matrix (NGM) method [1] have been developed to allow the direct computation of R_0, provided that some conditions are fulfilled, such that the model has an initial disease-free equilibrium state. However, in vector-borne diseases, this is only accomplished when the vector population is *stationary*, this is, when the number of vector deaths are balanced with the same amount of vector births. However, many situations could lead to *non-stationary* vector populations, such as increasing or decaying populations.

Some authors have explicitly considered more general cases in which the demographic rates are not identical or even time-dependent with a given periodicity. In the first case, one obtains an asymptotic stationary vector population, but not an initial disease-free equilibrium. Nevertheless, the basic reproduction number of these models is often computed by means of the traditional methods from the asymptotic value of the population [2], i.e. the post-pandemic disease-free equilibrium. Here we show that it is not enough to study the asymptotic behaviour of the model to derive the epidemic threshold. In the case of periodic demographic rates, it has been shown that the time-averaged basic reproduction number defines the epidemic threshold under some circumstances and even a generalisation of the NGM method has been developed [3].

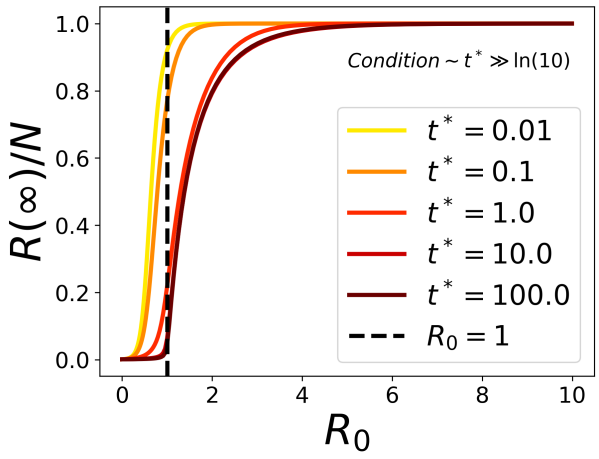

Fig. 1. Failure of the asymptotic theory to derive the epidemic threshold depending on the time-scales of the model. t^* is the time for the vector population to reach its asymptotic value.

We develop a compartmental model of vector-borne transmitted diseases that allows to describe growing and decaying vector populations. We show how and when standard methods fail to estimate the R_0 of the model and provide an alternative way to compute it. It turns out that the validity of the standard methods depends on on some time-scales of the model. Furthermore, we discuss and apply some approximations that allow to reduce the model in favour of simpler ones, with both fewer compartments and fewer parameters. In particular, we show that if some of the parameters fulfil certain conditions, it is possible to reduce the original model with 5 compartments and 4 parameters to an effective SIR model. The result is that a model in which hosts do not interact directly, but through vectors, in a certain limit yields and effective host to host interaction, what is assumed in some studies without suitable confirmation.

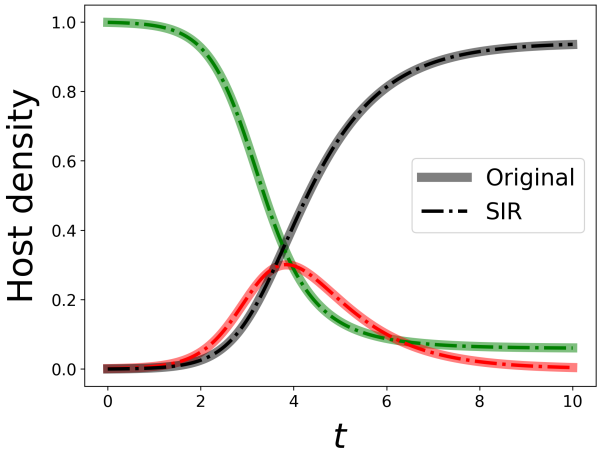

Fig. 2. Approximation to the SIR model in the suitable parameter range

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