Modelling parasite-induced marine diseases of immobile hosts

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Marine infectious diseases are more prevalent in recent times due to climate change and other anthropogenic pressures, posing a substantial threat to marine ecosystems and the conservation of their biodiversity [1]. An important subset of marine organisms are sessile, for which the most common mechanism for disease transmission is direct contact with waterborne parasites. Only recently, some deterministic compartmental models have been proposed to describe this kind of epidemics, being these models based on non-spatial descriptions where space is homogenised and parasite mobility is not explicitly accounted for [2]. These models have been able to describe experimental data in some specific situations, and thus are a good start point to develop more complex models. Indeed, in realistic situations epidemic transmission is conditioned by the spatial distribution of hosts and the parasites mobility patterns. Thus, the interplay between these factors is expected to have a crucial effect in the evolution of the epidemic, so calling for a explicit description of space.

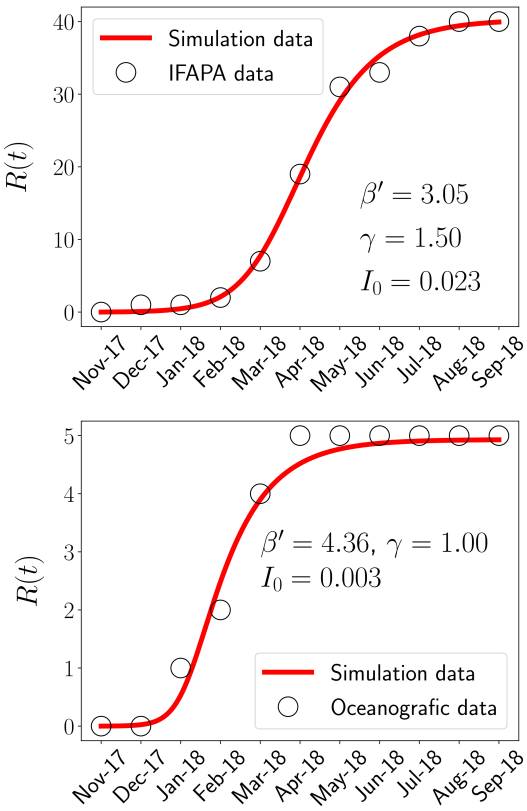

Fig. 1. Model fit using two experimental data sets of the mass mortality event of *Pinna nobilis*.

First, we built a mean-field spatially-homogeneous compartmental model and performed and extensive analytical study [3]. As a result, we were able to show that the model has an exact reduction via a conserved quantity and an approximate one that yields the original SIR model with effective coefficients. The model and its reductions were validated with experimental data of the mass mortality event of *Pinna nobilis* [4] (Fig. 1).

Then, we develop a spatially-explicit individual-based version of the model [5]. We investigate the impact of spatial disease transmission, performing extensive numerical simulations and analytical approximations. Specifically, the effects of parasite mobility into the epidemic threshold and the temporal evolution of the epidemic are assessed. We show that larger values of pathogen mobility have two main implications: more severe epidemics, as the number of infections increases, and shorter time-scales to extinction. Moreover, an analytical expression for the basic reproduction number of the spatial model, $\tilde{R}_0$, is derived as function of the non-spatial counterpart, R_0, which characterises a transition between a disease-free and a propagation phase, in which the disease propagates over a large fraction of the system. This allows to determine a phase diagram for the epidemic model as function of the parasite mobility and the basic reproduction number of the non-spatial model (Fig. 2).

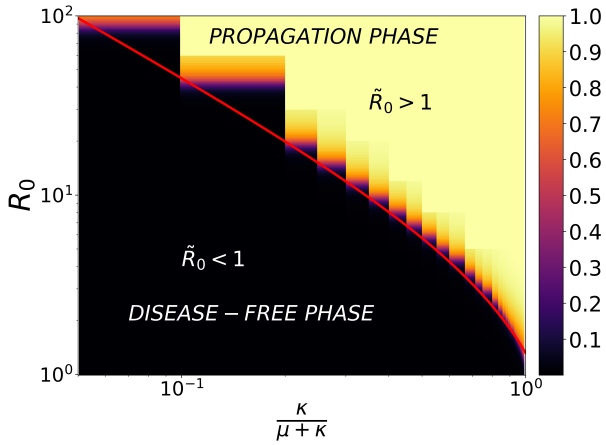

Fig. 2. Phase diagram showing the transition between the the disease-free phase and the propagation phase for several values of the parasite mobility and R_0. The colour code represents the density of dead individuals in the final state of the epidemic computed by the average over 1000 realisations.

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[4] García March et al., Biol. Cons. **243** (2020)

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