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Discrete stochastic metapopulation model with arbitrarily distributed infectious period

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ABSTRACT

In this study, a stochastic discrete-time model is developed to study the spread of an infectious disease in an n-patch environment. The model includes an arbitrary distribution of the (random) infectious period T, and the results are used to investigate how the distribution of T may influence the model outcomes. General results are applied to specific distributions including Geometric, Negative Binomial, Poisson and Uniform. The model outcomes are contrasted both numerically and analytically by comparing the corresponding basic reproduction numbers $\mathcal{R}_0$ and probability of a minor epidemic (or probability of disease extinction) $\mathbb{P}_0$. It is shown analytically that for $n = 2$ the reproduction numbers corresponding to different distributions of T can be ordered based on the probability generating function ϕ_T of T. In addition, numerical simulations are carried out to examine the final epidemic size $\mathcal{F}$ and duration of the epidemic $\mathcal{D}$ of a two-patch model.

1. Introduction

Deterministic and stochastic epidemic models have commonly assumed that the disease stages, particularly the infectious period (IP), follow an exponential distribution (continuous-time) or a Geometric distribution (discrete-time). The very property of these distributions that makes these models tractable, the memoryless property, is biologically unrealistic for most infectious diseases. It has been shown that models with these simplifying assumptions may generate misleading assessments on disease control strategies [1,2].

One of the more realistic alternatives to the exponential (Geometric) distribution for the IP that has been considered is the Gamma (Negative Binomial) distribution, which is a natural generalization due to its relationship with the exponential (Geometric) distribution. When a Gamma distribution is considered, the so called "linear chain trick" can be used to reduce the system of integro-differential equations to a system of ordinary differential equations (see, for example, [1,3–5]). The key idea in this approach is to introduce multiple substages for the IP, each of which follows an exponential distribution. A similar idea is applied in stochastic models to allow the use of Gamma distribution for the IP, while still preserving the Markov property of the process. Such models were first developed and studied in [6,7] and more recently in [8,9].

Stochastic models with an arbitrary distribution for the IP were first considered in [10–12], but Sellke's construction [13] helped derive stronger results such as those in [14,15]. Some recent studies have focused on understanding the effect of disease stage distributions on the model outcomes (see, for instance, [16–19]).

In [20], a patch model is used to study the spread of an epidemic through a population divided into n sub-populations (patches), in which individuals move between the patches according to the law of a continuous Markov chain (dynamic population epidemic model). In this framework, infected individuals make contacts with members currently in the same patch. In a more recent study on a continuous-time patch model [21], an expression for the basic reproduction number $\mathcal{R}_0$ and the extinction probability of the epidemic are derived in terms of the IP distribution. It was shown that for a two patch model $\mathcal{R}_0$ is maximized by an IP with constant length. For three or more patches, however, it is very difficult to draw general conclusions about the effects of IP distribution on $\mathcal{R}_0$ or the extinction probability. In the current study, we extend some of the results in [21] to an analogous discrete-time model.

Most epidemic models are in the continuous-time setting, studies on discrete models have been very limited. Mathematical formulations of continuous-time models are in general complicated when an arbitrarily distributed IP is included, particularly when the models also include control measures such as quarantine and isolation (e.g., [1]). This may make it challenging for modelers to communicate with biologists and public health policymakers. Analogous discrete-time models can be formulated in a way that is much easier to understand for non-mathematicians (see, for example, [2,22,23]). Another major

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