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Reproduction numbers for discrete-time epidemic models with arbitrary stage distributions

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Using an approach similar to that for continuous-time models, derivations of $\mathcal{R}_0$ and $\mathcal{R}_C$ for discrete-time epidemic models with arbitrary stage distribution are presented, and the formulas are shown to be consistent with those obtained from biological considerations. Both models with specific distributions for the infectious stage and models with an arbitrarily distributed (bounded) infectious stage are considered. Results show that the formulas for $\mathcal{R}_0$ and $\mathcal{R}_C$ can be expressed in terms of disease transmission rates and the means of stage distributions. Examples of Susceptible-Exposed-Infected-Recovered models as well as a model with disease control (e.g. isolation or hospitalization) are presented.

Keywords: reproduction number; discrete-time model; epidemics; arbitrarily distributed stage durations

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1. Introduction

When mathematical models are used to study the disease transmission dynamics of a pathogen, the reproduction number $\mathcal{R}_0$ and the control reproduction number $\mathcal{R}_C$ play a critical role. Various approaches have been developed for the derivation of an analytical expression for $\mathcal{R}_0$ ($\mathcal{R}_C$), which can provide helpful insights into the disease prevalence and control as well as the evolutionary dynamics of the pathogen. These studies include both continuous-time models (see, e.g., [3,6,8,9,12,16,17]) and discrete-time models (see, e.g., [1,4,5,7,11,14,19]). This paper focuses on the use of the next generation matrix approach for the derivation of analytic expressions of $\mathcal{R}_0$ ($\mathcal{R}_C$) for discrete-time epidemic models, particularly, under the assumption of arbitrarily distributed infectious period.

We have previously studied discrete-time epidemic models, in which we focused on modelling the effect of disease control (e.g. drug treatment, quarantine and isolation) on the reduction in the control reproduction number $\mathcal{R}_C$ and the final epidemic size (see [2,11]). In both papers the formulas for $\mathcal{R}_C$ were obtained and justified from the usual biological interpretations, namely the average number of secondary infections generated by a typical infected individual during the entire period of infection in a wholly susceptible population. In this paper, we adopt the method used in [1] and present the derivation of $\mathcal{R}$ (either $\mathcal{R}_0$ or $\mathcal{R}_C$) using the next generation matrix approach. That is, in the discrete-time case

$$\mathcal{R} = \varrho\big(F(I - T)^{-1}\big), \tag{1}$$

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