Basic Reproduction Number in a Growing Population

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Abstract The basic reproduction number of a fast disease epidemic on a slowly growing network may increase to a maximum then decrease to its equilibrium value while the population increases, which is not displayed by classical homogeneous mixing disease models. In this paper, we show that, by properly keeping track of the dynamics of the per capita contact rate in the population due to population dynamics, classical homogeneous mixing models show similar non-monotonic dynamics in the basic reproduction number. This suggests that modeling the dynamics of the contact rate in classical disease models with population dynamics may be important to study disease dynamics in growing populations.

Keywords Basic reproduction number, Population dynamics.

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1. Introduction

Contact networks are graphs representing the person-to-person contact structure in a population, in which the nodes represent individuals and the edges represent contacts (see, e.g., [1] and [8, Chapter 17]). They are more realistic than homogeneous mixing models to describe the heterogeneous and long-term nature of human contacts. Not surprisingly, they give predictions that cannot be easily reproduced in homogeneously mixing models. For example, on networks, the Susceptible-Infectious Susceptible models (or SIS, for diseases without acquired immunity) have a larger basic reproduction number than that of the Susceptible-Infectious-Removed models (or SIR, for diseases with lifetime acquired immunity) with the same disease and contact parameters [7], due to that fact that the long-term contacts allows multiple transmissions along an edge for SIS models, but not for SIR models. In addition, network SIS models introduces correlations in the infection status of neighboring nodes [4]. These cannot be observed in homogeneous mixing models.

Interestingly, Yuan et al. [10] shows another feature of network disease models, that the basic reproduction number $\mathcal{R}_0$ may display non-monotonic behavior in a growing population, i.e., $\mathcal{R}_0$ may increase to a maximum then decrease to an equilibrium value while the population increases to an equilibrium. There have been extended studies in homogeneous mixing disease models with population dynamics

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(see, e.g., [5,6] and [2, Section 10.2]). These studies assume that the per-capita contact rate either is a constant, or scales monotonically with the population size. Yet, none has shown such non-monotonic dynamics in the basic reproduction number as predicted by the network models.

We conjecture that this non-monotonic behavior is the result of precise counting of contacts in networks models, which has always been neglected in homogeneous mixing models. Specifically, for a population with N individuals and a per capita contact β, i.e., a total contact rate if βN in the population, when one individual leaves, his/her contacts are also removed. Because contacts are mutual, this must cause the peers of his/her contacts to have a lower contact rate. On the other hand, if one extra individual comes in with a contact rate β, he must contact others who already have a contact rate β, and thus increase their contact rate. We propose that if we properly count for the change in per capita contact rate by counting the dynamics of total contact rate in the population, then the homogeneous mixing models will show similar non-monotonic behavior in $\mathcal{R}_0$.

In Section 2, we construct a mathematical model that incorporates the dynamics of the per capita contact rate due to a slow population dynamics, and study the basic reproduction number of a fast disease dynamics (during which the population size can be regarded as a constant). This model is analyzed in Section 3 and is shown to have a non-monotonic dynamics for $\mathcal{R}_0$. Concluding remarks are given in Section 4.

2. Model

The main goal of this paper is to model the change of the per capita contact rate in a growing homogeneously mixed population. To do so, we assume a simple population dynamics: the births (or immigrations) are assumed to be a constant λ, and the per capita death rate μ is also a constant. Thus, the population size $N(\tau)$ at time τ can be modeled as

$$\frac{dN}{d\tau} = \lambda - \mu N \, .$$

Here we model the total contact rate in the population at time τ, $C(\tau)$, and then compute the per capita contact rate $\beta(\tau)$ from $C(\tau)$ as

$$\beta(\tau) = \frac{C(\tau)}{N(\tau)} \, ,$$

because we assume a homogeneous population, and thus every individual has the same per capita contact rate at time τ. This idea is well summarized in [3, Page 33].

Assume that each incoming individual brings in β_0 contacts per unit time, to random individuals in the population. Thus, the total $\lambda\beta_0$ incoming contact rate causes an increase of the same amount in the total contact rate $C(\tau)$ among the original individuals the population. Thus, $C(\tau)$ increases by $2\lambda\beta_0$ per unit time. On the other hand, when an individual leaves (or dies), he/she takes away his/her $\beta(\tau)$ contacts per unit time, and at the same time, causing a decrease of $\beta(\tau)$ in the total contact rate $C(\tau)$ among the remaining individuals. Thus the total rate of contacts in the population decreases by an amount

$$2\mu N(\tau)\beta(\tau) = 2\mu C(\tau) \, .$$