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Estimating Finite-Population Reproductive Numbers in Heterogeneous Populations

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Abstract

The basic reproductive number, $\mathcal{R}_0$, is one of the most important epidemiological quantities. $\mathcal{R}_0$ provides a threshold for elimination and determines when a disease can spread or when a disease will die out. Classically, $\mathcal{R}_0$ is calculated assuming an infinite population of identical hosts. Previous work has shown that heterogeneity in the host mixing rate increases $\mathcal{R}_0$ in an infinite population. However, it has been suggested that in a finite population, heterogeneity in the mixing rate may actually ***decrease*** the finite-population reproductive numbers. Here, we outline a framework for discussing different types of heterogeneity in disease parameters, and how these affect disease spread and control. We calculate "finite-population reproductive numbers" with different types of heterogeneity, and show that in a finite population, heterogeneity has complicated effects on the reproductive number. We find that simple heterogeneity *decreases* the finite-population reproductive number, whereas heterogeneity in the intrinsic mixing rate (which affects both infectiousness and susceptibility) *increases* the finite-population reproductive number when $\mathcal{R}_0$ is small relative to the size of the population and *decreases* the finite-population reproductive number when $\mathcal{R}_0$ is large relative to the size of the population. Although heterogeneity has complicated effects on the finite-population reproductive numbers, its implications for control are straightforward: when $\mathcal{R}_0$ is large relative to the size of the population, heterogeneity decreases the finite-population reproductive numbers, making disease control or elimination easier than predicted by $\mathcal{R}_0$.

Keywords: Basic Reproductive Number, Heterogeneity, Super-spreaders

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1. Introduction

The effect of heterogeneity on disease dynamics is a foundational question in infectious disease modeling. Recently, renewed attention has been given to the impact of heterogeneity on the basic reproductive number, $\mathcal{R}_0$ (31; 45; 36). $\mathcal{R}_0$ is the average number of secondary infections from a single infectious individual in an otherwise totally susceptible

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