



Basic stochastic transmission models and their inference

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Abstract

The current survey paper concerns stochastic mathematical models for the spread of infectious diseases. It starts with the simplest setting of a homogeneous population in which a transmittable disease spreads during a short outbreak. Assuming a large population some important features are presented: branching process approximation, basic reproduction number R_0 , and final size of an outbreak. Some extensions towards realism are then discussed: models for endemicity, various heterogeneities, and prior immunity. The focus is then shifted to statistical inference. What can be estimated for these models for various levels of detailed data and with what precision? The paper ends by describing how the inference results may be used for determining successful vaccination strategies. This paper will appear as a chapter of a forthcoming book entitled *Handbook of Infectious Disease Epidemiology*.

1 Introduction

The current chapter aims at presenting some basic stochastic models for the spread of infectious diseases in human (or animal) populations, and to also describe how to perform inference about important model parameters, such as the basic reproduction number R_0 and the critical vaccination coverage v_C . Naturally, there is some overlap, but also differences, with the current chapter and other overview papers, in particular two by the same author. However, [4] has more focus on the stochastic analysis of models and only briefly touches upon inference procedures, and [5] describe briefly many different inferential aspects with extensive references

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