



Who is the infector? General multi-type epidemics and real-time susceptibility processes

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Abstract

We couple a multi-type stochastic epidemic process with a directed random graph, where edges have random lengths. This random graph representation is used to characterise the fractions of individuals infected by the different types of vertices among all infected individuals in the large population limit. For this characterisation we rely on theory of multi-type real-time branching processes. We identify a special case of the two-type model, in which the fraction of individuals of a certain type infected by individuals of the same type, is maximised among all two-type epidemics approximated by branching processes with the same mean offspring matrix.

Keywords: Epidemics, Multi-type branching process approximation, Susceptibility processes, Directed random graphs

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1 Introduction

Mathematical models have proven to be successful in understanding infectious disease dynamics. Often, the focus is on (controlling) the beginning of an epidemic. In many of those models branching process approximations and the concept of the basic reproduction number R_0 (which corresponds to the offspring mean of the approximating branching process) play an important role. In the current paper we consider the entire epidemic outbreak instead. We do so in a setting where there are multiple types of infected individuals. Suppose that a large epidemic outbreak

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