MODELLING PREVENTIVE MEASURES AND THEIR EFFECT ON GENERATION TIMES IN EMERGING EPIDEMICS

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ABSTRACT. We present a stochastic epidemic model to study the effect of various preventive measures, such as uniform reduction of contacts and transmission, vaccination, isolation, screening and contact tracing, on a disease outbreak in a homogeneously mixing community. The model is based on an infectivity process, which we define through stochastic contact and infectiousness processes, so that each individual has an independent infectivity profile. In particular, we monitor variations of the reproduction number and of the distribution of generation times. We show that some interventions, i.e. uniform reduction and vaccination, affect the former while leaving the latter unchanged, whereas other interventions, i.e. isolation, screening and contact tracing, affect both quantities. We provide a theoretical analysis of the variation of these quantities, and we show that, in practice, the variation of the generation time distribution can be significant and that it can cause biases in the estimation of basic reproduction numbers. The framework, because of its general nature, captures the properties of many infectious diseases, but particular emphasis is on COVID-19, for which numerical results are provided.

1. Introduction

While the reproduction number is usually seen as a dynamic quantity, changing over the course of an epidemic, the generation time distribution is often seen as a static object. For example, during the recent COVID-19 pandemic, major efforts have been made to continuously estimate reproductions numbers, while often outdated estimates of the generation time distribution have been employed in the estimation. The distribution of the generation time, which we define here as the time between the infection of a secondary case and the infection of the corresponding primary case, is not an intrinsic property of an infectious disease, on the contrary, it depends on the environment and on the behaviour of the individuals among whom the disease spreads. Consequently, the generation time distribution can be subject to variations, for example, recent studies hint that generation times of SARS-CoV-2 have significantly shortened during the course of the pandemic [2, 11, 22, 27]. When doing inference, it is important to investigate the extent of these variations and take them into account, when substantial.