The effect of multiple characteristic time scales on the nonlinear dynamics of epidemics

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Abstract. We exploit a dynamical model for describing the spread of epidemics with application to the COVID-19 epidemic. We identify multiple characteristic time scales governing such a spreading process and demonstrate their effect on the nonlinear dynamics of the epidemic. We discuss the influence of nonlinear incidence rates and consider a possibility for a variable basic reproduction number.

Introduction

The spread of epidemics is governed by various factors. There are entire classes of models in terms of complexity or approximations to describe spreading processes like epidemics, in particular, dynamical systems (such as SIS/SIR models and their extensions) [1–3]; stochastic models, e.g. [4]; models with spatial flows, e.g. diffusion [5]; and models allowing for nontrivial spatial structure or topology, e.g. [6, 7]. One common feature in the majority of these models is the presence of kinetic coefficients or parameters that characterise the probability of elementary processes per unit time and their characteristic frequencies. These parameters determine a set of characteristic time scales that are peculiar to any spreading process. The purpose of this work is to identify these multiple time scales and to demonstrate their effect on the spread of epidemic, with the recent COVID-19 pandemic (see, e.g. [8]) taken as a case study.

Results and discussion

We have proposed a dynamical model for the simulation of spreading processes, in particular, epidemics [9]. Our model is an extension of the SIQR (susceptible-infected-quarantine-recovered) [10], SIRP (susceptible-infected-recovered-pathogen) [11, 12], and EITS (environmental infection transmission system) [13] models used earlier to describe various scenarios of epidemic spread. It takes into account two possible routes of epidemic spread: direct from the infected compartment to the susceptible compartment and indirect via some intermediate medium or fomites. The model also accounts for the so-called “quiet” (asymptomatic) spreaders, who have no apparent symptoms of infection but can infect others. In this work we analyse the effect of characteristic time scales governing the spread of the epidemic. We discuss several different forms of nonlinear incidence functions that determine the pathogen transmission rates and identify the inherent time scales. We also consider a possibility for a variable basic reproduction number determined by a characteristic decay time scale and estimate its effect on the positions of the epidemic peaks.

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