

# Compartmental epidemic models and their qualitative properties

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Most of the living populations have to cope with different diseases. Some of these diseases are communicable and can decrease the size of the population dramatically. This is why people are eager to understand the mechanism of epidemics and try to prevent their outbreak and propagation by efficient and affordable means (e.g. hygiene, vaccination). One of the tools of the investigation of epidemics may be the construction of mathematical models and the analysis of the solutions of these models.

In 1927, Kermack and McKendrick created an epidemic model (also known as SIR model) in the form of a system of ordinary differential equations

$$\begin{aligned}S' &= -aSI, \\I' &= aSI - bI, \\R' &= bI,\end{aligned}$$

where  $I = I(t)$ ,  $S = S(t)$  and  $R = R(t)$  denote the number of infective, susceptible and removed (by immunity or death) individuals as a function of time  $t$ , respectively. The contact rate  $a$  and recovery coefficient  $b$  are positive known numbers. This model has been improved several times taking into account also births, deaths, latent periods, reinfections, incubations etc. These models are called compartmental models because they divide the population into some subpopulations, so-called compartments (e.g. susceptibles, infectives, removed).

In our talk, after giving a short history of epidemics and a review of the compartmental models we turn to the main drawbacks of these models: the models assume that the population is homogeneous, that is they do not take into the account the different spatial positions of the individuals. There are several methods to bring also spatial dependence into the picture. For example, it is possible to allow the motion of the individuals in the population. This concept results in a system of reaction diffusion equations. Another possibility is to divide the original population into subpopulations and connect them somehow into a network according to some prescribed rules for the disease propagation. We will consider a third approach, which is similar to the last one but the division is carried out by an equidistant spatial mesh and not according to some geopolitical considerations.

We will define discrete one-step iterations in order to model the disease propagation. We assume that the speed of the motion of the individuals can be neglected compared to the speed of the disease and we neglect the natural births and deaths. We define the basic qualitative properties, such as nonnegativity and monotonicity, of this discrete model and give the sufficient conditions of the properties in the form of some bounds for the time-step. The discrete model can be considered as a discretization of some continuous models. We show that these continuous models may have wave form solutions. Numerical test results will be presented.

(This work is a joint work with István Faragó, MTA-ELTE Numerical Analysis and Large Networks Research Group.)