Exploring the Epidemic Curve

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Imagine a large population of individuals, of which some proportion contracts a new disease. Each infected randomly makes contact with any member of the population at one-to-all contact rate β. If the contacted individual is susceptible, *i.e.* has never encountered the disease, a new contamination occurs. Infected individuals recover at rate γ and subsequently become permanently immune against the disease, meaning that they cannot transmit nor contract it anymore.

This epidemic model has famously been introduced by Kermack and McKendrick in 1927, and is referred to as the compartmental *SIR* model. It can be formalised using a dynamical system, which describes the dynamics of the proportion of susceptible (s), infected (i) and recovered (r) individuals over time:

$$\begin{cases} \dfrac{ds}{dt} = -\beta si \\ \dfrac{di}{dt} = \beta si - \gamma i \\ \dfrac{dr}{dt} = \gamma i. \end{cases}$$

It is worth noticing that even though it is a simplified vision of a real epidemic, this model and its variations are prone to studying pertinent questions, such as:

Starting from a small number of infected individuals in a large population, will there be a major epidemic outbreak? If so, which fraction of the population will be contaminated? What is the effect of the population demography (births and deaths) on the epidemic?

In order to answer these questions, different mathematical points of view are useful, ranging from the above dynamical system to probabilistic models such as the stochastic *SIR* model, the Sellke construction and discrete-time branching processes.

The key points of this Bachelor Thesis are:

- Studying key characteristics of the epidemic: reproduction number, final epidemic size, endemic equilibrium when demography is taken into account.

- Understanding the interest and limitations of the different mathematical model formulations, as well as the relationships between them.

- Implementing numerical simulations illustrating the previous points.

References

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