

Chapter 2

The Basic Reproduction Number

ABSTRACT

The reproduction number is an important tool in infectious disease epidemiology that conveys both the present status of the disease and the likelihood of it persisting in the future. Next-generation matrices (NGMs) serve as a natural basis for defining and calculating the categories of individuals that can be recognized. The purpose of this chapter is to give details on the construction of NGM matrix with the consideration of different types of compartmental models that can be used in the analysis of the COVID-19 disease. The goal in this chapter is to provide a complete detailed procedure on how to construct a NGM simply by starting with the model specifications. Within this chapter, the authors define how to find the salient features of the NGM based on the three domains: NGM with a large domain, NGM with a small domain, and NGM with a classical domain.

INTRODUCTION

The value of basic reproductive number R_0 is regarded as one of the most important quantities in the study of infectious diseases epidemiology. A mathematical equation that describes the basic reproductive equation and its corresponding number can be used as a measure for the transmissibility of a disease. It is an indicator of the number of new infections that occur when an infectious individual is introduced into a susceptible or naive population. It

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is an indicator of the number of new infections that occur when an infectious individual is introduced into a susceptible or naive population. It is meant to explain the growth or decay of an endemic disease in a simple and clear way. It is likely that the disease will infect a susceptible population when its threshold value is greater than unity, and it will die out when it is less than unity (Diekmann, O., Heesterbeek, J. A. P., & Roberts, M. G. (2010). A related parameter to the basic reproductivity number is the exponential or Malthusian growth parameter r (Ma, J. (2020)). Malthusian parameter classification states that when r goes above zero, the disease invades the host population, but when R goes below zero, the disease dies-off.

In outbreak situations, R_0 is one of the quantities that must be estimated in order to design, control and for taking strict measurements against activated infections. From a theoretical standpoint, it is crucial for the analysis and interpretation of models evidencing infectious diseases. There is hardly a paper in the literature on dynamic epidemiological models that does not address R_0 . It is defined as the average number of new cases of an infection caused by one typical infected individual, in a population consisting of susceptible only.

Generally, the basic reproduction number formula are derived using three main approaches, that is statistical Li, Wu, Yao, (2020) stochastic (Riou & Ithaus (2020), Wu, Leung, & Leung (2020), and mathematical (Obeng-Denteh & Fosu (2014,2015 &2016)). The mathematical approach has several subdivisions and the most common is the use of the next generation matrix (NGM). In all these cases, the basic reproductive formula is obtained from the Jacobian matrix. The Jacobian matrix is the first partial derivatives of the given system of equations. The differential equations are also deduced from the compartmental diagrams.

A host/infectious agent system consists of several traits of individuals with epidemiological relevance. For instance, age, sex, and species. The case will only be considered if these traits divide the population into a finite number of discrete categories. Then one can create a matrix that shows how many individuals in each category were newly infected and how many individuals were infected in successive generations. A matrix for which K is usually the denotation is called a next-generation matrix (NGM); it was introduced in Diekmann et al. (1990), who suggested R_0 as the dominant eigenvalue of S . This chapter demonstrates how to construct the NGM for any such system. It is important to understand that the structure of the NGM can be related to its epidemiological interpretation, and that this interpretation can be used in order to extract relevant information from it in a systematic manner (Arienzo & Coniglio, 2020, Sahafizade & Sartoli, 2020,Zhou et.al,2020).

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