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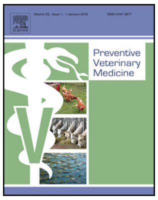

Complex system modelling for veterinary epidemiology

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ABSTRACT

The use of mathematical models has a long tradition in infectious disease epidemiology. The nonlinear dynamics and complexity of pathogen transmission pose challenges in understanding its key determinants, in identifying critical points, and designing effective mitigation strategies. Mathematical modelling provides tools to explicitly represent the variability, interconnectedness, and complexity of systems, and has contributed to numerous insights and theoretical advances in disease transmission, as well as to changes in public policy, health practice, and management. In recent years, our modelling toolbox has considerably expanded due to the advancements in computing power and the need to model novel data generated by technologies such as proximity loggers and global positioning systems. In this review, we discuss the principles, advantages, and challenges associated with the most recent modelling approaches used in systems science, the interdisciplinary study of complex systems, including agent-based, network and compartmental modelling. Agent-based modelling is a powerful simulation technique that considers the individual behaviours of system components by defining a set of rules that govern how individuals ("agents") within given populations interact with one another and the environment. Agent-based models have become a recent popular choice in epidemiology to model hierarchical systems and address complex spatio-temporal dynamics because of their ability to integrate multiple scales and datasets.

1. Introduction

Mathematical models have been applied in epidemiology from the onset of the discipline. The first mathematical model of the transmission of an infectious disease was published in 1766 when Daniel Bernoulli developed a model to evaluate the effectiveness of vaccination for smallpox in England (Bernoulli and Blower, 2004). Greenwood et al. (1936) published the first quantitative transmission experiments in 1936; these were analyzed by Kermack and McKendrick (1936a,b) in their highly influential series on the mathematical theory of epidemics the same year. The application of mathematical models has become its own subdiscipline within epidemiology, and has been described as mathematical, theoretical, or computational epidemiology. Despite the long-standing tradition of modelling in epidemiology, a major expansion in modelling has taken place over the last two decades thanks to the confluence of advances in both computational power

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Abbreviations: ABM, agent-based model; RTLS, real-time location system; R_0, basic reproduction number; ODD, overview, design concepts, and details.

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and modelling methodology, as well as the need for tools to support complex decision making regarding disease control. For example, controlling disease in agricultural settings and/or in the food supply can be regarded as complex systems problems. Pathogen transmission and dissemination are determined by multiple interrelated elements that are influenced by ecological, evolutionary, environmental, and management drivers that act on different scales of time, space, and organizational complexity. For example, herd immunity, the protection of susceptibles that results from the presence of immune individuals that reduce transmission in the population, originates from threshold behaviour associated with the nonlinear nature of pathogen transmission (Fine, 1993). Modelling methods are essential to systems science, the interdisciplinary study of complex systems, because modelling tools explicitly represent the variability and interconnectedness of such systems (Luke and Stamatakis, 2012). In addition, models have been proposed as an approach to enhance causal thinking in epidemiology, as they can effectively deal with interrelated causes acting at different levels (e.g. individual and population levels) (Galea et al., 2010). Addressing the interdependence and complexity of the factors underlying disease causation is challenging, but it also is a necessity to design effective policies. When we are unable to take into account system complexity when predicting policy outcomes, we create "policy resistance," in which implemented interventions fail to deliver or may even aggravate the targeted problem (Sterman, 2000).

The objective of this paper is to provide an overview of modelling approaches that are also used in the interdisciplinary field of systems sciences and are of more recent application in veterinary epidemiology, namely agent-based models (ABMs) and network models. We discuss the principles, advantages, and challenges associated with these approaches. As examples, we present some applications of our own research in addressing pathogen transmission in cattle populations. We integrated real-time animal position data with ABMs to understand how the dynamic contact structure influences the transmission of indirect- and direct-transmitted diseases in cattle and to assess the implications in common modelling assumptions and model complexity.

2. Overview of the modelling approaches commonly used in epidemiology

Compartmental, network, and ABMs are some of the most common modelling approaches used in epidemiology (Fig. 1). In compartmental models, individuals in the population are divided into subgroups, and the changes in the number of individuals in each subgroup are tracked over time based on their epidemiological states (e.g. susceptible, exposed, infected, recovered) (Fig. 2). Compartmental models can be deterministic or stochastic. The outcome in a deterministic model is predicted entirely by the model equations and initial values. Given the same model and same initial values, we should get exactly the same result every time we simulate the model. On the other side, stochastic models incorporate the effect of chance. They predict the probability of various outcomes. In general, stochastic models are more difficult to analyze, and we often turn to simulation to investigate the model behaviour. Compartmental models are often considered an oversimplification because some of the underlying assumptions are considered unrealistic, particularly the assumptions underlying the contact process. Common assumptions in compartmental models include homogeneous mixing (each individual has the same probability of contacting any other individual in the whole population) and infection hazard, which is often dependent on the density of individuals in the population (Begon et al., 2002).

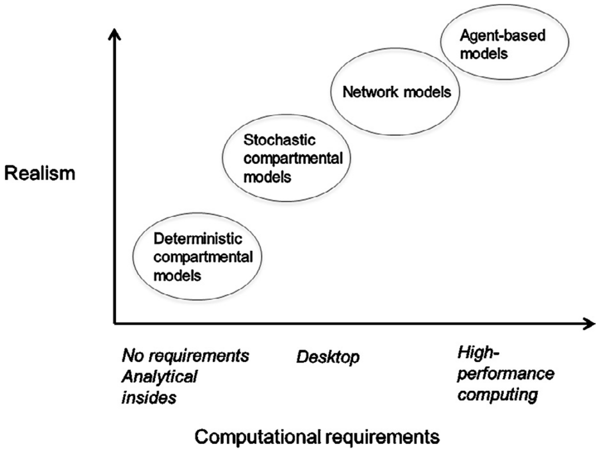

Fig. 1. Trade-offs between model realism and computational requirements for the most common modelling approaches. Both compartmental models and network models may be analyzed analytically and through computational simulations. Agent-based models are analyzed through computational simulations. Simulating large, agent-based models is computationally intensive and may require high-performance computing.

Modelling approaches such as network models or ABMs overcome these problematic assumptions underlying compartmental models. Network models simulate disease transmission by describing more realistic contact patterns among individuals in the population. Agent-based models (also referred to as individual-based models) simulate explicitly each individual in the population (Fig. 2). Herds, enterprises, and other aggregated units can also be described as agents. Agent-based models can incorporate complicated patterns of interaction among individuals in the population, and are able to handle individual variability. Individuals (also called agents) can be characterized by a given number of flexible attributes that influence disease transmission (e.g. level of colonization, antimicrobial use, susceptibility, infectiousness, age, vaccine status, etc.). Network models and ABMs are not mutually exclusive model classifications. Agent-based models often include a network structure that represents agents' interactions.

As these powerful modelling tools become more widely available, it may be tempting to want to use the approach that allows us to create the most realistic model of the problem at hand. The increased realism of the models, however, comes with a price. As a general trend, there is a trade-off between relaxing model assumptions to increase model realism and the needed computing power, data to parameterize the model and tractability of the models (Fig. 1).

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