



EDITORIAL

A Tale of Two Fields: Mathematical and Statistical Modeling of Infectious Diseases

The managing editor of *Osong Public Health and Research Perspectives* (PHRP) attended the Casablanca International Workshop in Mathematical Biology: Analysis and Control, Morocco, June 20–24, 2011. PHRP was welcomed by the community, especially by the infectious disease-modeling group. They welcomed a new public health journal that contains articles for applied mathematical modelers. It is an asset to have such strong supporters for PHRP.

Mathematical models for public health experts are varied. The classical disease-transmission model was created by Kermack-McKendrick in 1927 [1]. In this model, disease transmission is conveniently conceptualized as passage among members of a population by moving among compartments. Actually, this is a special case of the Susceptible-Infectious-Removed (SIR) compartmental model. SIR functions well for infectious or communicable diseases with immunity against re-infection or disease with no immunity. Another model divides I-class into two classes with an exposed period between being infected and becoming infectious, which yields Susceptible-Exposed-Infectious-Removed (SEIR) and Susceptible-Exposed-Infectious-Susceptible (SEIS). We can consider Susceptible-Infectious-Removed-Susceptible (SIRS) models with temporary immunity [1]. In the simple Susceptible-Infected-Susceptible model, the deterministic dynamic structure shows us a great deal about the behavior of stochastic paths and brings to our attention questions that pertain to the stochastic model: What is the nature of the stochastic path as it varies near the deterministic equilibrium? Starting from the deterministic equilibrium, what is the distribution of time until the stochastic hits zero? We should point out that the stochastic models that we have discussed here are simple ones, involving no more than two linked stochastic equations [2]. The basic reproduction number R_0 is the

number of secondary infections caused by a single infective agent introduced in an entirely susceptible population over the course of the infection of this single infective and determines whether there is an epidemic in a population [1]. Stochastic modeling with compartmental stochastic models is often utilized. The dynamics of an Ordinary Differential Equation system informs us of the deterministic skeleton on which the behavior of corresponding stochastic systems are built [2].

Statistical modeling has two tracks to reach conclusions from data. One assumes that the data are generated by a given stochastic data model, whereas the other uses algorithmic models and treats the data mechanism as unknown. Logistic regression is frequently used in public health because it produces a linear combination of the variables with weights that give an indication of the variable importance. The end is a neat result of how the prediction variables affect the response variable plus confidence intervals for the weights. Assume also that each one with a different approach to data modeling fits a model to the same dataset and that each one applies standard goodness-of-fit test, looks at residuals, etc, and is convinced that their model fits the data. Yet the two models give different pictures of nature's mechanism and lead to different conclusions [3]. Computer-generated simulation is becoming increasingly important in inference of given data, but still one of the most hackneyed methods to estimate disease-related phenomena is multiple regression [4].

In this issue two modeling approaches are presented. A compartmental deterministic mathematical model was introduced to predict the evolution of obesity in a population and to propose strategies to reduce its incidence. The authors took obesity as an epidemic and developed a model based on Susceptible-Infected-Susceptible transmission. Obesity was regarded as an infectious disease caused by

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social peer pressure or social contact. These social contacts had influences on the probability of transmission of a sedentary lifestyle and unhealthy nutritional habits. From these considerations they proposed an epidemiologic-type model to study the epidemic evolution of obesity [5].

Statistical modeling was adopted to estimate seasonal influenza patients in Korea using sentinel surveillance data. This report followed the traditional statistical modeling track. The authors present two regression models: first, they estimated monthly reporting rates (W1) from sentinel clinics of the influenza surveillance system, and then estimated hospital-visit patient numbers for the sentinel clinics. They also estimated weight of scale of treatment of national hospital/clinics to sentinel hospital/clinics (W2). The weight by month and province (W3) was estimated as the last step. The authors obtained the final number of influenza patients with multiple linear regression models using the above weights [6].

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