An Epidemic Aggregate and Individual-Based Model in a Patchy Environment

Phang Piau, Ang Kean Siang, Jane Labadin

Department of Computational Science and Mathematics,
Faculty of Computer Science and Information Technology, Universiti Malaysia Sarawak,
Kota Samarahan, Sarawak, Malaysia
pphang@fit.unimas.my, angkeansiang@live.com, ljane@fit.unimas.my

Abstract – The spatial heterogeneity of susceptible-infected-recovered type of compartmental models are commonly expressed in ordinary differential equation based patchy models, in which all individuals are regarded as having the same type of epidemiological profile and demographic characteristics. However, these patchy aggregate models are often complicated to be constructed especially for three or more patches. Nevertheless, with the help of System Dynamics Modeler in NetLogo, we can conveniently construct a three-patch susceptible-infected-susceptible (SIS) model. A scenario analysis of three residential areas in which individuals are allowed to migrate among those areas was carried out. The same analysis was then carried out by an individual-based model simulated with agent-based modeling technique, in NetLogo as well. The simulation show that the results of individual-based model agree well with the aggregate model by carefully setting the parameters value involved. Hence, individual-based models could be potentially extended as a visualization tool for observing the evolution of epidemic dynamics taking into account weather conditions, landscape patterns and individual behaviours.

Keywords – epidemic patchy model; aggregrate model; individual-based model; scenario analysis

I. INTRODUCTION

The complex nature and emergence of health phenomena and disease causality pose the huge challenges in epidemiology [1], i.e. the study of the spread of disease and its control measures. The epidemiological and demographic aspects of host population are usually incorporated into susceptible-infected-recovered (i.e. SIR) type of compartmental models in the form of ordinary differential equations (ODEs) (see, for example, [2-3] and many others) in mathematical epidemiology. SIR-type of rate equations can be categorized under aggregate models which are suitable to formally analyze and control the global evolution of the epidemic system. However, these mechanism-based SIR-type models assume the individuals in the population are well-mixed and the environment is homogenous, moreover the dispersal or migration terms are often simply added into initial non-spatial model. Considering the natural landscapes are typically far from homogeneous and uniform, it make sense to incorporate spatial heterogeneity parameters to produce a better epidemiological model.

Although ODE patch-based models (e.g. [4-6]) and partial differential equations (PDE) reaction-diffusion models (e.g. [7]) are among the widely-used mathematical models incorporating spatial effects into modeling various disease transmission phenomena, to construct an equation-based spatial structured model is often complicated. For instance, patchy models still remain a challenge when the number of patches is greater than or equal to 3 [8]. Not only that, since the spatial position of a single individual can change across the environment significantly on short time scales in this modern societies, the number of state variables needed to uniquely characterize it become very large and often implies large computational time. Thus, individual-based models [e.g. [9-10]] that explicitly represent each individual in one or more populations are of great importance in describing individual-environment interactions as well as for scenario analysis, i.e. what-if analysis as the epidemiological data is usually not completed or sparse [11].

In this paper we focus our attention on susceptible-infected-susceptible (SIS) model for the disease transmission in patchy environment by two different modeling approaches, namely equation-based aggregate model and rule-based individual-based model. The former is a top-down whereas the latter is a bottom-up modeling approach.

For the aggregate model, patchy SIS model can be viewed as multi-compartmental SIS models. Each compartment is assumed to be homogeneous patch in which all individuals are regarded as having the same type of epidemiological profile and demographic characteristics. When they are connected, the host population is allowed to disperse among the patches with certain immigration and emigration rate of susceptible and infective individuals so as to incorporate spatial heterogeneity of the epidemic system. However, the resulting governing equations could be challenging to solve for a non-mathematics discipline students, especially when the number of patches is large. Thus, for this work, we used the System Dynamics Modeler in NetLogo [12] to rapidly simulate our aggregate model to observe the global behaviour of the evolution of epidemic dynamics in each patch.

Then, we employed the agent-based modeling simulation platform in NetLogo [12] to simulate our individual-based model through imposing probabilistic rules at the individual level in each patch, so as to prototype simple yet realistic

"what-if" analysis for a disease persistence or extinction scenario within and across three patches computationally. The computer simulations developed in this work are primarily serves as an example of experimenting the interaction of many variables to produce a visualization of comparison between the results of aggregate and individual-based model. The parameters included were of those the most essential ones for a SIS model. Thus, simulation outputs presented in this paper are only some preliminary results for understanding a possible complex epidemic system by two different modeling approaches.

The rest of the paper is organized as follows: in the section II mathematical formulations for three patches model are presented. In section III we present the model implementation of our individual-based model. In section IV both the results of aggregate and individual-based models are discussed. Finally in section V we conclude by giving some final remarks and future works.

II. MATHEMATICAL FORMULATIONS OF AGGREGATE MODEL

We follow the patchy SIS epidemic model in [4] and construct our three-patch aggregate model (i.e. $1 \leq i \leq 3$). Unlike the numerical results of mass action epidemic model presented in [4], we presented a standard incidence epidemic model as shown in the following system of ODEs.

$$\frac{dS_i}{dt} = B_i(N_i) - \beta_i \frac{S_i I_i}{N_i} + \gamma_i I_i - \mu_i S_i + \sum_{j=1}^{3} a_{ij} S_j \quad (1a)$$

$$\frac{dI_i}{dt} = \beta_i \frac{S_i I_i}{N_i} - \gamma_i I_i - \mu_i I_i + \sum_{j=1}^{3} b_{ij} I_j \quad (1b)$$

where
S_i = the number of susceptible in patch i
I_i = the number of infective in patch i
B_i = birth rate per capita in patch i
μ_i = death rate per capita in patch i
a_{ij} = immigration rate of susceptible individuals from patch j
    to patch i
b_{ij} = immigration rate of infective individuals from patch j
    to patch i

with the basic reproduction number, $R_{0i} = \dfrac{\beta_i}{\mu_i + \gamma_i - b_{ii}}$. (2)

Following [4], the relation of the immigration and emigration rates of respective susceptible and infective individuals among three patches are shown below.

$$\sum_{j=1}^{3} a_{ji} = 0, \quad \sum_{j=1}^{3} b_{ji} = 0, \quad 1 \leq i \leq 3 \quad (3)$$

Equations (3) implies that the total immigration rate of susceptible (or infective) individuals from patch i to patch j is equal to the emigration rate of susceptible (or infective) individuals in patch i. However, only the dispersal rates of infective individuals have an effect on the basic reproduction number, as shown in (2). The basic reproduction number is kept constant in standard incidence model since it is not affected by the number of susceptible at any time.

With the help of System Dynamics Modeler in NetLogo, we construct the System Dynamics diagram which made of four elements, namely "stock" for representing the susceptible and infectious population for three patches, "flow" for bringing susceptible and / or infective into or out of a "stock" according to right-hand side of eqs. (1), "variable" for inputting the parameters value (i.e. infection and recovery rate, birth and death rate, dispersal rate), "link" for transmitting a number from a "variable" to a "flow". By constructing System Dynamics diagram, the procedures will be generated as NetLogo code by its built-in mechanism and one is able to obtain numerical solutions to his / her aggregate model. However, we omitted our System Dynamics diagram here due to space constraints.

With this tool, we present a scenario analysis for three patches in which each patch represents a residential area with unique epidemiological profile and demographic characteristics. Patch 1 is a residential area located nearby industrial area with a relative high infection rate and death rate. Patch 2 is a rural area with sparse population and less job opportunities, and therefore the resident are inclined to migrate, especially to patch 3 with attractive living conditions and good medical facilities indicated by high recovery rate and hence the lowest death rate among the three patches. The interface of our aggregate model is given in Fig. 1. The numeric value appeared in each "slider" is the parameter value of our scenario analysis.

In our NetLogo interface, the parameters values (i.e. birth and death rate, infection and recovery rate, dispersal rate) as well as initial conditions (i.e. initial susceptible and infected) to the patch under observed can be easily adjusted through its respective "sliders" while the dependent variables (i.e. the number of susceptible and infective individuals over time) can be visualized through either graphs or reported through "monitor". These visualizations provide convenience for doing sensitivity analysis as well as for the purpose of teaching and learning. For instance, if we set the birth and death rates as well as all the dispersal rates in patch 2 to zero, the "monitor" of R02 (i.e. the basic reproduction number of patch 2) will immediately give value 1. It means that the epidemiological profile of the patch 2 alone without dispersal in our scenario analysis is indeed a population with endemic.

With such interface, the effect of dispersal on the outbreak of disease in three patches can be roughly observed by running the simulations with different combinations of parameters value.