Implementing CASMIM for Epidemic Simulations

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ABSTRACT

This paper outlines the design and implementation of Huang et al.'s (2004) Cellular Automata with Social Mirror Identity Model (CASMIM), a small-world epidemiological model that accurately represents daily contact among individuals. The interactive capabilities of this epidemiological simulation tool are shown by describing the underlying network for a specific disease, giving a demonstration using a specific epidemic transmission example, and adding public health policy interventions to the model to assess their effects. Various simulation tool functions are described in detail. Source code is available via the author's web site.

1. INTRODUCTION

The 2003 SARS outbreak triggered a number of efforts to create epidemic computer simulation models to help public policy makers and epidemiologists understand the dynamics of epidemic transmission and assess the effects of various public health policies[1-3]. Several researchers have recently attempted to simulate potential transmission scenarios for flu viruses (especially for avian flu) involving geographic-social contact networks[4, 5]. Some are using differential equations and compartmental models to derive R_0 (a re-transmission parameter)[6, 7], while others prefer simulating disease transmission via large geographic information systems that monitor human movement and daily contacts[4, 5].

Although compartmental models can be implemented quickly, they cannot be used to clarify the effects of interactions between individuals. In contrast, large geographic information systems can show accurate epidemic transmission details, but they require significant time and effort to develop—especially systems that monitor daily human movements on a geographic plane. I established the CASMIM system published by Huang C.Y., Sun C.T., Hsieh J.L., and Lin H[2], to strike a balance between model accuracy and development complexity, while still maintaining robustness and broad coverage.

Details of several "what-if" experiments will provide to demonstrate CASMIM's functions and interactive capabilities for examining factors that affect epidemic transmission. These experiments are examples of a Problem-Based Learning (PBL) approach that was developed for medical education in the early 1970s and is currently used in over sixty medical schools [8]. Two characteristics make PBL compatible with what-if epidemic simulation system experiments: a) the epidemiological simulation tool can help users gain a sense of *engagement* with real-world epidemic transmission, and b) *interaction flexibility* allows for the use of simulation tools to show how complex systems work under different circumstances—for instance, the execution of various public health policy suites [9]. Epidemic transmissions are usually complex, and single answers often do not exist. Users can model realistic situations via the repeated interactive manipulation of parameters.

2. BACKGROUND

The spread of a contagious disease reflects a close relationship between social networks and individuals who come into contact with each other[2]. A random interaction hypothesis makes it easier for epidemiologists and public health specialists to construct SIR models that represent ranges of possible transmission dynamics for epidemic outbreaks, infectious origins, and disease parameters based on data collected during previous outbreaks of contagious diseases.

However, modern transportation modes and changes in lifestyles have rendered the traditional SIR model incapable of accurately reflecting the transmission dynamics of contagious diseases. Recent statistical analyses and computational simulations of social networks have shown that the global topological characteristics of social networks exert considerable influence on the overall behavior of easily transmitted diseases[11, 12].

Huang et al.'s CASMIM is a small-world computation simulation model that conceptualizes individuals as elements and their most frequently visited places as logically abstracted mirror identities—for example, homes, train stations, workplaces, and restaurants. The mirror identity concept utilizes simple social networks to a) preserve the properties of elements that interact with their neighbors within two-dimensional lattices, and b) reflect such activities as long-distance movement and daily visits to fixed locations[2]. For this reason, the mirror identity concept in CASMIM is suitable for describing epidemics in modern societies. The model has clustering and small-world properties that allow it to simulate epidemic transmission dynamics.

3. SYSTEM IMPLEMENTATION

The simulation tool implements CASMIM by using Borland C++ Builder to encode the underlying social network, disease status transition process, public health policies, and user interface.

3.1. Underlying Social Network

This network is a two-dimensional lattice in which each cell contains a mirror identity belonging to one individual. The entire population is represented by a one-dimensional list. A brief description of individuals and their mirror identities is given in Tables 1-2.

Table 1. Individual class and its attributes.

Name	**Type**	**Description**
ID	Number	A unique number used to identify the individual.
Disease_Status	Character	The individual's disease status.
Attributes	Class	Useful epidemiological information about and personal properties of the individual.
Mirror_Identities	Object Array	A list of the individual's mirror identities.

Table 2. Mirror identity class and its attributes.

Name	**Type**	**Description**
ID	Number	A unique number used to identify a mirror identity.
(X, Y)	Location	Mirror identity location on a 2D lattice.
Home, Hospital	Boolean	Used to identify a mirror identity staying at home or in hospital isolation.

Three steps for initializing underlying social network constructed by individuals and their mirror identities are a) using a normal distribution to pre-determine the number of mirror identities belonging to each individual according to a pre-defined average number of mirror identities; b) locating the mirror identities on a 2D lattice;

and c) building relationships among individuals according to adjacent relationships between mirror identities.

3.2. Personal Disease Status Transition

Integration of the SIR disease status system proposed by Kermack and McKendrick makes it possible for CASMIM to simulate an epidemic [10]. According to the CASMIM approach, every individual has an epidemiological status (*S*, *I*, or *R*) and a geographic mobility status (normal, quarantined, or isolated). Status transitions are determined through a combination of links with adjacent neighbors and probabilistic causes (e.g., infection rate and detection rates for such symptoms as fever). Basic personal disease status transition mechanisms are shown in the left Gray-part of Figure 1. When a patient or susceptible individual goes to a hospital to seek medical treatment, the infection rate increases according to the number of sick neighbors.

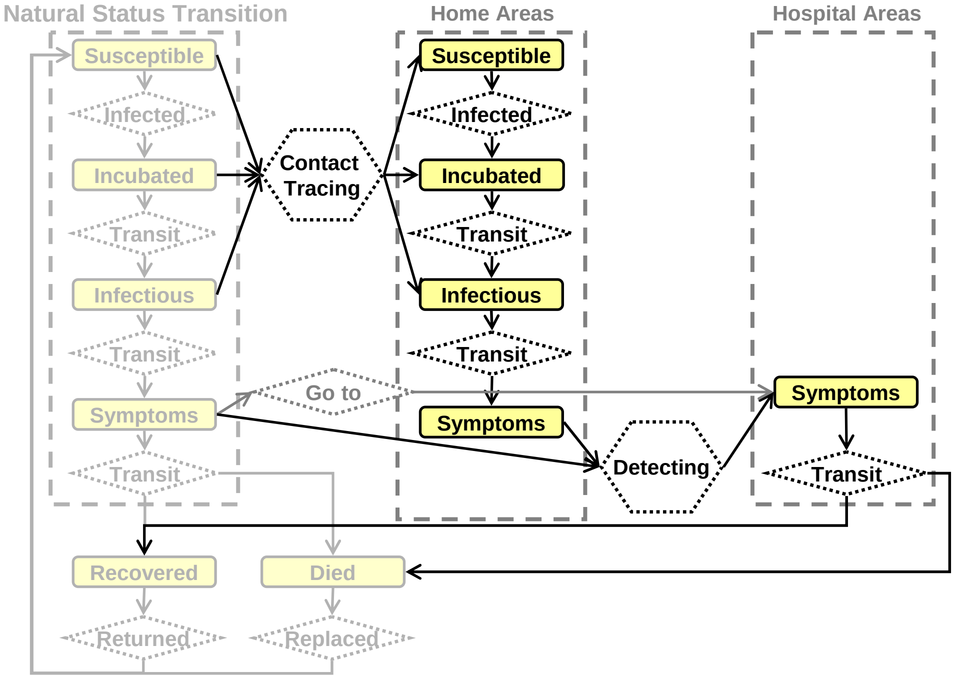


Figure 1. The left Gray-part is natural disease status transition with normal medical system using the SARS example. The right part is full social interventions, all of which lead to changes in social mobility.

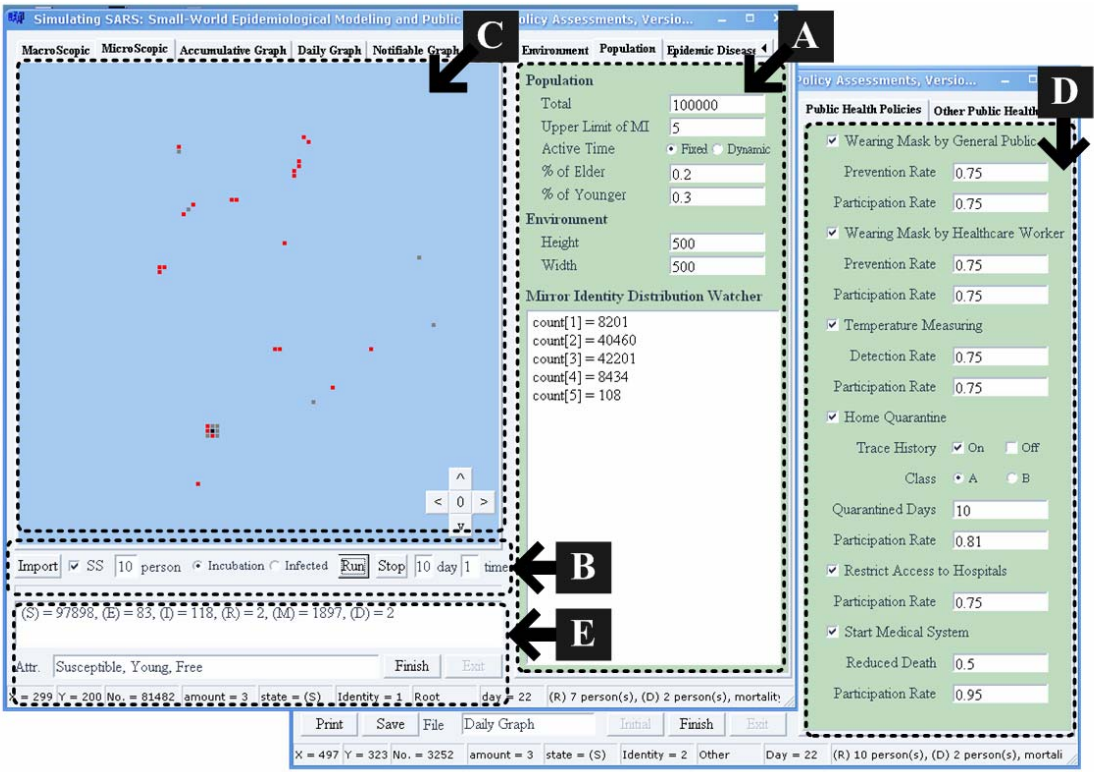
3.3. Intervention of Social Events

One advantage of CASMIM is its use of the mirror identity concept to reflect individual geographic mobility in special areas. This characteristic is particularly useful for analyzing public health policies, which not only influence infection and contact rates, but also change an individual’s social mobility potential. Using health policies executed by the Singaporean government during the SARS outbreak as an example, mask wearing and reduced contact policies decreased the probability of becoming infected and the home quarantine, hospital visitation ban, and body temperature-taking policies restricted social mobility. Figure 1 illustrates the intervention of a contact tracing mechanism that forced potentially infected individuals to stay at home and the detection mechanism used to identify patients with symptoms and consequently send them to local hospitals.

3.4. User Interface

The user interface can be broken down into several parts. The first is designed to help users build an underlying social network by inputting such parameters as population size and average number of mirror identities

(Fig. 2 Part A). The second consists of pre-defined epidemiological parameters related to individual disease status transition. These parameters are set according to recommendations made by epidemiologists. The third consists of imported cases that are input with their epidemiological properties and options for day-by-day simulations (Fig. 2 Part B). The epidemic transmission dynamic is shown via macro- and micro-view windows that allow for observations of detailed transmission along the two-dimensional lattice (Fig. 2 Part C). The health policy input dialogue allows for activating or disabling health policies day-by-day. Users can manipulate participation rate and policy efficiency values as needed (Fig. 2 Part D). Simulation results are shown as daily reported, accumulated, and home quarantine curves. Statistical curves can be updated as day-by-day simulations are run (such as figures 4-6). At the bottom of the simulator is a system information watcher that provides simulation data (Fig. 2 Part E).



Population
Total 100000
Upper Limit of MI 5
Active Time ● Fixed ○ Dynamic
% of Elder 0.2
% of Younger 0.3
Environment
Height 500
Width 500

Mirror Identity Distribution Watcher
count[1] = 8201
count[2] = 40460
count[3] = 42201
count[4] = 8434
count[5] = 108

☑ SS 10 person ● Incubation ○ Infected 10 day 1 time

(S) = 97898, (E) = 83, (I) = 118, (R) = 2, (M) = 1897, (D) = 2

Attr. Susceptible, Young, Free

X = 299 Y = 200 No. = 81482 amount = 3 state = (S) Identity = 1 Root day = 22 (R) 7 person(s), (D) 2 person(s), mortality

File Daily Graph

X = 497 Y = 323 No. = 3252 amount = 3 state = (S) Identity = 2 Other Day = 22 (R) 10 person(s), (D) 2 person(s), mortali

☑ Wearing Mask by General Public
Prevention Rate 0.75
Participation Rate 0.75
☑ Wearing Mask by Healthcare Worker
Prevention Rate 0.75
Participation Rate 0.75
☑ Temperature Measuring
Detection Rate 0.75
Participation Rate 0.75
☑ Home Quarantine
Trace History ☑ On ☐ Off
Class ● A ○ B
Quarantined Days 10
Participation Rate 0.81
☑ Restrict Access to Hospitals
Participation Rate 0.75
☑ Start Medical System
Reduced Death 0.5
Participation Rate 0.95

Figure 2. User Interface of CASMIM.

4. EXAMPLE EXPERIMENTS

4.1. The small-world properties of CASMIM

The first experiment was conducted to examine the effect of average degree of separation between people who visit three fixed locations on a daily basis. The number of an individual’s mirror identities represents the number of fixed places that are visited every day. The focus of this experiment was on the relationship between population size and degree of separation, which highlights how people and their mirror identities in a simulated society are tied together in short-distance relationships. According to the results shown in Figure 3, an increase in total agent population was accompanied by a slow, logarithmic increase in average degree of separation for the entire underlying contact network. The average degree of separation remained sufficiently low to characterize the underlying network as a small-world social network model.

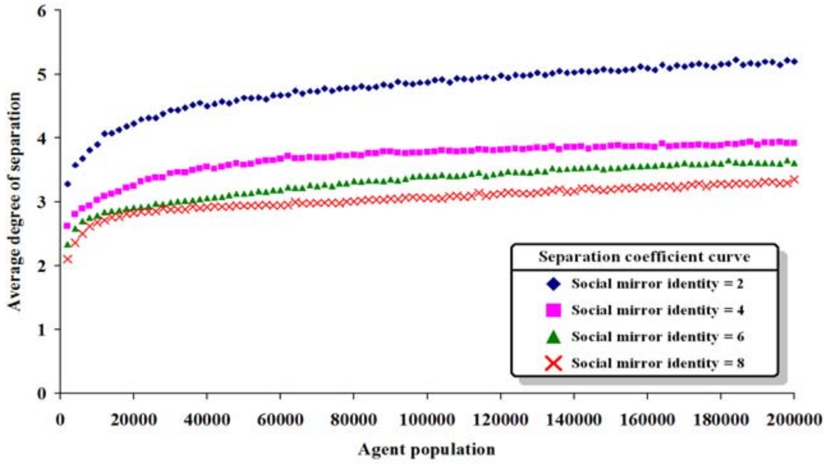


Figure 3. Increase in total population is accompanied by a slow logarithmic increase in degree of separation.

4.2. Epidemic Simulation Capability

Epidemic computer simulation tools allow for quick and repeated interactive manipulation to assist in understanding real-world epidemic transmission using “what-if” experiments. I used the Singapore dataset from Huang et al.’s paper to run the simulation. Imported cases, disease characteristics, and health policy execution were inputted manually on a day-by-day basis according to a timeline published by the Singaporean health authority. Policy efficiency and public participation rates were set up according to suggestions from public health experts.

4.2.1. Disease spread without any control measures.

This experiment can lead to quick insights into whether a medical system can meet the challenges of a new epidemic. Using the SARS simulation as an example, the severity of such symptoms as high fever and heavy coughing meant that almost all patients had to go to a hospital for medical treatment; based on the situation in Singapore, I assumed the operation of a normal medical system. This what-if experiment was easily run using the basic disease transmission rule mentioned in Section 3.2 and Figure 1; results are shown in Figure 4. Based on a SARS reproduction number (*R0*) of 2.56, the results indicate an exponential increase in this scenario.

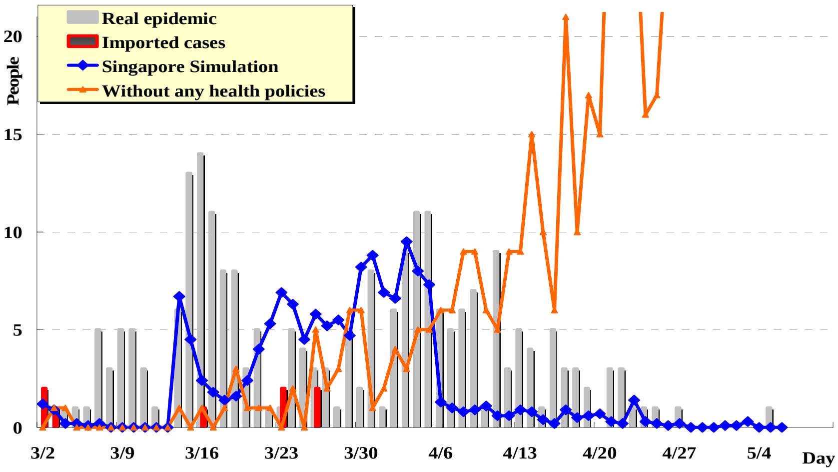


Figure 4. SARS simulation result and original Singapore epidemic curve.

4.3. Effects of public health policy interventions.

Since public health policy execution is a tradeoff between individual health and social cost, a repeatable and flexible computer simulation tool can help in the simultaneous assessment of public health policy efficacy and social cost. Once again I used public health policy interventions from the Singaporean simulation of imported cases from Huang et al.'s research as the trigger and executed health policies day-by-day. I tested three scenarios.

4.3.1. Effects of the removal of a single health policy

Real-world analyses of the influence of a single policy on an epidemic outbreak are very difficult, but simulations allow for the disabling of individual policies in order to measure their effectiveness. According to the results shown in Figure 5, a) a larger number of individuals would have become infected if the general public had maintained its normal rate of contact with neighbors, and b) disease propagation would have been more difficult to control if most people did not follow the mask-wearing policy.

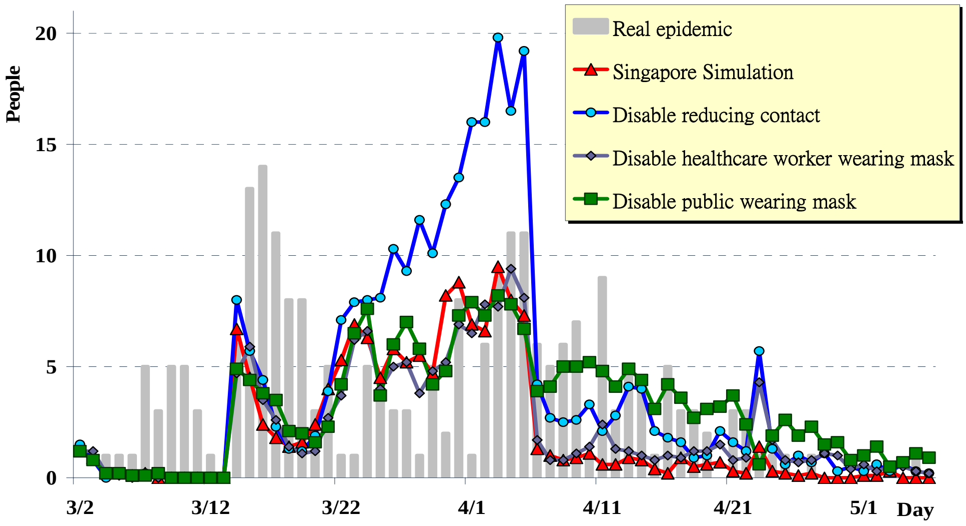


Figure 5. Comparison of scenarios in which individual health policies are disabled.

4.3.2. Effect of early health policy execution

Certain health policies are less effective when they are implemented too slowly, therefore health policy makers and researchers are interested in determining what might have happened had such policies been executed more quickly. I ran a simulation of the Singapore situation with a body temperature measuring policy enacted on 3/23 and compared the results with actual data from executing the policy on 4/22. According to the results shown in Figure 6, earlier enactment triggered a sudden increase in reported cases on 3/24. I therefore concluded that earlier execution of this policy would have been very effective in detecting infected SARS patients and reducing disease propagation.

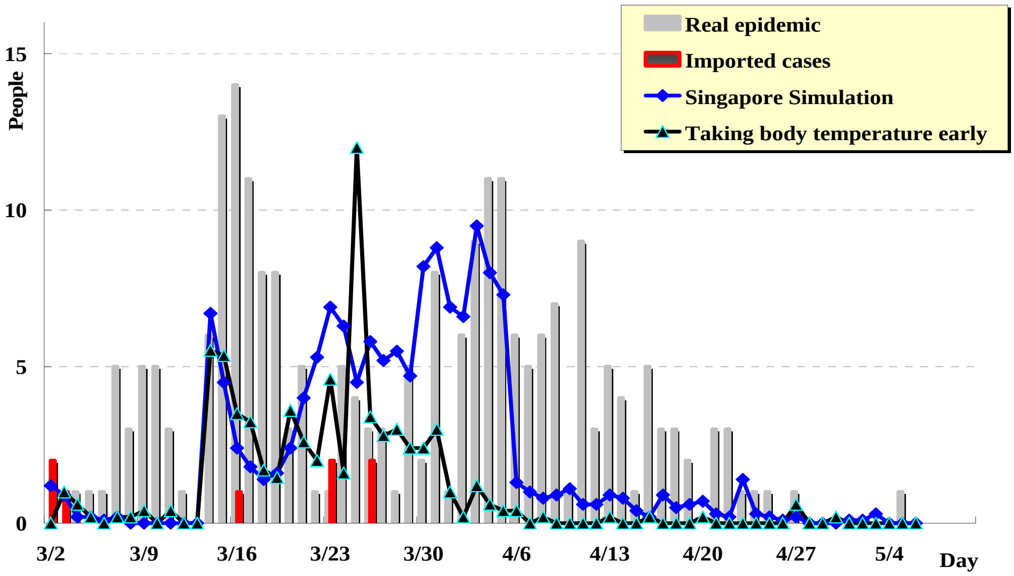


Figure 6. Simulation results of original Singapore simulation and a possible scenario in which a body temperature measurement policy is quickly enacted.

5. CONCLUSION

I used this paper to introduce a simulation tool named CASMIM that implements a social network-based epidemiological simulation model for studying emerging infectious diseases. The model can help users to a) gain a sense of engagement with real-world epidemic transmission and b) review the effects of health policies by manipulating efficiency and time parameters associated with various health policies. The flexibility and extensibility of the mirror identity concept in CASMIM allows for successful simulations of multiple geographic health policies (e.g., home quarantine, hospital isolation, and the presence of super-spreaders). I offered several “what-if” experiment examples to show users how they can manipulate my proposed tool to perform epidemic simulations. I plan on expanding CASMIM for simulating scenarios for flu—a standard type of air transmission epidemic. Those interested can download a copy of this simulation tool (including C++ source code, executable application, sample experiment, instruction manual) from http://www.cis.nctu.edu.tw/~gis93813/SARSTool/.

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