TOWARDS A FRAMEWORK FOR HOLISTIC ANALYSIS OF HEALTHCARE SYSTEMS

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ABSTRACT
We present a work in progress towards building a framework for holistic analysis of Healthcare Systems (HSs) through a disciplined stratification of concerns and a systematic integration of simulation processes in different layers. A lot of simulation-based research efforts can be found in the literature where HSs are studied with focus on perspectives such as the allocation of scarce health care human and infrastructural facilities to meet the needs of patients, disease spreading within an hypothetical community, and so on. The different perspectives are often studied in isolation with constant parameters as abstractions of the influences of other phenomena on the system under study. We propose a methodology for a "loosely" integrated simulation where independent simulation processes of disparate concerns in HS exchange live updates of their influences on one another. We think this approach will take the results obtained closer to the reality of the interactions between health phenomena and help stakeholders take more realistic decisions.

INTRODUCTION
HSs are complex systems of distributed subcomponents governed by complex health processes, inter-organizational workflow, and various services (Barjis 2011). Applications of Modeling and Simulation (M&S) to HSs usually target specific aspects of healthcare problems. Some of these studies include minimizing patients' waiting times in outpatient clinics (Mustafee et al. 2012; Topaloglu 2006), monitoring the flow of patients for efficient utilization of healthcare facilities (Mes and Bruens 2012; Morrice et al. 2013) and epidemiology researches to institute required policies in HSs (Kasaie et al. 2013; Worth et al. 2010). Other areas include studies of human population and healthcare delivery (Charfeddine and Montreuil 2010) and HS management efficient use of scarce human and infrastructural resources for healthcare services delivery (Ma and Demeulemeester 2013; Harper 2002; Persson and Persson 2009).

Discrete Events Simulation (DES) methods have been used recently to study problems related to the performances of HSs (Gunal and Pidd 2010; Mes and Bruens 2012). Other methods combine simulation with optimization techniques, Data Envelopment Analysis (DEA), and goal programming, to study different aspects of healthcare problems (Ahmed and Alkhamis 2009; Topaloglu 2006).

Interestingly, simulation processes to address different healthcare problems are often done in isolation. Since in reality, the system under study exists amidst other systems and phenomena that may influence its internal processes, a common approach to model such influences is to represent them as parameters in the model under study to experiment with different hypothetical values of the parameters in separate simulation runs. For instance, in a simulation of the allocation of healthcare resources to tackle the spread of a disease in an environment, the model may include some parameters as abstractions of the coefficients of the levels of infections, awareness, migration, etc. in the community. Then some hypothetical sets of values of the parameters are used for separate simulation runs to investigate the performance of the resource allocation. In reality, however, some (or all) of these coefficients could change within the periods of each simulation runs examined thereby making the modeler's assumption about them obsolete. Conversely, a simulation model of the epidemic itself may contain abstractions of coefficients mentioned previously including a parameter representing the level of healthcare resource allocations which are all maintained constant for different simulation runs of the epidemic model.

We argue that there is need to explore more pragmatic approaches to make situations, and hence, the results obtained as close as possible to reality. Therefore, we propose the parallel simulation of independent disparate simulation models of different problems whose outputs may influence one another and systematically transmit live updates and feedbacks between them. For instance, if we may simulate the epidemic model described previously concurrently with models that are sources of its parameters (i.e., levels of resource allocation, awareness, migration, etc.) and allow them to communicate new values of the parameters to one another. This approach will result in more accurate forecasts of the effects of the interactions between the different components of HSs and their responses to issues. We provide more details on the proposal in the next section, followed by a simple example as illustration; then we provide concluding remarks and directions for future work.

HEALTHCARE SYSTEM MODELING
Considering the complexity of the HSs and the diversity and requirements of simulation objectives in the domain, we propose a four-layered stratification of common M&S objectives for better placement of problems and selection of suitable formalisms to model the problems in a framework. Figure 1 shows the formulated layers in dashed boxes with double arrows representing the mutual interactions between them.

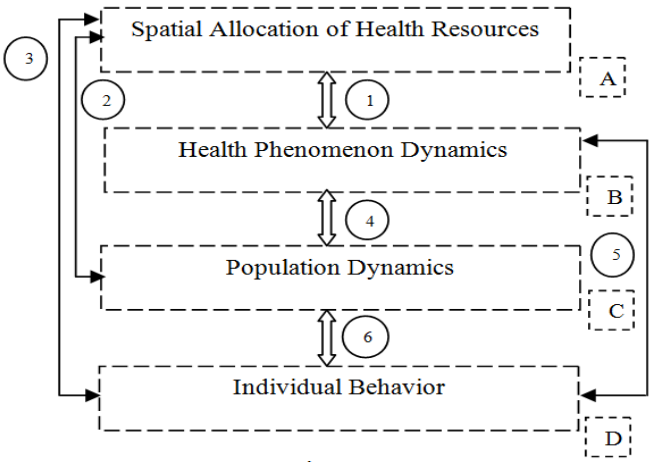

Figure 1: Layers of concerns in Healthcare Systems

At layer A, the Spatial Allocation of Healthcare Resources represents resources (human and infrastructural) allocated to meet demands for healthcare services. Problems in this layer can usually be described as discrete events systems as it often involves scheduling of resources for specific services delivery and responses to service requests. A suitable formalism to model problems in this layer is the Discrete Events System Specification (DEVS) (Zeigler et al. 2000).

The Health Phenomenon Dynamics layer (layer B) represents the group of investigations of health-related phenomena in a community that may lead to a change in the demands for healthcare services. Examples of such phenomena include the disease spreading due to epidemics, seasonal occurrences, person-person contact, etc. Cellular Automata is usually used to model problems in this domain.

Layers C represents the category of problems to study how the dynamics in the population of a community may influence or be influenced by other health issues or the allocation of healthcare resources in the environment. Such dynamics in population may include birth, death, immigration and emigration rates. Such problems may be modeled with formalisms like Differential Equations.

The individual behavior at level D describes the category of problems involving the investigations of human behaviors and personal habits such as educational level, physical state, emotion, cognition and social status in relation to other healthcare concerns and allocations of resources. Problems in this category may be modeled with Petri nets.

INTEGRATION OF HS SIMULATION LAYERS

In this section we describe the notion of "loose" integration between models in the different layers described in the previous section. Let us assume that Figure 2 represents the loose integration of simulation models, one in layer A and the other in layer C. We use the term "loose" integration to describe our notion of parameter integration here to indicate that the simulations models involved are not tightly coupled together as is usually the case in the couplings between the ports of models in the same layer; Rather, each model runs independently in its own experimental frame. Each model provides an input and an output interface similar to the update and notifier methods of the Observer for each of its input and output parameters. Therefore, when the simulations run concurrently, each output parameter notifies all its observers whenever there is a change in its value.

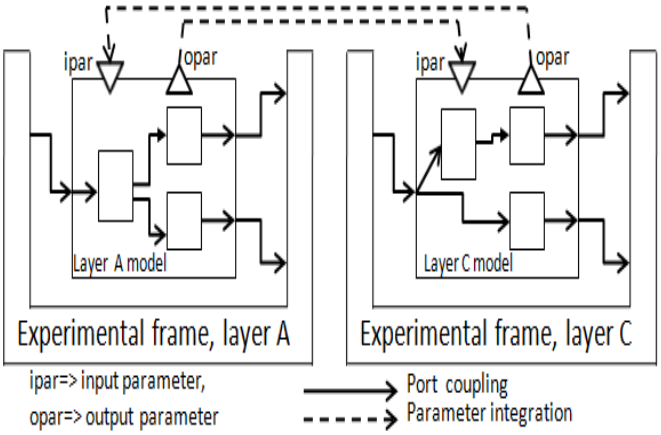

Figure 2: Loose integration of models in different HS layers

CASE STUDY

In this section, we report our experiment with the model by White (White et al. 2009) for simulating disease spreads during epidemics. This study falls within layer B in our classification presented in Figure 1 and it is modeled with the two-dimensional Cellular Automata (CA).

Each cell of the CA is considered to represent a square area of the land in which the epidemic is propagating in a population and the state, $s_{a,b}^{t} \in [0,1]$, of any cell (a,b) at any time, t, represents the ratio of infected population to the total population of the cell. Also, it is considered that the state of any cell, (a,b), at any time t depends on the states of its eight neighboring cells, $V^{*} = \{(\alpha,\beta) | a-1 \leq \alpha \leq a+1, b-1 \leq \beta \leq b+1\} - \{(a,b)\}$ and that of the cell itself in the previous time step. They proposed a local transition function for each cell (a,b) at a time step $(t+1)$ as:

$$s_{a,b}^{(t+1)} = g\left((1-P(t))s_{a,b}^{t} + (1-s_{a,b}^{t})\left[\varepsilon s_{a,b}^{t} + \sum_{\alpha,\beta \in V^{*}} \mu_{\alpha\beta}^{(a,b)} s_{a+\alpha,b+\beta}^{t} \right] \right)$$

Where: $P(t) = 0.2t + 0.2$ is a measure of the infected population that has recovered from the disease within the last time step, g is a discretization function that returns a value in [0,1], (see White et al. 2009) for more details. The real parameters ε and $\mu_{\alpha\beta}^{(a,b)}$ are characteristics of the epidemic and the environment with $\mu_{\alpha\beta}^{(a,b)} = c_{\alpha\beta}^{(a,b)} \times m_{\alpha\beta}^{(a,b)} \times v$ where $c_{\alpha\beta}^{(a,b)}$ and $m_{\alpha\beta}^{(a,b)}$ are abstractions of connections/links and movement of infected people respectively between cell (a,b) and its neighboring cells V^{*} and v is the virulence of the epidemic. The authors presented a simulation of the model with the following constant assumptions of the parameters: $\epsilon = 0.4$, $c_{\alpha\beta}^{(a,b)} = 1$ indicating that there exist connections/transportation links between every cell and its neighbors; $m_{\alpha\beta}^{(a,b)} = 0.4$ representing the movement of infected people between the different cells and $v = 0.4$.

Our Proposal

We claim that instead of constant parameters as abstractions of other healthcare concerns in the present simulation, it would be reasonable to have real models of the situations running concurrently and exchanging feedbacks with the disease spread simulation. We believe that the results obtained from this approach will give more accurate representation of reality. For instance, in reality, an outbreak

within a cell can lead to change in the pattern of movements between the cell and its neighboring cells; a model of this situation can find its place in layer B of Figure 1. It is also noteworthy to mention that this model of the movement pattern may be influenced by other factors such as the activities of healthcare facilities in the cell under study and its neighboring cells (models in layer A of Figure 1) and individual habits and characteristics such as awareness, immunity or vaccinations (layer D models).

We cannot provide elaborate models of all factors in this short paper due to space limitations; we have, however, repeated the same simulation twice for the same number of time steps. In the first simulations, we maintained the constant values proposed by the authors (i.e., White et al. 2009) and in the second, we used randomly generated numbers between 0 and 1 as the values of $m_{\alpha\beta}^{(a,b)}$ (the movement of people between the cells) which were assumed to be coming from an independent simulation running concurrently. We present the results in the next subsection.

Simulation Results

Recall that the state of any cell (a, b) represents the ratio of the infected population to the total population which is a real number within the range [0.0, 1.0]. For simplicity, the values are rounded to one place of decimal to have a finite state set, $S = \{0.0, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0\}$. The color code chosen to represent the states of the cells in successive time steps are given in Table 1:

Table 1: Color code for states of cells

States	.0	.1	.2	.3	.4	.5	.6	.7	.8	.9	1.0
Colors											

The simulation was done with an hypothetical space divided into 200 by 200 cells. Figure 3 and Figure 4 show the spread of the disease within the same group of cells when all parameters are fixed and when the parameter representing population dynamics was varied respectively. Each of the two figures shows the levels of spread in nine successive time steps. We see from Figure 3 that with fixed parameters, the disease spread appears to subside in successive time steps from step 3 with most cells having infection rates of below 30% at the ninth time step. However, with a varied population dynamic parameter in Figure 4, the rate of disappearance of the disease is slower and the infection rates within most cells are still above 50%.

For further comparison of our results, we observed the evolution of the epidemic within a selected cell at the centre of the space under study. The graphs of the infection rates against time steps for fixed and varied population dynamics parameter are provided in Figure 5 and Figure 6 respectively. The graphs also show significant difference in the evolution of the disease within this cell.

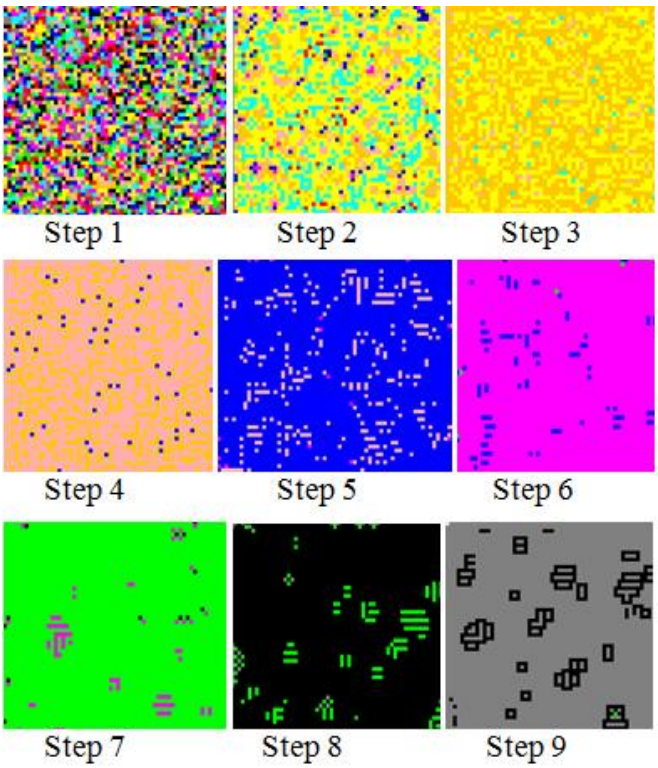

Figure 3: Disease spread with fixed environmental parameters

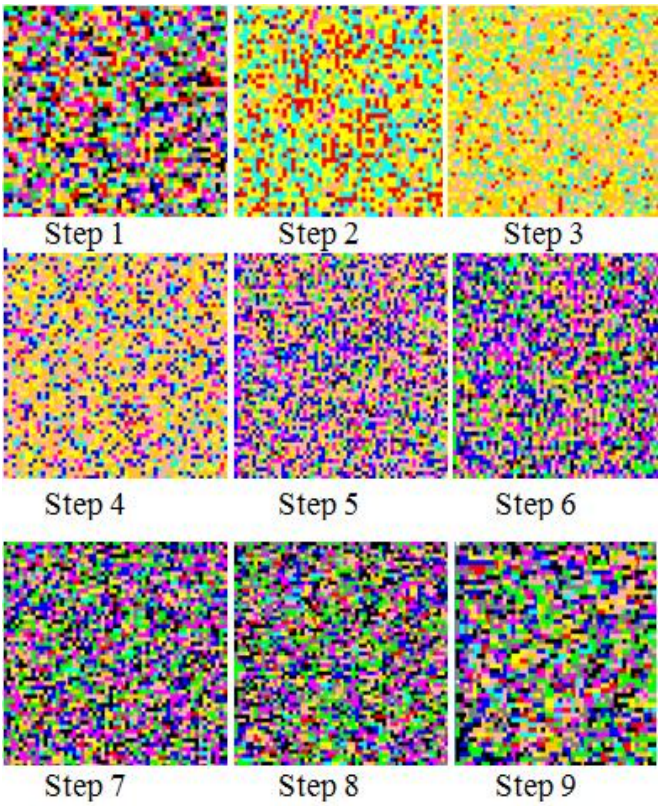

Figure 4: Disease spread with varied population dynamics parameter

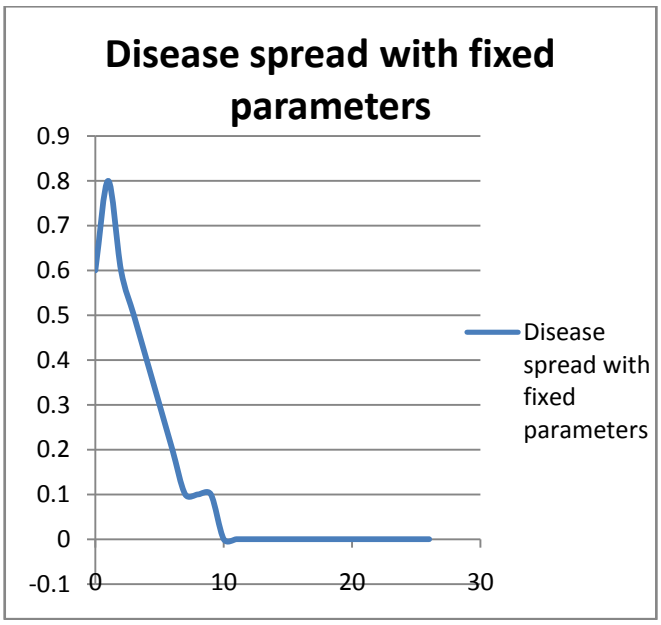

Figure 5: Infection rates against time steps within cell (100, 100) with fixed population dynamics parameter

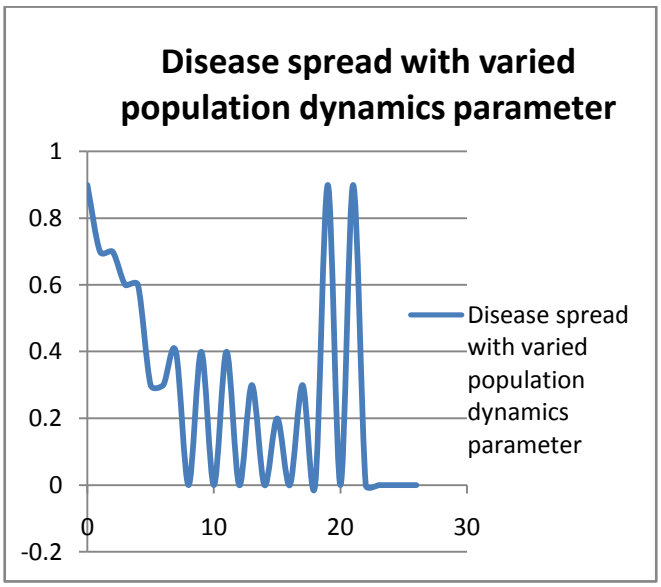

Figure 6: Infection rates against time steps within cell (100, 100) with varied population dynamics parameter

CONCLUSIONS

In this short paper, we have presented an ongoing research towards a framework for integrated simulation of different aspects of healthcare systems with exchange of live updates as influences between independent simulation processes.

We proposed disciplined stratification of healthcare concerns that are often investigated with simulation into four categories and a systematic integration of the simulation processes in the four categories by mutual exchange of live parameter updates. Our approach is different from the state-of-the-art in that different healthcare concerns are usually studied in isolation while other health phenomena that may affect them are represented by some fixed-valued parameters. We believe that such influences are often not fixed in reality as the different components of Healthcare systems are expected to respond to other concerns and adjust some internal activities. In future research, we intend to develop the proposed loose integration mechanism into a framework to coordinate the exchange of influences among the studies such that every simulation process publishes changes in its variables that may be required by other processes in real time without disrupting their activities. Such framework can be used to establish a liaison between existing healthcare simulation environments for holistic analysis of healthcare systems.

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