HOW HEALTH CARE SYSTEMS REACT ON EPIDEMICS

Patrick Einzinger[1], Michael Gyimesi[2], Günther Zauner[1]

[1]dwh Simulation Services,
1070 Vienna, Neustiftgasse 57-59, Austria
[2]Technical University of Vienna,
1040 Vienna, Wiedner Hauptstraße 8-10, Austria

patrick.einzinger@drahtwarenhandlung.at (Patrick Einzinger)

Abstract

Standard approaches to simulating epidemics of infectious diseases include the classic SIR-model and agent based simulations. Another interesting application for modelling and simulation are studies of the dynamics of whole parts of health care systems and their reimbursement schemes. We show how to integrate the transmission of infectious diseases into a model of this type. It is agent based and consists of three main agent types: Patients, Medical Providers and Medical Problems. The latter represents different diseases which patients can contract. Each patient implements a statechart for every medical problem type. These statecharts model the random generation of new diseases and corresponding medical problem objects which control disease progression and the treatment pathways a patient takes. A central "Health Market" object manages provider search of the patients. As an example, we integrate influenza as an infectious disease into the model with a separate object type "InfluenzaEpidemic" that stores the characteristics of every new epidemic during simulation time. Transmission of the disease takes place between agents which are connected by a network based on spatial relations. Each agent stores his past infections so he does not get the same virus strain twice. Experiments show that this resembles the behaviour of SIR-models and that this model can provide insight into the impact of epidemics on the utilization of the health service system and its reimbursement.

Keywords: Epidemics, SIR-Model, Health Services Research, Agent based modelling.

Presenting Author's biography

Patrick Einzinger was born on March 19th 1984 in Tulln, Austria. He studied technical mathematics at the University of Technology in Vienna and graduated with a diploma thesis on a System Dynamics model of the financing of Austrian regional health insurances. Currently he is working on simulation studies at dwh simulation services and continues his academic career towards a PhD.

1 Introduction

Infectious diseases and epidemics are a major topic of health services research. Unlike chronic illnesses which are often caused by general morbidity, an unhealthy lifestyle or aging, an epidemic spreads through social contacts between humans and affects people of all age groups, especially children.

Infections create a positive feedback loop which dominates the system until not enough susceptible people remain to allow further spreading of the disease. New cases can emerge dramatically in a short period of time and lead to organizational problems for society (capacity of medical providers, absenteeism at work etc.) as well as increased mortality.

Dynamic models of infectious diseases have a long tradition. One of the most famous is the SIR-model of Kermack and McKendrick which separates the population into homogenous compartments of susceptible (S), infected (I) and recovered (R) individuals. However, such global models ignore spatial effects and the possible behaviour of individuals [1].

In agent based simulation, the infectious disease spreads locally through interaction of agents which represent individuals. Approaches reach from modelling contact networks between agents [2] to explicitly integrating submodels of households and workplaces [3], but to our knowledge none of the past modelling studies implemented structures of the health services system, like service providers (e.g. physicians) and their reimbursement.

In this study we show how to integrate an epidemic influenza model into an existing agent based framework for modelling outpatient health care and effects of different reimbursement systems in Austria [4]. In the original model people develop medical problems with certain probabilities, but it does not contain reasons for the emergence of diseases (like physiologic attributes of the agents, or interrelation of illnesses between different agents as in the case of infectious diseases). However, it is possible to add these features to the existing model structure.

2 Methods

2.1 Model of the Health Service System

The basic model – implemented in AnyLogic 6.5.0, an object-oriented multi-paradigm simulator from XJ Technologies, based on the Java programming language - consists of three main agent types: “Patients”, “Medical Providers” and “Medical Problems” (typical medical problems are, for example, acute diseases like influenza or chronic health problems like hypertension). The main idea is that patients randomly develop new medical problems.

2.1.1 Patients

We model a patient population which is spatially distributed on a map of Austria. The simulation initialises each patient inside a polygon symbolizing the Austrian border.

It was not possible to do simulations of eight million agents, as would be Austria’s population, because this consumed too much memory. With fewer agents the distances on the map between patients and medical providers become unusually large. One has to pay attention to this problem. Additionally the ratio of medical providers and patients must be similar to the real ratio. For example for 10.000 patients we chose to model 150 general practitioners.

Patients in the model have age and sex as variables. They are initialised according to the corresponding distributions from official statistics. The model uses these variables to calculate the dying probabilities of each patient, as the population changes dynamically.

Usually the generation of diseases (and probably also treatment and reimbursement) would depend on age and sex too. However in the case of modelling just influenza we ignore the influence of both. Realistically the immune answer is weaker for children and the elderly. With reliable data available the model could incorporate this fact easily.

Each patient implements a statechart for every type of medical problem. The simplest version of these statecharts would have two states, one where the agent does not have the medical problem, and one where he has actually developed it and has not recovered yet (the according statechart for influenza is shown in Fig. 1). However, these statecharts could be more complicated, for example if the medical problem can start in different disease stages.

In general the modelling of the development of each disease with a simple statechart reflects the idea that the main fact that is important at the patient level is if he or she has this specific disease or not. It is not necessary to implement further information about the diseases, their progression and their treatment in the patients themselves, but in own medical problem objects.

2.1.2 Medical Problems

The medical problem objects implement specific information about the disease, for example disease progression and possible treatment pathways in the healthcare system, with help of statecharts. They are modelled as agents because in AnyLogic just agents have message passing features that we use for the medical problems. When the patient develops a medical problem (the corresponding statechart leaves the state where the agent does not have the disease), he is assigned an instance of the specific problem type.

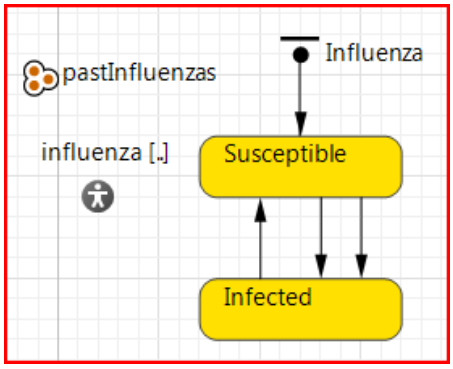

Fig. 1 Statechart of influenza infection inside the patient object. Collection variable for past infections and object influenza [..] (which stores an object of type Influenza when an infection takes place).

The problem classes reflect the idea that each disease has its own attributes and that disease progression and treatment pathways are characteristic for different illnesses.

A patient infected with influenza, for instance, would develop the need for a first consultation from a general practitioner. After this consultation that would provide him with medical services or medication, he might need a blood test at a laboratory (for checking if it is really an influenza infection) and optionally a second consultation.

In the model a "Need" statechart maps these possibilities in the form of one or more treatment pathways. Each state symbolises that the patient needs consultation of a medical provider. Additionally it contains information on the possible provider types (for example a consultation in the treatment pathway could be possible at a medical provider of type general practitioner or of type internist) and on "service packages". Each service package contains a list of services. At consultations the medical provider accounts for the services of exactly one service package.

As an example, service package 1 could contain just the usual lump compensation, whereas service package 2 would contain additionally an intramuscular injection. Different service providers (for example of different types) can choose different service packages for the same disease.

2.1.3 Medical Providers

The medical provider agent class represents all medical providers that have a contract with public health insurances in Austria, for example physicians, laboratories or other specialists working in health care. The "type" parameter in this class indicates the particular type of the provider (e.g. general practitioner, internist).

Additionally there can be parameters that influence treatment decisions of providers. In the case of influenza, not every general practitioner or internist might automatically prescribe neuraminidase inhibitors (like Oseltamivir). Furthermore certain medical providers might not be capable of providing some services, for example physicians that do not have a device for sonography would not offer sonographies to their patients. Further iterations of the model could handle this with a list of possible services for every medical provider.

For handling of their patients providers have two queues with different priorities, where the patients can register themselves: "queue" and "queueToday". Medical Providers treat all patients in "queueToday" on the same day and before all patients in the normal queue. This is important for modelling diseases where emergencies can occur. Each queue is served according to the First In, First Out (FIFO) principle.

Providers have their working capacities for each day of the week stored in an array called "workingFor". In base run we set the capacity per day (integer values) to be uniformly distributed on the interval [5, 10]. The working capacities signify how many patients a provider can treat per day.

2.1.4 Patient-Provider Interaction

Medical providers and patients are spatially randomly distributed on a map of Austria. With appropriate data, distributions that allow agglomerations (regions with higher agent density) would be possible too.

In reality several criteria influence patient's provider search. To keep it simple we just use the provider's distance to the patient to determine the patients preferred provider of a particular provider type. However patients do not search directly for a provider, but they send a message with the particular provider type that they want to consult to a global "HealthMarket" object. This object returns a provider of the appropriate type with an acceptably small distance to the inquiring patient.

Further model iterations could implement far more complicated provider selection strategies just by substituting the "HealthMarket" object. This would allow a real "market" situation where on one hand patients have a need and on the other hand providers offer different treatment styles and capacities for treating patients (as the required time might be a factor in selection of a provider). Thus we suggest further research on factors influencing patient's selection of medical providers.

In the model, patients store providers that they have found through "HealthMarket" as their preferred providers. They will just consult another provider if their preferred one cannot treat them with the desired priority.

If patients have a need for treatment and have chosen a particular provider they register in one of his service queues. Medical providers will treat people from their queues until they reach their daily limit as given in

"workingFor". After treatment the patient receives a message that he has been treated and all statecharts of his medical problems that need a consultation of this provider type can transit to the next state in their treatment pathway.

2.2 Implementation of an Epidemic Model

The easiest way to implement influenza epidemics into the model would be to let patients randomly develop influenza with probabilities dependent on the time of the year, as most cases of influenza occur – at least in Austria – in winter during the first weeks of the year. For a model that concentrates mainly on reimbursement and considers many different diseases this is a useful approach.

However, in this paper we want to couple the model with a classic SIR-type epidemic model. Therefore an additional object type "InfluenzaEpidemic" represents particular influenza epidemics with different virus strains. Each time the event "startEpidemic" is scheduled it creates a new instance of the epidemic.

The epidemic object could implement an SIR-model with the well-known differential equations, which are shown in Eq. (1).

$$\begin{aligned} \frac{dS}{dt} &= -\beta \cdot S \cdot I \\ \frac{dI}{dt} &= \beta \cdot S \cdot I - g \cdot I \\ \frac{dR}{dt} &= g \cdot I \end{aligned} \qquad (1)$$

As the agent part of the model should simulate at least the progress of the disease and its treatment for each agent individually, we do not need the part of the differential equations where infected patients recover, so the continuous equations would just control the new infections of agents.

Tab. 1 Timeouts of state transitions between consecutive states of disease progression (Asymp.Inf. = AsymptomaticInfectious). The transition to the state Symptomatic takes place after one day. The other timeouts are uniformly distributed.

Original state	Destination	Timeout
Asymptomatic	Asymp.Inf.	uniform(0, 2)
Asymp.Inf.	Symptomatic	1
Symptomatic	NonInfectious	uniform(3, 5)
NonInfectious	Final State	uniform(4, 9)

This coupling has serious disadvantages. For one, the performance is weak because all event conditions in the model are tested at each step of the differential equation solver. Furthermore, the model has to pick susceptible agents randomly to infect them accordingly to the change dI/dt. Of course this change is continuous, but agents can only be infected one by one. Altogether this is not a natural solution.

Therefore (and for reasons described in Section 1), we have chosen to incorporate spatial relations and individuality of the agents for the disease transmission. The statecharts inside patients which model disease generation consist of the states "Susceptible" and "Infected". The state "Recovered" is implicitly modelled because a collection variable stores past influenza epidemics that infected the agent. Agents develop immunity against all influenza virus strains they have been infected with.

The influenza disease object implements both a statechart that models disease progression and a statechart that controls the treatment pathway. The disease progression states are: Asymptomatic (the patient is infected, but has no signs of infection and cannot infect others), AsymptomaticInfectious (the patient can infect others, but has still no signs of infection), Symptomatic (the patient develops symptoms and notices his disease) and NonInfectious (the patient still has symptoms, but is not infectious anymore). The timeouts until state transitions are shown in Tab. 1.

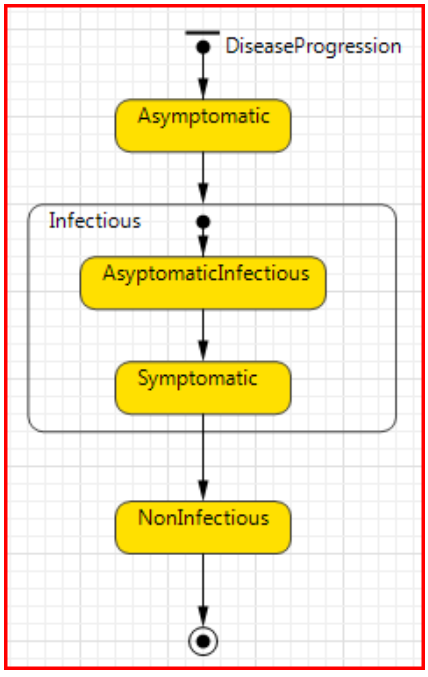

Fig. 2 Statechart of the disease progression of influenza. Patients are not instantaneously infectious. Just in the infectious state (asymptomatic and symptomatic) they may infect other individuals.

Patients potentially transmit the disease as long as they are in state "Infectious" of the influenza progression statechart. A cyclic event – with a uniformly distributed timeout between zero and two days – sends a message with a reference to the particular influenza epidemic object to another person that is connected with the transmitter. The connections

in the model form a small-world network, i.e. most connections link nearby agents, but some are random. Each agent has 20 connections, 95% of which connect neighbours.

An important parameter of each epidemic is the infectivity. We model infectivity as the probability of a successful infection if a susceptible patient receives an infection message. The default value for infectivity is 0.05, which means that 1 out of 20 infection messages lead to an actual infection.

There are three different possible treatment pathways:

1. The patient has one consultation with a general practitioner. The general practitioner receives a lump compensation, and he may or not may prescribe neuraminidase inhibitors.
2. The patient waits longer than 3 days for his first consultation. Then he deletes himself from the queue of the general practitioner and just waits until the end of his influenza.
3. At the first consultation the general practitioner takes a blood sample and sends it to a laboratory for a test for the influenza virus. After this the patient comes to the general practitioner for a second consultation.

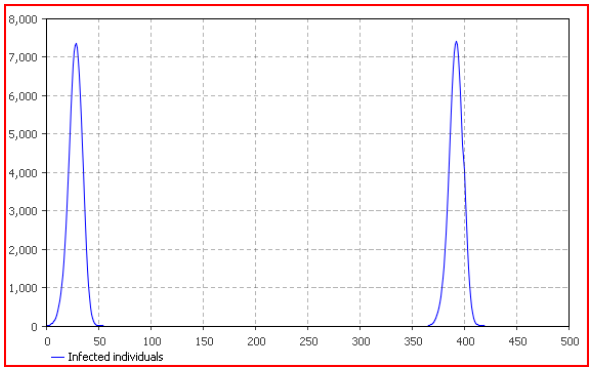

Fig. 3: Infected individuals of two consecutive influenza epidemics.

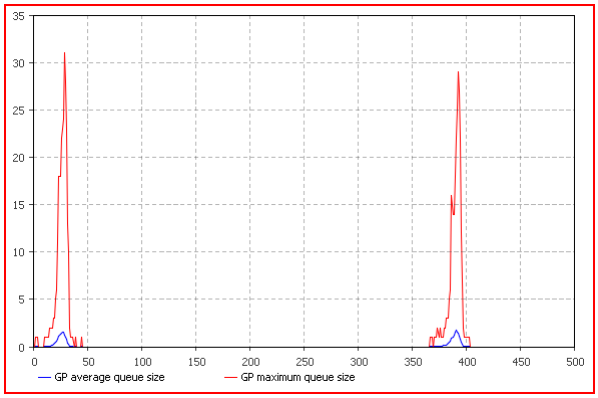

Fig. 4: Patients in the queue of general practitioners – average and maximum queue sizes during the two influenza epidemics.

Note that these treatment pathways are by no means empirically attested; they are just for illustrative purpose. For example, prescription of antibiotics might be far more common in influenza-like-illnesses than prescription of neuraminidase inhibitors. However antibiotics have no effect on the influenza virus, whereas the latter can shorten the length of the infection by about a day on average [5]. Therefore the patient transits in the disease progression statechart one day faster if he or she receives neuraminidase inhibitors.

The java class “Services” creates a HyperSQL database at runtime. Additionally it stores prices of services and handles writing of services to the database (together with date of service, patient id and id of the provider). The method *servicesCosts(long providerId, Service service)* in the Services class calculates total costs per service type for a particular provider from the database. For most services this gives the amount of services multiplied with the service price, however lump compensations are counted at most once per quarter, provider and patient.

3 Results

Simulations took place with 10.000 patients. The base run shows the typical SIR-type behaviour (Fig. 3). Here the second epidemic took place one year after the first. Additionally, the output incorporates average and maximum queue sizes (Fig. 4) and reimbursement of the providers (of course this reimbursement is just a partial one as it results from only one disease).

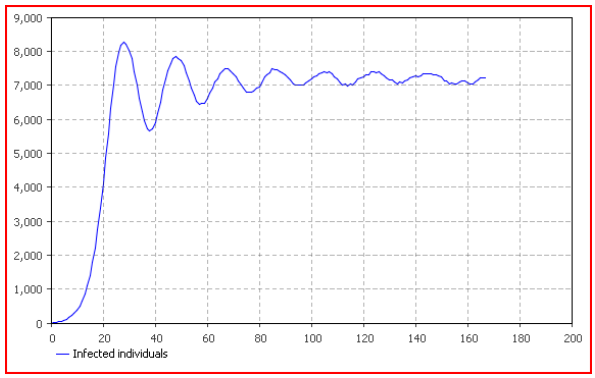

Fig. 5: Infected individuals of one epidemic if patients do not develop immunity. Damped oscillations occur.

If the agents do not store the epidemics they have already had (essentially an elimination of the “recovered” state) we get a different picture with oscillations like in Fig 5. In general, the maximum queue sizes of the general practitioners are a few times the average queue sizes.

The cost information for general practitioners (Fig 6. and Fig 7.) and laboratories shows that in the second scenario overall costs rise almost linearly over the whole simulation time, whereas in the base run the rise of costs is by far not so tremendous.

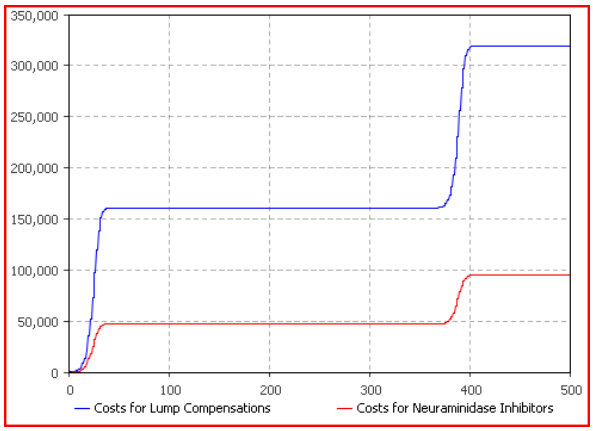

Fig. 6: Base run, development of overall costs for lump compensations and neuraminidase inhibitors during two influenza epidemics.

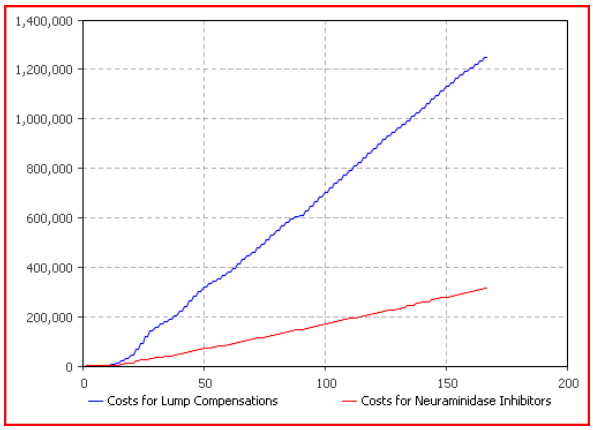

Fig. 7: Simulation without immunity. Development of overall costs for lump compensations and neuraminidase inhibitors during one epidemic which never dies out.

One interesting effect is the influence of neuraminidase inhibitors on progression of an epidemic. Therefore we conducted a parameter variation experiment where the probability of neuraminidase inhibitor prescription varied from 0 to 1 with steps of 0.2. Results (Fig. 8) show that neuraminidase inhibitors can at most slightly delay an epidemic. Tab. 2 lists costs for lump compensations and neuraminidase inhibitors in the parameter variation experiment.

4 Conclusions

The proposed model incorporates both the spread of epidemics and effects of health system structure and reimbursement. Therefore it can lead to a broader understanding of the influence of epidemics on health systems.

The results of the simulations show that the model gives plausible development of infections and costs for the considered services. Moreover, it offers a rich structure for integrating further knowledge on various aspects of health care systems.

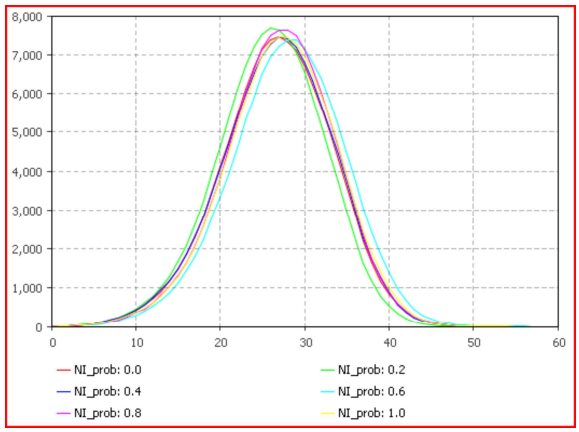

Fig. 8: Infected individuals in parameter variation experiment with six different values for probability of neuraminidase inhibitor prescription.

Further possible experiments with the developed model are simulations with limited capacity of providers, simulations of vaccination strategies and implementations of different strategies on micro level (strategies of doctors) and macro level (system strategies). Additionally the infection probability per contact could be varied or calibrated with real data.

Tab. 2 Overall costs for lump compensations (Costs LC) and neuraminidase inhibitors (Costs NI) in the parameter variation experiment. Probability of neuraminidase inhibitor prescription varies from 0 to 1 with steps of 0.2.

NI_probability	Costs LC	Costs NI
0.0	160854.7	0.0
0.2	160347.9	28805.2
0.4	161162.4	63185.6
0.6	160402.2	82375.6
0.8	159967.8	114736.0
1.0	160782.3	147500.4

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