The cholera spread Simulation

N Baturina^{1,*} and G Anisimova^{1,2}

¹Don State Technical University, 1, Gagarina sq., Rostov-on-Don, 344000, Russia

²FKUZ "Rostov-on-Don Research Anti-Plague Institute"

Abstract. One of the frequently used modern epidemiological methods is the Simulation of disease spread. We used AnyLogic simulation. During the model construction, we take into account the specific cholera features. They are: the pathways of infection transmission, the course duration and the duration of the incubation (latent) period, the possibility of vaccination, etc. Two approaches are presented here: system-dynamic model and agent-based one. The system-dynamic model is used for strategic modelling of the epidemiological situation, it reflects the global trends. The agent-based approach allows describing the individual behaviour of each agent - person, who independently form events conditioning transitions between states. Used together they make it possible to reflect different aspects of the epidemiological process development. The combination of these two models gives more possibilities for their application in a real situation: give the opportunity to impose tactical nuances on strategic modelling.

1 Introduction

Research epidemiological methods are quite diverse [1, 2]. They are classic methods, such as statistical analysis, like trend and forecast [3, 4], as well as modern methods, like simulation and so on. One can choose the research method in dependence of the research objectives and the special disease peculiarities. Usually, by using different approaches a more detailed analysis can be carried out [5].

One of the frequently used method is the Simulation of disease spread. There are many different methods of building a model. In many ways, the choice of the concrete methods of building a Simulation model is determined by a specific disease.

The specific features depending on the disease, which must be taken into account when constructing the model, includes the pathways of infection transmission, the course duration and the duration of the incubation (latent) period, the possibility of vaccination, etc.

In addition, it is necessary to take into account the specifics of the territory: both physical-geographical and climatic features, as well as social, cultural characteristics, including the population density and closeness of communication between the people, the traditions of the region and so on.

The ways of transmission of cholera infection by contact, water and food were taken into account to build this model of cholera spread. It was taken into account the influence of

* Corresponding author: baturinata@mail.ru

importation on the spread of infection, as well as a decrease in the rate of spread due to vaccination.

We considered two approaches: system-dynamic and agent-based one. Used together they make it possible to reflect different aspects of the epidemiological process development. It was used AnyLogic simulation.

The system-dynamic model assumes a high level of aggregation of objects. Here individuals are not distinguishable, the peculiarities of their behavior are not taken into account, and therefore this model is more intended for strategic modeling of the epidemiological situation. It may reflect global trends, for example, one of the most important in the spread of cholera feature - the flows of infection importation.

In contrast to the system dynamics model, the agent-based model is individual-oriented. It allows taking into account the behavior and psychology of people (attitudes towards travel, vaccinations during an epidemic, preventive measures to reduce the risks of infection).

2 Stochastic model of the epidemic spread as a model of system dynamics

The developed model of system dynamics is an extension of the classic SEIR model [6], which takes into account the ways of infection (contact, water and food), as well as imports.

Figure 1 shows a diagram of the levels and flows of the model, in Table 1 - their description, as well as a description of the parameters and variables used in the diagram. The model parameters were chosen both fixed and random with given distribution laws.

Fig. 1. Diagram of levels and flows.

Mathematically, a system-dynamic model is a system of differential equations that are solving numerically when the model is running. In our case, the functioning of the model is described by the following system of differential equations (the description of the variables is given in Table 1):

$$\frac{dS}{dt} = r_{SN} - r_{EC} - r_{EW} - r_{EF} - r_{SO}$$

$$\frac{dE_C}{dt} = r_{ED} + r_{EC} - r_{IC}$$

$$\frac{dE_W}{dt} = r_{EW} - r_{IW}$$

$$\frac{dE_F}{dt} = r_{EF} - r_{IF}$$

$$\frac{dI}{dt} = r_{IC} + r_{IW} + r_{IF} - r_R$$

$$\frac{dR}{dt} = r_R$$

$$S(0) = N - r_{SD} p_D \qquad I(0) = r_{SD} p_D$$

$$E_C(0) = E_W(0) = E_F(0) = R(0) = 0$$

Here

$$r_{SN} = i_N \qquad r_{SO} = i_O$$

$$r_{EC} = \frac{S}{N} \cdot I \cdot i_C \cdot p_C \qquad r_{EW} = \frac{S^2}{N} \cdot i_W \cdot p_W \qquad r_{EF} = \frac{S^2}{N} \cdot i_F \cdot p_F$$

$$r_{IC} = \frac{E_C}{t_{in}} \qquad r_{IW} = \frac{E_W}{t_{in}} \qquad r_{IF} = \frac{E_F}{t_{in}} \qquad r_{IW} = \frac{I}{t_{il}}$$

Several types of system dynamics models were considered (the model parameters are fixed, random, set using control elements).

Figure 2 shows the simulation results when parameters changes by using controls. The model makes it possible to trace the dynamics of the epidemic spread.

Table 1. Parameters and variables of the system dynamics model.

Name	Designation on flow diagram	Brief designation
Parameters		
Total Population	TotalPopulation	N
The probability of infection transmission by contact Water food	Infectivity Infectivity Infectivity	pC pW pF
Proportion of infected visitors (deliveries)		pD
Intensity of infection contact Water food	RateInfectiousC RateInfectiousW RateInfectiousF	iC iW iF
Intensity of incoming flow	RateFlowInput	iN
Intensity of outgoing flow	RateFlowOutput	iO
The duration of the incubation (latent) period	IverageIncubTime	t _{in}
Duration of infection	IverageIllnessDuration	t _{il}

Levels		
Number of susceptible	Susceptible	S
Number of infected		
Contact	ExposedC	E _C
Water	ExposedW	E _W
Food	ExposedF	E _F
The number of infected in the active phase of the disease	InfectiousC	I _C
	InfectiousW	I _W
	InfectiousF	I _F
Number of recovered	Recovered	R
Flows		
Visitor flow rate	SusceptibleFlowInput	r _{SN}
Flow rate of leaving	SusceptibleFlowOutput	r _{SO}
Infestations flow rate		
Contact	ExposedRateC	r _{EC}
Water	ExposedRateW	r _{EW}
Food	ExposedRateF	r _{EF}
Infection flow rate		
Contact	InfectiousRateC	r _{IC}
Water	InfectiousRateW	r _{IW}
Food	InfectiousRateF	r _{IF}
Recovery flow rate	RecoveredRate	r _R

Fig. 2. The dynamics of epidemiological process, obtained using the system dynamics model.

3 Stochastic agent-based model of epidemic spread

There were considered several types of agent-based models (model parameters are fixed, random, set using control elements, various options for transitions between blocks).

Three state diagrams determine Individual behavior: a health state diagram, a location diagram, and a vaccination diagram (Figure 3). The description of the parameters and variables used in the diagrams is given in Table 2.

Table 2. Parameters and variables of the agent-based model.

Name	Designation
Infection intensity	iInf
Waterborne contamination intensity	iW
Food contamination intensity	iF
Contact contamination intensity (trip contamination)	iT
Contact intensity (trip)	iGoTr
Vaccination intensity	iVac
The probability of waterborne contamination	pW
The probability of food contamination	pF
The probability of contact contamination	pT
The probability of taking action to vaccinate	pVac
The probability of getting vaccinated	pGoVac
The probability of contact (trip)	pGoTr
Duration of the incubation period	tInc
Duration of the disease	tIll
Trip duration	tTr
Start vaccination time	tVac
Maximal number of infected for trip refusal per 100 person	MaxNInfTr
Minimal number of infected to start vaccination per 100 person	MinNInfVac
Current daily infected number per 100 person	NInfI
Maximal daily contaminated number per 100 person	kMaxNInf

Fig. 3. Statecharts of the agent-based model.

The Vaccination diagram specifies the states VacNo "not vaccinated" and Vac "vaccinated". It is believed that since the onset of the epidemic, there are already a certain

number of vaccinated people, determined by the pVacNo parameter (proportion of those not vaccinated). The Vaccination diagram uses internal and external transitions. The internal transition is triggered by a timeout with the tVac parameter, which determines the time after which the vaccination activities begin. It includes the sending of notifications inviting everyone who has not yet been ill to vaccinate, and the vaccination. The external transition between the states VacNo and Vac is carried out with a given probability pGoVac with additional restrictions taking into account the number of cases at the current moment and the current states of the agent in the StateHealth and Location diagrams.

The simulation results are displayed on time charts and diagrams (Figure 4). Here's the change of

- a) the number of infected over time;
- b) the ratio between the number of person in the four groups (susceptible, latent, infected and recovered);
- c) the ratio between the number of person staying at home and in the trip;
- d) the ratio between unvaccinated and vaccinated.

Fig. 4. Timelines and charts of the agent model.

One can use these agent-based models to predict the time of the disease peak, to determine the index of contagiousness depending on the external model parameters, to determine events (timing, intensity, etc.) to prevent the infection growth.

4 Conclusion

The combination of these 2 models gives more possibilities for their application in a real situation. A system-dynamic model designed for strategic modeling of the epidemiological situation, reflecting global trends, in combination with an agent-based model, will also allow using tactical nuances. This will make it possible to influence the situation, to reduce the epidemic growth rate and reduce the peak of the disease.

The agent-based approach in combination with the system-dynamic model seems to be the most promising, since it is more realistic. It allows describing the individual behavior of each agent - person, who independently form events conditioning transitions between states.

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