

System-Dynamic simulation of the Cholera spread

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Abstract. One of the frequently used modern epidemiological methods is the simulation of disease spread. We used AnyLogic simulation. System-dynamic model is presented here. It may be used for strategic modelling of the epidemiological situation and reflects the global trends. During the model construction, we take into account the specific cholera features, such as the pathways of infection transmission, the course duration and the duration of the incubation (latent) period, the possibility of vaccination, etc. Different cholera strains correspond to different parameter values. Anylogic makes it possible to visualize the epidemic spread in movement at various values of the model parameters and it looks like cartoon. It also gives the possibility to select and clarify the parameter values. For convenience, when building the model, we used sliders. They help in the selection of parameters to change quickly the values of the model parameters, including the effect of vaccination on the process of the disease spread. We were able to compare the results obtained by simulating the disease spread with specific data on real cholera spread. Our results of the study indicate that the used model can be effectively applied for forecasting. By analyzing the results of modeling with varying parameters, it is possible to predict the dynamics of the cholera spread.

1 Introduction

It is very actual today to have any forecast or trend for different disease spread.

One of the most interesting method is the simulation modeling, and it finds more and more widespread use.

Simulation modeling in the study of the epidemics spread processes is increasingly being used [1-7]. This is due to the development of simulation tools, the ability to play the model in real time, taking into account various factors affecting the ongoing processes. They allow to visualize the picture of these processes, convenient for analysis.

One may dream to create the universal model for any diseases. But it would be too simple to have the same model for anyone disease. The matter is that the spread rules are different for each one disease. But the real problem is to analyze disease spread, taking into account

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the specific features, peculiarities of each disease. So, we can discuss only one of them - that is cholera [8-9].

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.

We considered in [10] two cholera spread approaches: system-dynamic and agent-based one. It was used AnyLogic simulation. Used together they make it possible to reflect different aspects of the epidemiological process development.

The system-dynamic model assumes a high level of aggregation of objects. In such model from [10] individuals are not distinguishable, the peculiarities of their behavior are not taken into account, 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.

This paper offer a modification of our system-dynamic model proposed in [10] in order to have more detailed analysis of the various model parameter influence on the dynamics of the cholera spread. Besides, additional factors have been added to the system, without which the epidemiological picture of the cholera spread would be incomplete. They are: the processes of vaccination, sampling from contaminated water or food sources, and importation of infection from outside.

2 Materials and methods

Our model of system dynamics is an extension of the classic SEIR model [10], which takes into account the ways of infection (contact, water and food), as well as imports, recovery, vaccination, etc.

Our model includes the following levels:

- people in a latent phase, infected by contact, water or food
- people in the active phase, infected by contact, water or food
- infected visitors in the active phase of the disease
- infected latent visitors
- visitors of the country and people leaving abroad
- recovered people
- vaccinated people

To examine the influence of each infection method on the epidemiological process of the cholera spread as a whole, it was necessary to isolate separate flows of infected by contact, water, food and the flow of imports. Figure 1 shows the structural diagram of the model, which includes the levels described above; input and output flows that determine the values of variable levels; model parameters on which flows depend. The description of the parameters, variable flows and levels are given in Table 1.

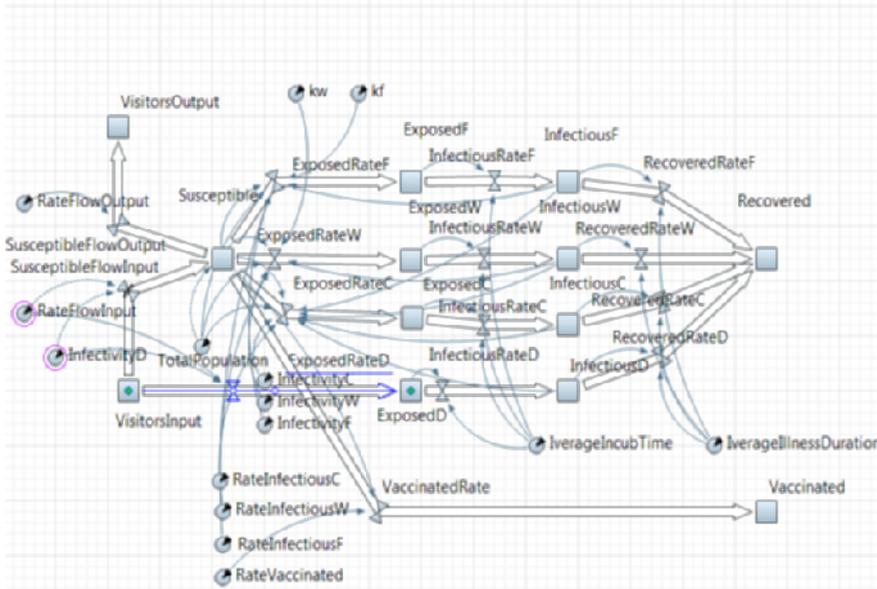


Fig. 1. The system-dynamic model of the cholera spread. Structural scheme.

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	InfectivityC InfectivityW InfectivityF	pC pW pF
Proportion of infected visitors (deliveries)	InfectivityD	pD
Intensity of infection contact Water food	RateInfectiousC RateInfectiousW RateInfectiousF	iC iW iF
Intensity of vaccination		iV
Intensity of incoming flow	RateFlowInput	iN
Intensity of outcoming flow	RateFlowOutput	iO
The duration of the incubation (latent) period	IverageIncubTime	tin
Duration of infection	IverageIllnessDuration	til
Infection rate parameter by		
Water	kw	kw
food	kf	kf
Levels		
Number of susceptible	Susceptible	S
Number of vaccination	Vaccinated	V
Number of infected Contact Water Food	ExposedC ExposedW ExposedF	EC EW EF

Number of infected latent visitors	ExposedD	ED
Number of infected visitors in the active phase of the disease	InfectiousD	ID
The number of infected in the active phase of the disease	InfectiousC	IC
Contact	InfectiousW	IW
Water	InfectiousF	IF
Food		
Total number of infected	Infectious	
Number of recovered	Recovered	R
Number of incoming visitors	VisitorsInput	VN
Number of outgoing visitors	VisitorsOutput	VO
Flows		
Visitor flow rate	SusceptibleFlowInput	rSN
Flow rate of leaving	SusceptibleFlowOutput	rSO
Infestations flow rate	ExposedRateC	rEC
Contact	ExposedRateW	rEW
Water	ExposedRateF	rEF
Food	ExposedRateD	rED
infected visitors (deliveries)		
Infection flow rate	InfectiousRateC	rIC
Contact	InfectiousRateW	rIW
Water	InfectiousRateF	rIF
Food	InfectiousRateD	rID
Deliveries		
Recovery flow rate	RecoveredRate	rR
Vaccination rate	VaccinatedRate	rV

As a result of solving the following system of differential equations one can determine the variables describing the cholera spread process in accordance to the scheme shown in Figure 1.

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

$$\frac{dE_C}{dt} = r_{EC} - r_{IC}, \quad \frac{dE_W}{dt} = r_{EW} - r_{IW}, \quad \frac{dE_F}{dt} = r_{EF} - r_{IF}, \quad \frac{dE_D}{dt} = r_{ED} - r_{ID}$$

$$\frac{dI_C}{dt} = r_{IC} - r_{RC}, \quad \frac{dI_W}{dt} = r_{IW} - r_{RW}, \quad \frac{dI_F}{dt} = r_{IF} - r_{RF}$$

$$\frac{dI_D}{dt} = r_{ID} - r_{RD}$$

$$\frac{dR}{dt} = r_{RC} + r_{RW} + r_{RF} + r_{RD}$$

$$\frac{dV}{dt} = r_V$$

$$S(0) = N - I_C(0) - I_W(0) - I_F(0) - I_D(0)$$

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

$$I_C(0) = I_W(0) = I_F(0) = I_D(0) = 1$$

Here

$$r_{SN} = i_N(1 - p_D) \quad r_{SO} = i_O \quad r_V = S \cdot i_V$$

$$r_{EC} = \frac{S}{N} \cdot I \cdot i_C \cdot p_C, \quad I = I_C + I_W + I_F + I_D$$

$$\begin{aligned}
 r_{EW} &= \frac{S^{kw}}{N} \cdot I_W \cdot i_W \cdot p_W & r_{EF} &= \frac{S^{kf}}{N} \cdot I_F \cdot i_F \cdot p_F & r_{ED} &= i_N \cdot p_D \\
 r_{IC} &= \frac{E_C}{t_{in}}, r_{IW} &= \frac{E_W}{t_{in}} & r_{IF} &= \frac{E_F}{t_{in}} & r_{ID} &= \frac{E_D}{t_{in}} \\
 r_{RC} &= \frac{I_C}{t_{il}}, r_{RW} &= \frac{I_W}{t_{il}} & r_{RC} &= \frac{I_F}{t_{il}} & r_{RD} &= \frac{I_D}{t_{il}}
 \end{aligned}$$

3 Results

The process of the epidemic spread begins if at least one infected person appears. The rate of change in the people number infected by contact is directly proportional to the total infected people number, regardless of the infection method, the number of susceptible to the disease, the intensity of contacts and the probability of infection during contact. The rate of change in the people number infected by water or food is proportional to the number of positive samples, the number of susceptible to the disease, the intensity of contact and the probability of infection in the process of contact with water or food sources. The rate of vaccination is directly proportional to the number of susceptible to the disease and the intensity of vaccination. To increase the flow of those infected by water or contact, the parameters of the infection rate by these ways were additionally introduced.

In order to investigate the influence of the model parameters on the epidemiological process, the slider type controls have been added to the model (Figure 2). They allow you to play the model, turning on or off certain factors (infection methods), vary the values of the parameters.



Fig. 2. Model control sliders.

Figure 3 a), b) shows the dynamic processes of the epidemic development in the vaccination absence. It is shown the results corresponding to the marked on the sliders

parameter values. In Figure a) the disease peak falls on about the sixtieth day and is equal to 64% of the total number of susceptible to the disease. In Figure b), corresponding to lower intensities of contacts and the probability of infection, the disease peak is more blurred, it is reached much later, about two hundred days and is equal to 30% of the total susceptible to the disease number. The graphs can also determine the percentage of infected by contact, water and food. The largest infected number falls on the waterway of infection that is correspondable to the epidemiological observation data.

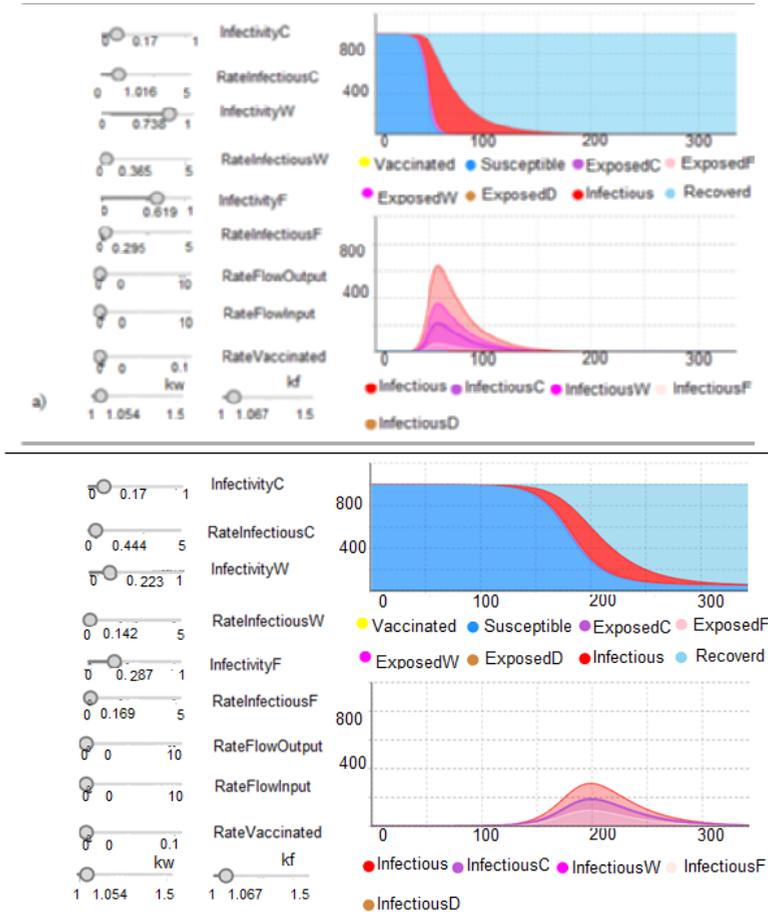


Fig. 3. a, b – epidemic spread in the vaccination absence.

The implementation events to population vaccination significantly changes the picture of the epidemic development, as one can see from the Figure 4. If one takes the same as in Figure 3 a) contacts intensities and the infection probabilities, than there is a decrease in the cases number and a right shift in the disease peak.

Analysis of the simulation results allows us to find the relationship between the rate of spread of the epidemic, its duration and the intensity of vaccination.

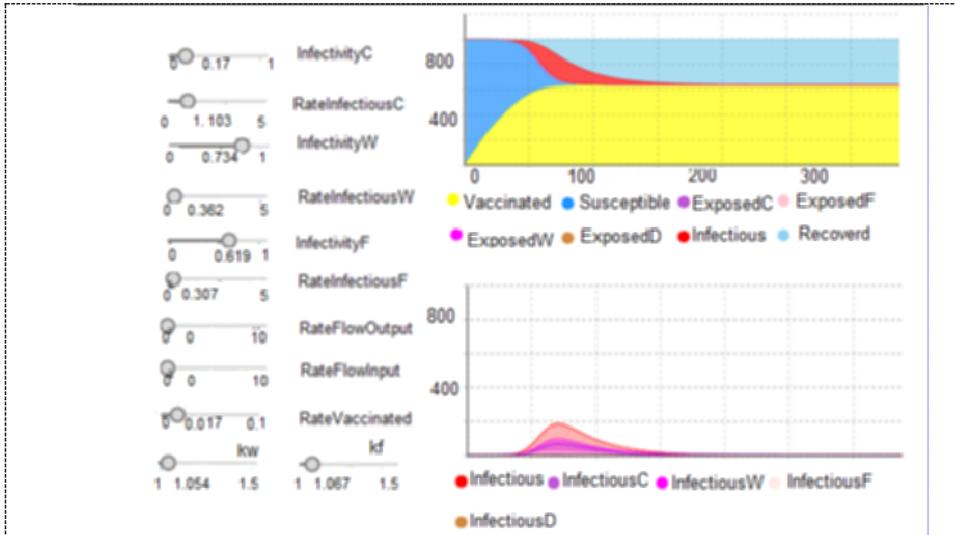


Fig. 4. Epidemic spread during vaccination.

4 Conclusion

Our previous paper presented the cholera spread simulation of two types, where we took into account the specific cholera features. We used AnyLogic simulation. Two approaches were presented there: system-dynamic model and agent-based one. The system-dynamic model is usually used for strategic modelling of the epidemiological situation, it reflects the global trends. The agent-based approach allows one to describe the individual behavior of each agent - a person who independently forms events that condition transitions between states.

Now we tried to examine the first one in more details. When constructing the model, we used the specific features of cholera, such as the most common methods of infection (by contact, water, food, import) and anti-epidemic events (vaccination).

Anylogic makes it possible to visualize the epidemic spread in movement at various values of the model parameters and it looks like cartoon.

The model gives the possibility to determine way of the influence on the infection spread dynamics of such model parameters as the intensity of infection, probability of the infection transmission, the intensity of anti-epidemic events, as well as to determine the number of infected in various ways, the duration of the delay in the onset, and the rate of its spread.

Our results of the study indicate that the used model can be effectively applied for forecasting. By analyzing the results of modeling with varying parameters, it is possible to predict the dynamics of the cholera spread (the number of vulnerable, latent, infected, recovered with different methods of infection), to determine the necessary intensity of vaccination to reduce the spread of the epidemic, to plan preventive and anti-epidemic events in order to combat the epidemic spread of the disease.

We plan to proceed the analysis of simulation results additional series of simulation experiments with various combinations of parameters. Based on the statistical data epidemiological observations on the cholera outbreak in previous years, using the developed model, it is possible to determine the appropriate values of our parameters. After that, we may use these parameters to forecast the real cholera outbreak.

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