Spread of epidemic

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1 Introduction

When disease spread quickly and affect many people we can call it epidemic. Some of the most unfamus epidemic thorough history are XIV century Black Death and Spanish Flu pandemic in 1918. Infected person is not significant, however when a great number of people is sick it creates serious health and economic threats. Goal of simulating spread of epidemic is to better understand how epidemic behave in time, how quickly it spreads depending on many factors.[4] It can also be used to picture how vaccination affect disease spreading and confirms that herd immunity is important.

2 Literature models

Main models for epidemic in cellular automata are as follows:

- SIR
- SEIR
- SIS
- SEIRS

where each letter stand for status types of persons:

- S - susceptible
- I - infected
- E - exposed
- R - recovered

The choosen model should represent a disease we want to model. SIR model assume that in recovery status individual get full immunity and on the other hand in SIS person can get sick even after successful treatment.[4]

The neighborhood we choose can greatly affect dynamics of disease spreading as stated in [1]. However more than type of neighborhood the type of connection between cells is important. There can be one, two three or none ways of transport. It affects equations and speed of spreading.[4]

Each cell is not an individual person, but a representation of square portion of land. That said there can be a cell with only infected people in it. People can move from one cell to another.[4]

During next step model calculate how many people will be in each cell in each of groups(susceptible,infected,exposed,recovered). Vaccinations, cell connections, neighbourhood and people spread are major factors in how disease will spread.

How and when cell change their status? This questions are answered, by mathematical equations with proper assumption about model.
When we assume that population count is constant we can use KedleMadroc model[] (hovewer it is regarded as simplified).

There are more mathematical models in literature:
SIR[]
SIS[]

3   Project goals

The aim of this project is to implement SIR model of epidemic spread in cellular automata with JAVA. Main programming reference will be code from laboratory classes where cellular automata was used. The UI will be created with JavaFX and SceneBuilder. If possible interface will have may parameters to choose, like: vaccination value, people spread in board(random,uniform, constant), epidemic model(SIR,SIS,SEIR,SEIRS), neighbourhood size and type, if not only simple parameters for one model will be present.

4   Implemented models

4.1   Neighbourhood

Cell can have Von Neman or Moore neighbourhood, it is possible to change it size (from 1 to 4).
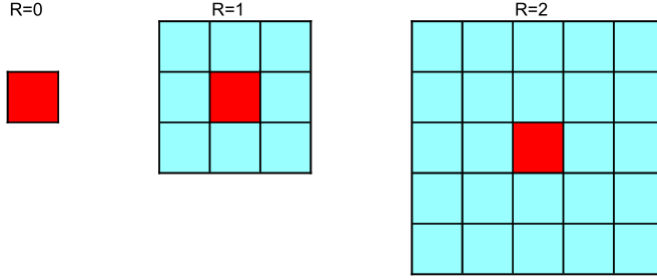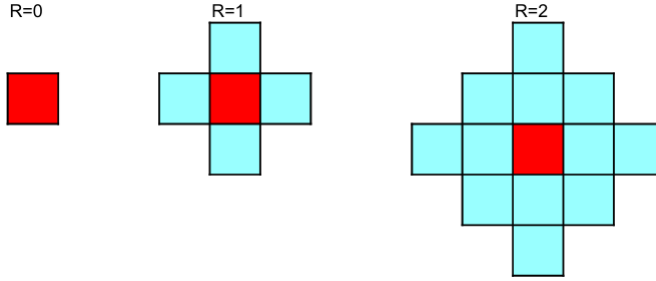
Figure 1: Moore neighbourhood

Figure 2: VonNewman neighbourhood

To not hardcode adding of neighbours to cell, following equations found on wolfram [2][3] were used:

$$N^M_{x_0,y_0} = \{(x,y) : \mid x - x_0 \mid \leqslant r, \mid y - y_0 \mid \leqslant r\} \tag{1}$$

$$N^V_{x_0,y_0} = \{(x,y) : \mid x - x_0 \mid + \mid y - y_0 \mid \leqslant r\} \tag{2}$$

- x_0, y_0 - target cell coordinates

- x, y - all other cells coordinates

- r - neighbourhood size

- $N^V_{x_0,y_0}$ - set of neighbours(VonNewman) cells for target cell

- $N^M_{x_0,y_0}$ - set of neighbours(Moore) cells for target cell

4.2 Epidemic models

Spread of disease between cells was modelled, by implementing transition equation proposed by[4]. It was decided to use it, because it takes into con-
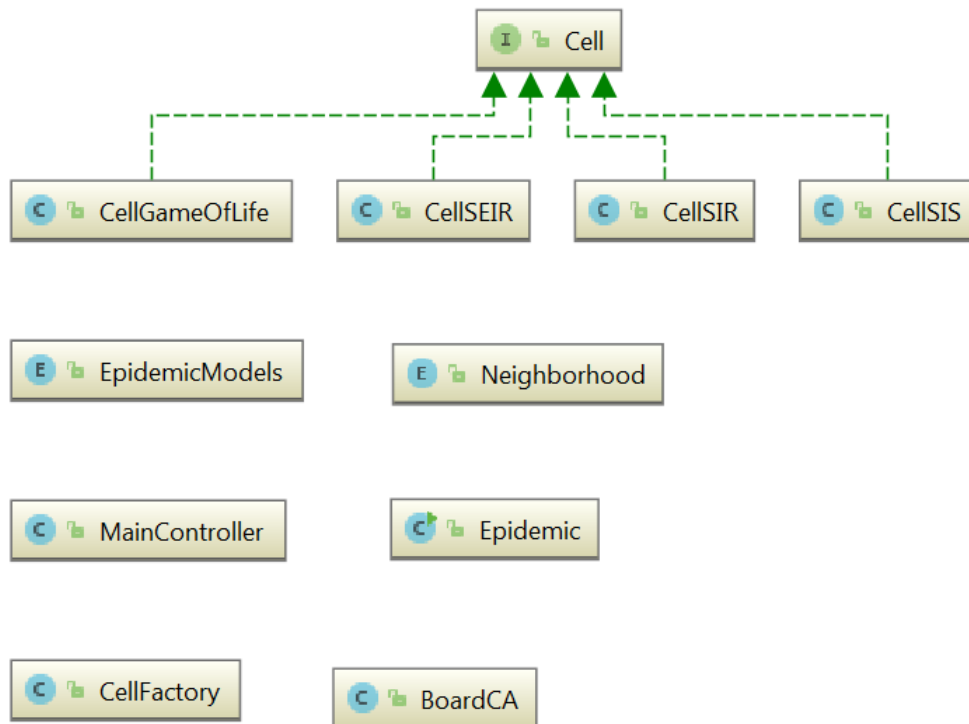
Figure 3: Class diagram

sideration:

- vaccination

- number of means of transportation

- each cell is small population not a individual

4.3 Code

Program was written in Java. Simulation is created, by use of Timeline class, which object is used to execute doIteration() function. To avoid writing a lot of if and switches Factory pattern was used for creating Cell object for chosen model.

4.4 Finished GUI

The user interface was created with JavaFX and SceneBuilder.
To start simulation:

- Choose model

- Choose neighbourhood type and size

- Set model parameters

- Click INIT button

- Change cell types, by mouse clicking(or draging) on board (it is possible to choose new type of cell, depends on chosen model)

- Change speed of simulation on slider(optional, default 1s)

- To start click START button

- To pause click STOP button(you can resume with START button)

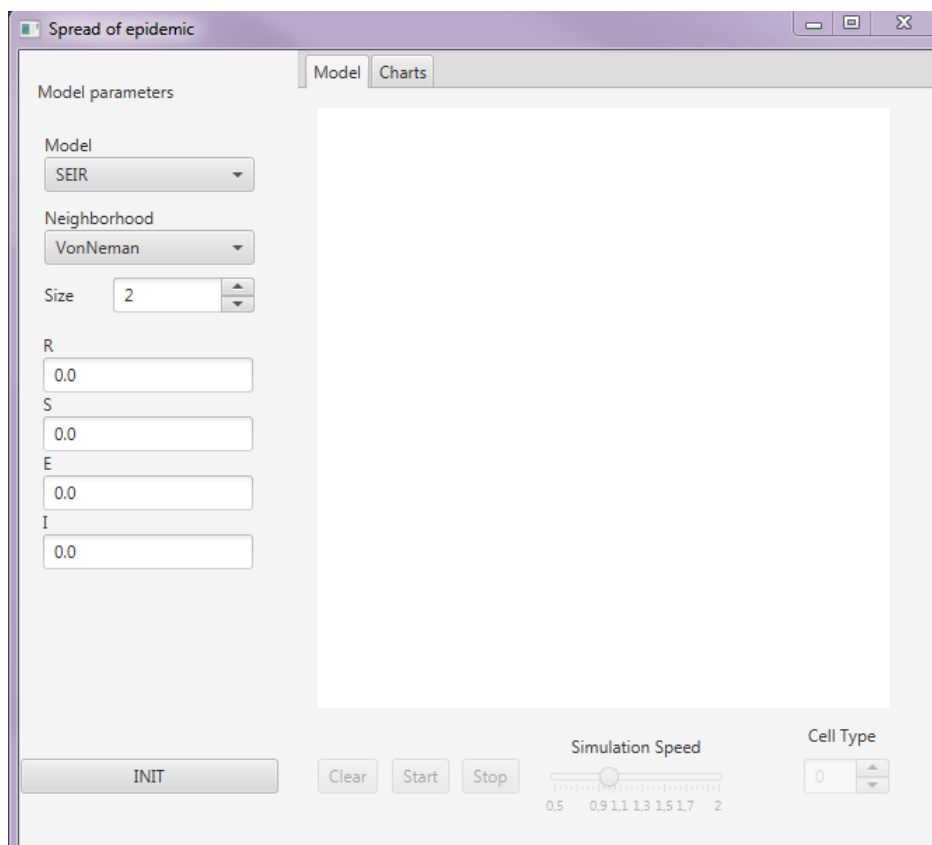- Use CLEAR button to terminate simulation and be able to set up a new one
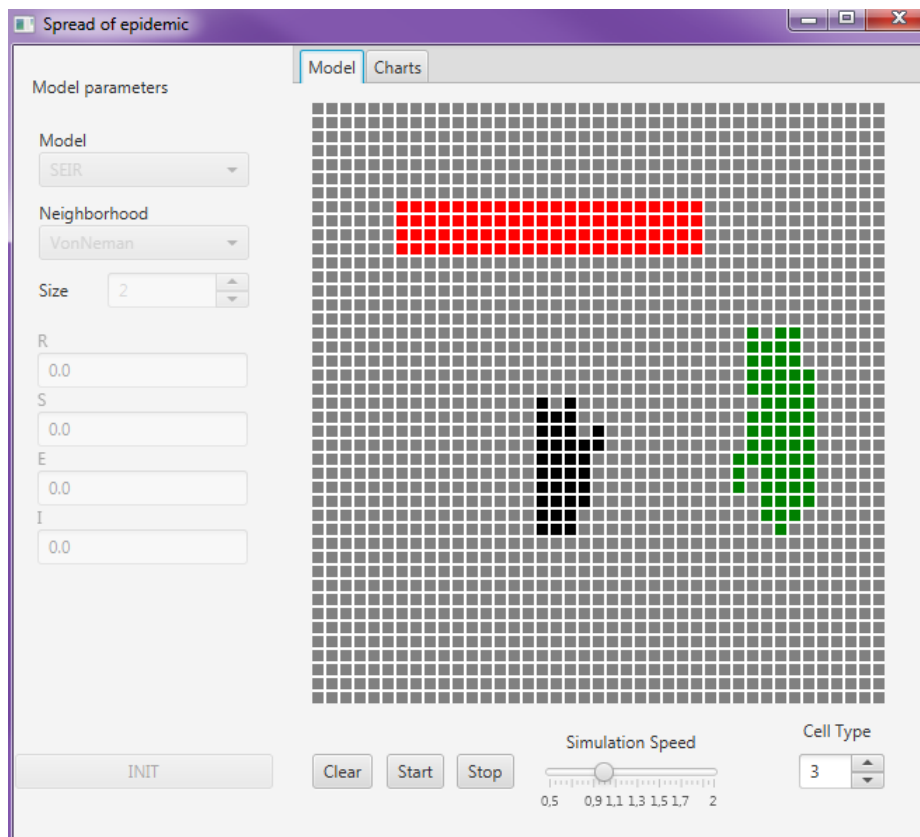

Figure 4: GUI when program start

Figure 5: GUI ready to start simulation

5 Summary

Bibliography

[1] Baki Cissé, Samira El Yacoubi i Abdessamad Tridane. *Impact of Neighborhood Structure on Epidemic Spreading by Means of Cellular Automata Approach*. Czer. 2013.

[2] Eric W. Weisstein. *Moore Neighborhood*. URL: http : / / mathworld . wolfram.com/MooreNeighborhood.html.

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[4] S. Hoya White, A. Martín del Rey i G. Rodríguez Sánchez. "Modeling epidemics using cellular automata". W: *Applied Mathematics and Computation* 186.1 (2007), s. 193 –202. ISSN: 0096-3003. DOI: https: / / doi . org / 10 . 1016 / j . amc . 2006 . 06 . 126. URL: http : / / www . sciencedirect.com/science/article/pii/S0096300306009295.