

Simulation model for infectious Virus in human population

Hardeep Singh, Student no. 3089450, Applied Computer science, University of Winnipeg

Abstract — the usage of simulation models for understanding social and biological phenomena became popular, nowadays. There are some phenomena that can't be tested in real world such as transmission of infection in human population. To manage risks, a simulation model can be made to test how people get infected by virus. The aim of this paper is to make such simulation model for spreading of infectious virus in human population and to know deaths caused by it. The simulation results shows what will happen in a real world if a people get infected from virus, and how many people will die from infection, depending on the infectiousness of the virus, population density, chance of recovery after getting infected and if they are not treated by doctors after getting infected. The experiment results depicted that to lower the number of deaths in real life caused by virus, there should be large number of doctors in the virus prone area, virus infectiousness rate should be low and recovery chances should be high. The properties of simulation model like emergence and self – organization are also discussed.

I. INTRODUCTION

Disease is a condition of the body, or some part or organ of the body, in which its functions get disturbed. Some diseases are infectious and some are non-infectious. This paper will focus on the infectious diseases caused by viruses. The diseases caused by various type of viruses are increasing day by day among people, which lead to thousands of deaths every year. The infectious virus spreads fast in population due to various reasons like density of population, way of interactions among people, virus infectiousness rate etc. The model used in this paper will assume that the population is well-mixed, so every pair of individuals is equally likely to interact with each other during any given interval of time. The death of a person will depend on the duration of infection, old age and if that person will not treated by a doctor. The whole infection cycle will be worked as if a susceptible person come in the contact with infected person will also get infected, if infected person is not treated by the doctor and duration of infection crosses the threshold value that person will die or if treated, than person will come under the category of healthy ones. The model will be initiated with some infected and healthy people, infectiousness rate of the virus and number of doctors in the system. At the end of the simulation, results shows how many people are died due to virus and how number of doctors in a given environment can make a huge difference to reduce the number of deaths in the system

II. RELATED WORKS

The literature of computer models for several biological problems is well researched over last few decades. There are many simulation models developed in past by researchers by

using different computer languages. Christoph Aschwanden [1] developed a spatial simulation model for infectious viral diseases by using Java programming language. The main focus of his study was on SARS and Common Flu. In his model, people can move freely in 2D environment and there is stochastic interactions among people. He arranged environment as houses stores, schools and other work places. Parameters used in this model was infectious period, recovery period, attack distance, attack rate and death rate. However, our simulation model is developed using Net logo for all kind of viral diseases. Moreover, our model have additional parameter like number of doctors, who can treat infected individuals.

Karl Mink and Mike Zdeb [2] used Statistical Analysis system (SAS) to make simulation model for spread of infectious disease. The spread of virus in there study is depended on several factors like environment required for virus to survive as they need a host for their survival, human factors like sharing needles when injecting drugs, drinking clean water, hand washing etc. Where, in our system virus spread through direct infectious contact between healthy and infected individual. The vision behind there model was to know how does population density influence the number infected and we also used population density to check how it make difference to number of infected people. In their paper they chose vaccination for specified infected people, but in our system every infected individual have equal chance to be treated by a doctor.

Alun L. Lloyd [3] made a mathematical computation model on infection dynamics in small-world networks. The focus of their study was how spatial structure of population can make impact on the spread of infectious diseases. They used a connected network or random graph in which infection could transfer from one individual to another. The parameters used is the distance between two individuals, degree or connectivity of nodes, and connectivity distribution. However, in our system we are not using networks, every healthy individual is equally likely to get infected when it came in contact with infected individual.

Stephan Carl [4] made a spatially-explicit, individual-based mathematical model that accounts for the spread of dengue infection as a result of human movement and mosquito dispersion is presented. However, our model can simulate different type of viruses by adjusting the parameter like infectiousness, chance of recovery and duration of infection. Important features of their model was use high quality outbreak data and mosquito trapping data for calibration and validation. In our model, we can define initial virus outbreak size of the virus in the system in term of number of infected agents.

III. METHODOLOGY

A virus in human population simulation model is comprising of number of people. In a given environment, some people are susceptible to be infected by virus or the immune ones, some are already infected by virus and rest are the doctors. The system will be initialized with some defined number of infected individuals and doctors. The carrying capacity of the system is set to 300. In other words, there can be at most 300 people in the system at one time. There are five types of individuals in the given environment:

1. *Healthy or susceptible*: - can get infected.(Green)
2. *Infected*: - Infected by virus.(Red)
3. *Immune*: - Cannot be infected. (Grey)
4. *Doctors*: - Agents who can make infected people healthy again. (Blue)
5. *Dead*: - dying due to infection, old age and infection duration. [1]

The whole system works on the basis of the following rules:-

1. In the given system, when a susceptible individual comes in contact with an infected one, it also get infected by virus. Density of population also affected the number of individuals infected per time unit. If number of people in the system are more at the start of the simulation, then there are chances that individuals may get infected quickly.

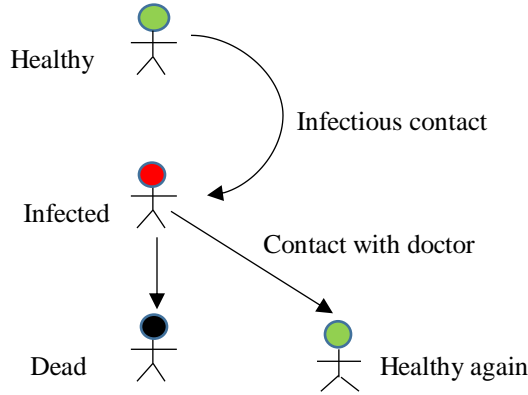


Fig 1. Infectious process

2. Reproduction among agents occurs only if current population of the system is less than the carrying capacity and leads to creation of a healthy offspring. The number of offspring per healthy agent can vary according to the value set for num-children. For example, if value of num-children is 5, then every healthy individual can have maximum 5 offspring in their lifetime.

3. Infectiousness is another parameter used in this system which can be set in according to, how quickly a virus can spread among people in a system. For example, if infectiousness of a virus is set to be more then it means virus will spread quickly in the system.

4. An infected person can get healthy again by two ways, first if it is treated by a doctor. In other words, if an infected agent

came in contact with a doctor, it will become healthy again. Secondly, if chance of recovery is more after getting infected.

5. A person in a system dies due to the following three reasons:-

- If an infected person do not treated by a doctor. In other words, if an infected agent do not came in contact with doctor, that person will die.
- It doesn't matter if that person is healthy or infected. The maximum years a person can live in system is set to 50 years.
- If duration of the disease for an infected individual crosses the specified number of weeks. That individual will eliminated from the system.

6. The percentage of infected people in system is calculated using the following formula:-

$$(\text{Infected people} / \text{total population of system}) * 100$$

- Similarly, immune ones are calculated using following formula:-

$$(\text{Immune people} / \text{Total population of system}) * 100$$

A. Self-organization

Self-organization is a process where a system reproduces itself with the help of its own logic and components. The self-organized systems do not need control by any external agent. The whole system is decentralized, distributed over all the components of system. The self-organized systems are robust and able to survive or self-repair in adverse environmental conditions. [6]

The virus in human population model discussed in this paper is also a self-organized system where there is no centralized agent. The system is showing self-organization when infected individuals are dying due to infection and total number of people in the system decreased. Then the healthy individuals reproduced and give birth to the new healthy offspring. The number of children one agent can have in lifetime is the value set for the num-children parameter. This self-organization and reproduction of agents leads to escalating the total number of people in the environment and help the system to maintain the maximum carrying capacity.

1. System shows self-organization when initial number people in the system are 120 and there are 25 doctors in the given environment. The infectiousness is set to 60% and initial number of infected individuals in the system are 30. Simulation results showing that number of people dying in the system are more and agents are reproducing to maintain the maximum carrying capacity of system.

2. When infectiousness set to 45% and outbreak size is 50, moreover, initial population is 150 along with 20 doctors in the system. A healthy individual can have up-to maximum 3 offspring. When we run simulation for this value initially people dies and agents self-organized and reproduces to maintain maximum carrying capacity value.

Fig.2 showing self-organization as when infected people died from the virus the total people in system decreased after that healthy individuals reproduce and there is increase in total number of people in the system.

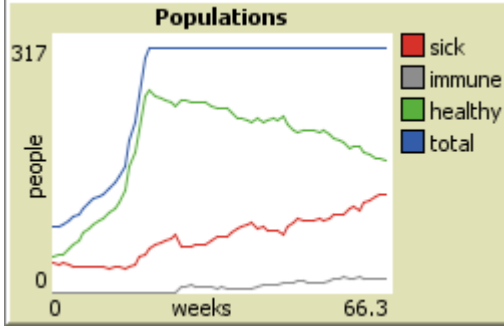


Fig 2. Showing self-organization

B. Emergence

Emergence is the second important property of a complex adaptive system. Emergence cannot be explained at the agent level alone, it can be study from the macro-level behaviour of the system. The macro behaviour of the system occurs by the local interactions of the agents.

In this model, emergence is obtained as the final state of the simulation model. Emergence is tested by adjusting values of infectiousness, chance-recover, and number of doctors. As the infectiousness percentage increases, agents will get infected very quickly and die and some are treated by doctors. Than our system shows emergence when all the infected people die or become healthy.

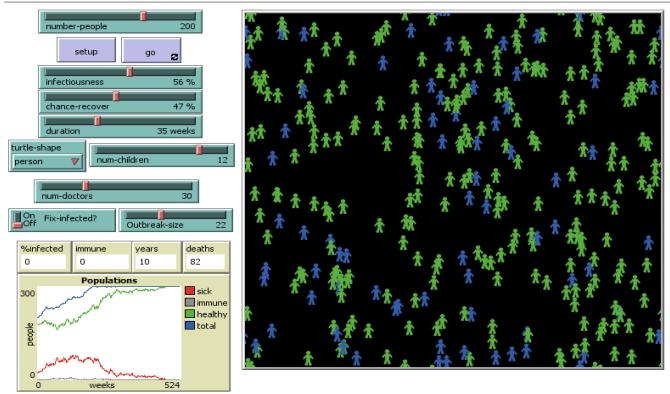


Fig 3. System showing emergence

Fig 2. Showing the macro state of the system when all the infected people are eliminated, some are treated by the doctors, others are died due to infection.

In table 1, experiments are performed by changing the values of number of doctors, infectiousness rate and chance-recovery. The number of deaths are calculated. Moreover, results are depicting that there are less number of deaths in the system and all infected agents are eliminated from system.

Chance-recover	Infectiousness	Doctors	Deaths
45%	28%	25	143
40%	60%	56	28
65%	15%	20	14
55%	40%	35	67

Table 1. Comparison of number of deaths to show emergence

IV. EXPERIMENTS

Experiments of this model is performed by changing the values of the parameters such as infectiousness, chance-recover and number of doctors and fixing all other parameter values.

Experiment 1.

In this experiment, value of infectiousness varies and all other parameter values are set initially.

The initial population in the system is set to 200 and each healthy individual can reproduce up-to 3 offspring in lifetime and system is maintaining the carrying-capacity of 300 people. Moreover, each infected individual has chance of recovery 45%. In addition, the number of doctors in the system is set 25 and the duration of infectiousness is set to 24 weeks, after that person may either recover or died in the system. The initial infected people in the system are 50.

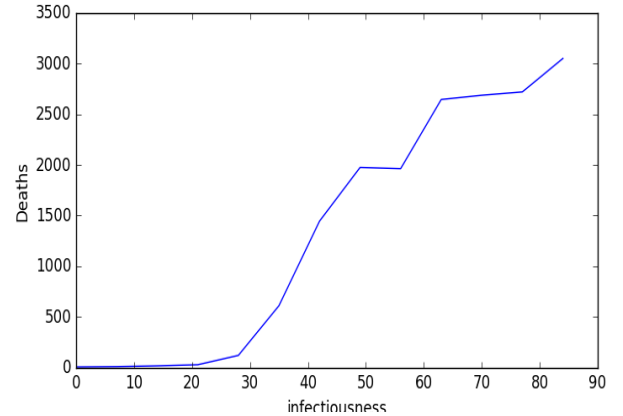


Fig 4. Results for 1st set of parameters

In fig 4, the experiment result showing that with the increase in the infectiousness of virus in the system there is huge increase in number of deaths. Apart from this, we came to know that the highly infectious viruses like Ebola can cause more number of deaths as compare to less infectious viruses like chickenpox, influenza and HIV.

Experiment 2.

In this experiment, value of number varies and all other parameter values are set initially.

The initial population of the system is set to 270, if an infected individual dies in system then healthy agent can reproduce up-to 6 children during whole simulation run. Moreover, the infectiousness is set to 60% and recovery chance of infected

individual is 40%. The infected individual can stay 20 weeks in the system after that either they recover or die due to infection. Initially, there are 30 infected people in the system.

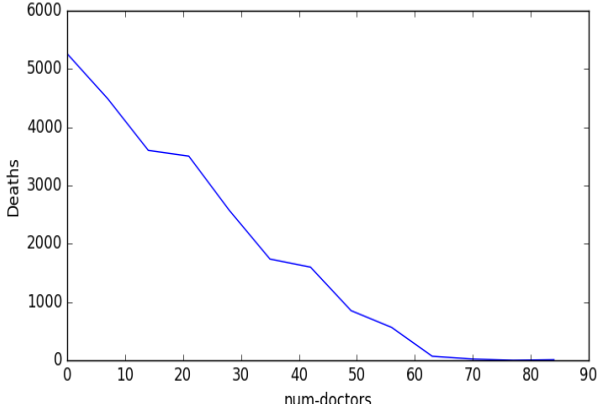


Fig 5. Results for 2nd set of experiment

In fig. 5. The experiment results showing that with the increase in number of doctors in the system then there is decrease in the number of deaths. Like, when there is 7 doctors in the system than 4300 people died due to infection and when number of doctors are 60, then deaths in system are around 15. Which shows there is big role of doctors in the real life to cure various types of viral diseases like influenza, tuberculosis etc.

Experiment 3.

In this experiment, value of recovery chances varies and all other parameter values are set initially.

The initial population of the system is 220 and each healthy can have maximum 5 children. Moreover, Infectiousness rate is set to 50% and an infected agent can live in the system up-to 25 weeks. After that the agent will die or recover from infection. The system is initialized with 25 doctors and outbreak-size is set to 20.

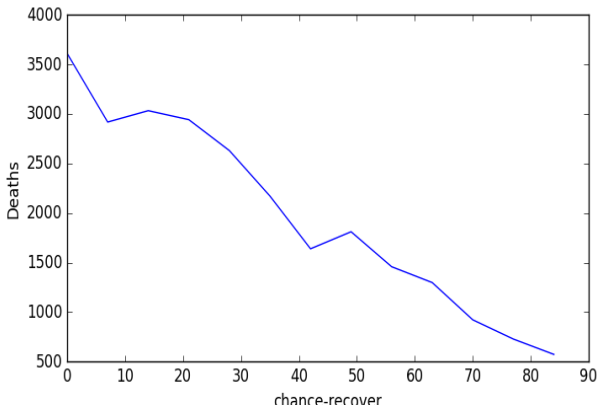


Fig 6. Results for 3rd set of parameters

In fig 6, results of the simulation run is showing that the diseases with the higher recovery chance leads to lesser number of deaths in the real life environment. Viruses like Hepatitis-B,

influenza, Common-flu have higher recovery chances and there are very less number of deaths due to these viruses.

V. DISCUSSION

In the existing model virus of Net logo, we have added new attributes like num-doctors, num-children and outbreak-size. Where value num-doctors make huge impact on the system as shown in the experiment no. 2. The large number of doctors in the system leads to decrease in the deaths of infected individuals. Moreover, num-children can make impact on the total number of people in the system. If the number-children set with the large value then system can maintain the maximum carrying capacity for the longer time. Apart from this outbreak-size can set the initial infected agents in the system.

When infectiousness rate is set to 70% or more then virus spread in the system more quickly. Chance-recover can affect the recovery from virus by infected agent. In addition, when duration is set to 30 weeks, then infected individual have more time to recover, otherwise it dies by infection.

VI. CONCLUSION

The simulation model for virus in human population is presented in this paper along with methodology used for it. There are some important real life parameters defined in this paper, which can make huge impact on the number of deaths due to different types of viruses. Parameters like infectiousness, chance-recover and doctors came among those parameters. The three experiments are conducted to demonstrate the importance doctors, infectiousness rate of virus and chance recovery after getting infected in real life. Experiments results indicates that number of deaths due to virus in real life can be less if, there are more doctors in the system, if infectiousness rate is low of virus, and if chance of recovery is higher after getting infected. The system self-organized when deaths occur by reproduction moreover, emergence is shown when all infected individuals are eliminated from the system.

In the future, new real life parameters can be added to this model like birth rates, immunity to know more about deaths in system. Moreover, a similar model can be made for the non-humans or animals and deaths can be calculated for them caused by viruses by setting parameters like population density, infectiousness, duration of infection, chance-recover etc.

REFERENCES

- [1] Christoph Aschwanden, Spatial simulation model for infectious viral diseases with focus on SARS and the Common Flu, 37th Hawaii International Conference on System Sciences, 2004.
- [2] Karl Mink, Mike Zdeb, Using SAS to model the spread of infectious disease, paper 174-29.
- [3] Alun L.Lloyd, Steve Valeika, Ariel Cintron-Arias, Infection dynamics on small-world networks, unpublished.
- [4] Stephen Karl, Nilimesh Halder, Joel k Kelso, Scott A Rithie and George J Milne, A spatial simulation model for dengue virus infection in urban areas, BMC infectious disease, 2014.
- [5] James A Yorke, Neal Nathanson, Giulio Pianigiani and John Martin, Seasonality and the requirements for perpetuation and eradication of viruses in populations, VOL. 109, February 1979, by John Hopkins University school of hygiene and public health.
- [6] Self-organization. In Wikipedia. Retrieved November 06, 2017, from <https://en.wikipedia.org/wiki/Self-organization>